

GenCore version 5.1.3
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OM nucleic - protein search, using frame_plus_n2p model

Run on: January 17, 2003, 09:57:04 : Search time 101.5 seconds
(without alignments)
6567.449 Million cell updates/sec

Title: US-09-743-492-1
Perfect score: 6444
Sequence: 1 gatccgcagcgaagactcc.....attgaataatcaattctt 3467

Scoring table:
BIOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 566448

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+_n2p_model -DEV=xlip
-O=/cgn2_1/USPRO_spool/US09743492/runat_17012003_093836_11545/app_query.fasta_1.3655
-DB=PIR_73 -QFMT=fastan -SUPERX=rrp -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=biomatch62 -TRANS=humand0 cdi -LIST=45
-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09743492 @cgn_1_1_178 @runat_17012003_093836_11545 -NCPU=6 -ICPU=3
-NO_XLIPY -NO_MMAP -LARGESQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV.TIMEOUT=120
-WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3236	50.2	1897	1	TDHUKL
2	3176.5	49.3	1290	2	A56493
3	3172	49.2	1898	2	A56216
4	3057	47.4	582	2	A57068
5	2926	45.4	1912	2	A56178
6	2874.5	44.6	1691	1	D54689
7	2874.5	44.6	1894	2	C54689
8	2867.5	44.5	1499	2	I50212
9	2850	44.2	1501	2	I58146
10	2847	44.2	1907	2	SS0893
11	2844	44.1	1863	2	S46217
12	2753.5	42.7	1496	1	A48758
13	2509	38.9	1231	2	SS3089
14	2503	38.8	2029	1	TDFFLK

15	2450.5	38.0	1437	2	T31093	probable protein-t
16	2377	36.9	2051	2	T30938	receptor tyrosine
17	1869	29.0	398	2	I56540	protein-tyrosine-p
18	1836.5	28.5	1585	2	T19121	probable protein-t
19	1551	24.1	802	1	A36065	protein-tyrosine-p
20	1538	23.9	1262	1	B48758	protein-tyrosine-p
21	1525	23.7	796	1	JC1285	protein-tyrosine-p
22	1518	23.6	829	1	A47373	protein-tyrosine-p
23	1429	22.2	700	1	SI2053	protein-tyrosine-p
24	1423	22.1	699	2	JC6132	protein-tyrosine-p
25	1307	20.3	1452	1	SI7670	protein-tyrosine-p
26	1306	20.3	1452	1	SI7669	protein-tyrosine-p
27	1243	19.3	1457	1	A48066	protein-tyrosine-p
28	1236	19.2	1440	2	JC6312	protein-tyrosine-p
29	1168	18.1	1445	1	A48148	protein-tyrosine-p
30	1166.5	18.1	1436	2	JC5290	protein-tyrosine-p
31	1162	18.0	1442	1	B48148	protein-tyrosine-p
32	1142	17.7	1422	2	T42636	protein-tyrosine-p
33	1135.5	17.6	1442	2	S72441	protein-tyrosine-p
34	1117.5	17.3	2314	1	A46151	protein-tyrosine-p
35	1089.5	16.9	1301	1	A41622	protein-tyrosine-p
36	1048.5	16.3	1237	2	A54080	protein-tyrosine-p
37	1038	16.1	1273	1	TDRTLT	leukocyte common a
38	1035.5	16.1	1304	1	A46546	leukocyte common a
39	1017	15.8	1291	1	A28334	leukocyte common a
40	1013	15.7	1200	2	T43148	protein-tyrosine-p
41	1011.5	15.7	1469	1	B36182	probable protein-t
42	894	13.9	1402	2	T42522	protein-tyrosine-p
43	876.5	13.6	1422	2	T30111	protein-tyrosine-p
44	702	10.9	1711	1	A55148	hypothetical prote
45	697	10.8	256	2	A40169	protein-tyrosine-p

ALIGNMENTS

RESULT 1

TDHUKL

leukocyte antigen-related protein precursor - human

N:Alternate names: Leukocyte common antigen homolog

N:Contains: protein-tyrosine-phosphatase (EC 3.1.3.48)

C:Species: Homo sapiens (man)

C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 22-Jun-1999

C:Accession: S03841; JI0051

R:Steuil, M.; Krueger, N.X.; Hall, L.R.; Schlossman, S.F.; Saito, H.

J. Exp. Med. 168, 1523-1530, 1988

A:Title: A new member of the immunoglobulin superfamily that has a cytoplasmic region

A:Reference number: JI0051; MUID:89035978; PMID:2972792

A:Accession: S03841

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-1897 <STR>

A:Cross-references: EMBL:Y00815; NID:g34266; PIDN:CNA68754.1; PID:g34267

C:Genetics: GDB:PTPRF; LAR

A:Map position: Ipr34-Ipr34

C:Superfamily: Leukocyte antigen-related protein; fibronectin type III repeat homolog

C:Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembra

F:1-16/Domain: signal sequence #status predicted <SIG>

F:17-1897/Product: leukocyte antigen-related protein #status predicted <MAT>

F:17-1250/Domain: extracellular #status predicted <EXT>

F:37-99/Domain: immunoglobulin homology <IMM1>

F:139-199/Domain: immunoglobulin homology <IMM2>

F:236-299/Domain: immunoglobulin homology <IMM3>

F:308-390/Domain: fibronectin type III repeat homology <FN3A>

F:403-489/Domain: fibronectin type III repeat homology <FN3B>

F:501-583/Domain: fibronectin type III repeat homology <FN3C>

F:596-685/Domain: fibronectin type III repeat homology <FN3D>

F:698-798/Domain: fibronectin type III repeat homology #status atypical <FN3E>

F:810-893/Domain: fibronectin type III repeat homology <FN3F>

F:905-989/Domain: fibronectin type III repeat homology <FN3G>

F:1001-1078/Domain: fibronectin type III repeat homology <FN3H>


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Db 1492 serGluLysArgSLeuLeuArgInPheGlnPheMetAlaTrpProAspHisGlyValPro 1511
QY 666 GAGTACCACCACTCCCTCGGCTTCCTACACAGGGGTCAAGGCCCTGCACACCCCTAGAC 725
Db 1512 GtUTyrProThrProIleLeuAlaPheLeuArgValLysAlaCysAsnProLeuAsp 1531
QY 726 GCAGGGCCCATGGTGTGACTGTCACAGCGGGGGTGGCGGACCGGCTTCATCGTG 785
Db 1532 AlaGlyProMetValValHisCysSerAlaGlyValGlyArgThrGlyCysPheIleVal 1551
QY 786 ATTGATCCATGTTGGAGCGATGAACACAGACAGCGGTGACATCTATGGCCACGTG 845
Db 1552 IleAspAlaMetLeuGlnuArgMetLysHisGluTyrThrValAspIleTyrGlnHisVal 1571
QY 846 ACCTGATGCGATCACAAGAGAACTACATGTCGACACAGGAGACCAAGTACGTTTCATC 905
Db 1572 ThrCysMetArgSerGlnArgAsnTyrMetValGlnThrGluAspGlnTyrValPheIle 1591
QY 906 CATGAGGCGCTGTGGAGCTGTGCACGTGGCGGCACACAGAGGTGCTGCCGCAACCTG 965
Db 1592 HisGluAlaLeuLeuGlnuAlaAlaMetCysGlyHisThrGluValLeuAlaArgAsnLeu 1611
QY 966 TATGCCACATCCAGAACGTGGCGCAAGTGCCTCCAGGGAGAGTGTGACCCGCAATGAG 1025
Db 1612 TyrAlaHisIleGlnLysLeuGlnValProProGlyGlnuSerValThrAlaMetGln 1631
QY 1026 CTGCACTCAAGTGTGTCGCCACGCTCCAAAGCCCAACAGCTCCGCTTCATCAGCGCAAC 1085
Db 1632 LeuGluPheLysLeuLeuLagIleSerLysAlaArgAlaSerArgPheIleSerAlaAsn 1651
QY 1086 CTGCCCTGCAACAAGTTCAGAAACCGGCTGGTGAACATATGCCCTTACGATGACCCGT 1145
Db 1652 LeuProCysAsnLysPheLysAsnArgLeuValAsnIleMetProTyrGluLeuThrArg 1671
QY 1146 GTGTGTCTCAGCCCACTCCGTGGTGTGAGGGCTGTGACTACATCATGACCACTCTCTG 1205
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Db 1692 AspGlyTyrArgGlnLysAlaTyrIleAlaThrGlnGlyProLeuLagIleuSerThr 1711
QY 1266 GAGGACTTGTGGGGCTATGAGGAGCAATTCACACATCATGCTCATGCTGACCAAG 1325
Db 1712 GluAspPheTrpArgMetLeuTrpGluHisAsnSerThrIleLeuValMetLeuThrLys 1731
QY 1326 CTTCGGAGATGGGCGAGGAGAATGCCACAGTACTGGCCACAGAGCGCTTCTGCTCGC 1385
Db 1732 LeuArgGluMetGlyArgGlyLysCysHisGlnTyrTrpProAlaGluArgSerAlaArg 1751
QY 1386 TACCACTACTTGTGTGACCCGATGCGTGAATACACATGCCCCAGTATATCTGCGT 1445
Db 1752 TyrGlnTyrPheValValAspProMetAlaGluTyrAsnMetProGlnTyrIleLeuArg 1771
QY 1446 GAGTTCAGAGTCACGAGATCCCGGAGTGGGAGTCAAGGACATCCGGAGTTCACAGTT 1505
Db 1772 GluPheLysValThrAspAlaArgAspGlyGlnSerArgThrIleArgGlnPheGlnPhe 1791
QY 1506 ACAGACTGGCCAGAGAGGCGCTGCCAAGACAGCGGAGGATTCATTGACTTCATCGGG 1565
Db 1792 ThrAspTrpProGluGlnGlyValProLysThrGlyGluGlyPheIleAspPheIleGly 1811
QY 1566 CAGGTGCATTAAGACACAGAGAGCAGTTTGGACAGAGATGGGCTATCACGGTGCACCTCA 1625
Db 1812 GlnValHisLysThrLysGlnPheGlnPheGlnAspGlyProIleThrValHisCysSer 1831
QY 1626 GCTGGGCTGGGGCGGCGGGGGTTCATCAGCTGAGCATGCTCTGGAGGGCGCAATGCGC 1685
Db 1832 AlaGlyValGlyArgThrGlyValPheIleThrLeuSerIleValLeuGlnuArgMetArg 1851
QY 1686 TATGAGGCGGTGTCACATGTTTTCAGACCGTGAAGACCCCTGCGTACAGAGCTCTGCGC 1745
Db 1852 TyrGluGlyValValAspMetPheGlnThrValLysThrLeuArgThrGlnArgProAla 1871

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QY 1746 ATGTCGACAGACAGACCAAGTATCAGTGTGCTACCGTGGGCGCTGGAGTACTCGGC 1805
Db 1872 MetValGlnThrGluAspGlnTyrGlnLeuCysTyrArgAlaAlaLeuGlnTyrLeuGly 1891
QY 1806 AGCTTGACCACTATGCAACG 1826
Db 1892 SerPheAspHisTyrAlaThr 1898

RESULT 4
A:57068
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type f - mouse (fragment)
M:Alternate names: leukocyte antigen-related protein LAR
C:Species: Mus musculus (house mouse)
C:Date: 03-Oct-1995 #sequence_revision 09-Mar-1996 #text_change 23-Jul-1999
C:Accession: A57068; S40280
R:Schaapveld, R.Q.J.; van den Maadenberg, A.M.J.M.; Schepens, J.T.G.; Olde Weghuis,
Genomics 27, 124-130, 1995
A:Title: The mouse gene Ptpnf encoding the leukocyte common antigen-related molecule
A:Reference number: A57068; MUID:95394448; PMID:7665159
A:Accession: A57068
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-582 <SCH>
A:Cross-references: GB:Z37988; NID:9993005; PIDN:CA86070.1; PID:9993006
R:Henricks, W.; Brugman, C.; Zeuwen, P.; Schepens, J.; Mieringa, B.
submitted to the EMBL Data Library, June 1993
A:Description: Assessment of the expression levels of murine protein-tyrosine phospho
A:Reference number: S40280
A:Accession: S40280
A:Molecule type: mRNA
A:Residues: 116-221 <HEN>
A:Cross-references: EMBL:Z23049; NID:9438135; PIDN:CAA80584.1; PID:9438136
C:Genetics:
A:Gene: Ptpnf
C:Superfamily: Leukocyte antigen-related protein; fibronectin type III repeat homolog
og
C:Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembra
E:1-582/Domain: Leukocyte common antigen cytosolic domain Homology (fragment) <IAC>
E:50-271/Domain: protein-tyrosine-phosphatase homology <PRP1>
E:339-562/Domain: protein-tyrosine-phosphatase homology <PRP2>
E:223/Active site: Cys (phosphocysteine intermediate) #status predicted
E:229/Binding site: substrate phosphate (Arg) #status predicted
E:514/Active site: Cys (phosphocysteine intermediate) #status predicted
E:520/Binding site: substrate phosphate (Arg) #status predicted

Alignment Scores:
Pred. No.: 2,24e-194 Length: 582
Score: 3057.00 Matches: 572
Percent Similarity: 99.14% Conservative: 5
Best Local Similarity: 98.28% Mismatches: 5
Query Match: 47.44% Indels: 0
DB: 2 Gaps: 0

US-09-743-492-1 (1-3467) x A57068 (1-582)
QY 81 ATGCGAGACACCACCACCCATCCCATACCGACCTGCGGACAAATCGAGCCCTCAAA 140
Db 1 MetArgAspHisProIleProIleThrAspLeuAlaAspAsnIleGluArgLeuLys 20
QY 141 GCCAACGATGGGCTCAAGTCTCCAGAGGTATGATGATCATGCAACCTGGACAGCAGTTC 200
Db 21 AlaAsnAspGlyLeuLysPheSerGlnGlyTyrGlnuSerIleAspProGlyGlnPhe 40
QY 201 ACCTGGAGCAATTCAAACCTGAGTGAACAACCCCAAGAACCGCTATGCGAATGTCATC 260
Db 41 ThrTrpGluAsnSerAsnSerGluValAsnLysProLysAsnArgTyrAlaAsnValIle 60
QY 261 GCCTACGACCACTCTGAGTCACTTACCTATGATGATGCGCTCCCGGAGTGAATAC 320
Db 61 AlaTyrAspHisSerArgValLeuLeuThrSerIleAspGlyValProGlySerAspTyr 80
QY 321 ATCAATGCCAACAATCATGATGCTACCGCAACAGAAATGCTTACATCGCCACGAGGGC 380

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Db	81	lLeasnlalaaSnTyrlLeasRgLyThYrArlgYsElInsaMaLaTyrlLeaLaThrlngLy	100
Qy	381	CCCCGCCCCGAGACCATGGCGGATTTCTGGAGAAAGGTGTGGGAGACGGCCAGCCACT	440
Db	101	ProLeuProGluThrMetGlyAspPheTrpArgMetValTrpGluGlnArgThrAlaThr	120
Qy	441	GTGGTCATGATGACACGGCTGGAGAGAAAGTCCCGGGTAAATGTATCATCAATCTGGCA	500
Db	121	ValValMetMetTrpArgLeuGlnGluLysSerArgValLysCysAspGlnTyTrpPro	140
Qy	501	GCCCGTGGCACCGAGACCTGGCGCTTATTCAGGTGACCCGTGTGGACACAGTGGAGCTG	560
Db	141	ValArGgLyThrlngLyThlThTyrlGlyLeuIlleGlnValThrLeuValAspThrValGluLeu	160
Qy	561	GCCACATCACTGTGCGGACCTTGACACTCCACAAGATGGCTCCAGTGAAGAGCTGAG	620
Db	161	AlaThrTrpThrMetArgThrPheAlaLeuHISLysSerGlySerGlnTyArgGln	180
Qy	621	CTGGCTCAAGTTTCAGTTCATGAGCTGGCCGACACCATGGAGTTCCTAGTACCACACTCC	680
Db	181	LeuArgGlnPheGlnPheMetAlaTrpProAspHisGlyValTrpGluTyTrpThrPro	200
Qy	681	ATCCGAGCCCTTCACAGCGGGGTGAAGAGCTGCAACCCCTTACAGCAGGGCCCATAGG	740
Db	201	IlleuAlaIlePheLeuAlaArgValLysLysAlaCysAsnProLeuAspAlaGlyProMetVal	220
Qy	741	GTGCATCGACAGCGGGGCTGGGCGCCGACCGGCTTCATCTGATGATGATGCATGTG	800
Db	221	ValHISysSerAlaGlyValGlyArgThrGlyCysPheIlleValIlleAspAlaMetLeu	240
Qy	801	GAGCGGATGAAGCACGAGAAACGCGTGGACATCTATGGCCAGCTGACCTGCATGCGATGA	860
Db	241	GluArgMetLysHISGluLysThrValAspIlleTyrlGlnHisValThrCysMetArgSer	260
Qy	861	CAGAGGACCTCAAGGTGGACAGCGGAGACCAAGTGTTCATCATAGAGCGCGTGG	920
Db	261	GlnArgAsnTyTrpMetValGlnThrGluAspGlnIrrTyValPheIlleHISGluAlaLeuLeu	280
Qy	921	GAGGCTGGCACGTGCGGCGACACAGAGAGTCCCTGGCCGCAACCTGTATGCCCCACATCCAG	980
Db	281	GlnAlaAlaMetCysGlnHISThrGlnValLeuAlaIleArgSnuLeuTrpAlaHISIlleGln	300
Qy	981	AAAGTGGCCCAATGTCCTCCAGGGGAGATGTGTACCGCCATGGAGCTCGATGTCAAGTTG	1040
Db	301	LysLeuGlyGlnValProProGlyGlnSerValThrAlaMetGluLeuGlnPheLysIleu	320
Qy	1041	CTGGCCACTCCAGGGCCCAACACTCCCGCTTATCAAGGCCCAACTGCCCTGGCAACAG	1100
Db	321	LeuAlaAsnSerLysAlaHISThrSerArgPheValSerLysAlaSnuLeuProCysAsnLys	340
Qy	1101	TTTCAGAACCGCGTGGTGAACATCATCCCTACGAATTGACCCGCTGTGCTGGCACGCC	1160
Db	341	PheLysAsnArgLeuValAsnIlleMetProTyrluLeuThrArgValLysLysLeuGlnPro	360
Qy	1161	ATCCGTGTGTGGAGGCGTGTGACTATCATCATGATCCACGTTCTCTGGAGGTATTATAGACAG	1220
Db	361	IleArgGlyValGluGlySerAspTyrlLeaAlaSerPheLeuAspGlyTrpArgGln	380
Qy	1221	CAGAAAGCTTACATAGCTTACACAGGGGCTCTGGCAGAGACACCGAGACTTTGGCGC	1280
Db	381	GlnLysAlaTyrlleAlaThrGlnGlyProLeuAlaGlnSerThrGluAspPheTrpArg	400
Qy	1281	ATGCGATGGGAGCAATTCACCATATGCTCATGCTGTGACCAAGTGGGGAGATGGGC	1340
Db	401	MetLeuTrpGlnHISAsnSerThrIlleIleValMetLeuThrLysLeuArgGluMetGly	420
Qy	1341	AGGGAGAAATCCACACAGTACTGGGCCAGCAGAGCGCTGTCTGCTACCAAGTACTTGT	1400
Db	421	ArgGlnLysCysHISGlnTyTrpProAlaGluArgSerAlaArgGlyGlnTyTrpPheVal	440
Qy	1401	GTTCACCCGATGGCTGAGTACACATGCCCGAGTATATCCGTGGTGAAGTCAAGGTCAAG	1460

Db 441 ValAspIromEAlaIagIuIyrAsnMetProGIInTYrIIleuAlaArgIuIphelysValThr 460

QY 1461 GATCCCGCGGATGGGATGCAAGACATCCGGCACTTCACATCCAGACTGGCCAGAG 1520
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Db 461 AspAlaIaArgAspGlyGlnSerAlrGThrIIleArgIuIphethrAspIrrProGlu 480

QY 1521 CAGCGCGTCCCAAGACAGCAGGAGGATTCATTGACTTTCATGCGGCGAGTGCATTAAGACC 1580
|||||
Db 481 GInGlyValrIrrPolrYsThrIryGluGlypHeIIeaSprHeIIegLyGlnAlaHisYsThr 500

QY 1581 AAGGACACATTTGGACAGCATGGATGGCCCTATCACGGTCGACATCGCAGTCCGGCGGCCGC 1640
|||||
Db 501 LysGIuGlnIrrpHeGlyGlnAspGlyProIIleThrValHisCysSerAlaGlyValIdIyArg 520

QY 1641 ACCGGGGTTCATCATCTGTGACATGCTCTGGAGCGCATCGCTATGAGGCGCTGTC 1700
|||||
Db 521 ThrGIyValrIrrpHeIIerThrIrrSerIIleValIleuGIuArgMetArgTyrGluValVal 540

QY 1701 GACATGTTTCACACGCTGAGACCCCTGGCTACACAGCCGTCGCGCATGGTGCAGACAGAG 1760
|||||
Db 541 AspMetpHeGlnThrYalIyThrIleuAlaGThrIrrAlaArgProIleMetValIdIrrGlu 560

QY 1761 GACCATATCACACTGTGTACCGTGGCGGCCCTGGAGTACCTCGGCGAGCTTGACCATAT 1820
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Db 561 AspGIInTYrGlnIleuCYsTYrIrrAlaIalalauGIuTYrIleuGlySerpHeAspHisTYr 580

QY 1821 GCACAG 1826
|||||

Db 581 AlaThr 582

RESULT 5

A56178

protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta precursor - human

M.Alternate names: protein-tyrosine-phosphatase BPTP-2

C.Species: Homo sapiens (man)

C.Date: 03-Oct-1995 #sequence,revision 03-Oct-1995 #text_change 21-Jan-2000

C.Accession: A56178; S12052; B44929

R.Pulido, R.; Krueger, N.X.; Serra-Pages, C.; Saito, H.; Streuli, M.
J. Biol. Chem. 270, 6722-6728, 1995

A.Title: Molecular characterization of the human transmembrane protein-tyrosine phosphatase delta isoforms.

A.Reference number: A56178; MUID:95204468; PMID:7896816

A.Accession: A56178

A.Status: preliminary

A.Molecule type: mRNA

A.Residues: 1-1912 <PDL>

A.Cross-references: GB:SI89929; NID:9755652; PIDN:AA041149.1; PID:9755653

R.Krueger, N.X.; Streuli, M.; Saito, H.
EMBO J. 9, 3241-3252, 1990

A.Title: Structural diversity and evolution of human receptor-like protein tyrosine phosphatase delta isoforms.

A.Reference number: S12049; MUID:91006018; PMID:2170109

A.Accession: S12052

A.Status: preliminary

A.Molecule type: mRNA

A.Residues: 390-1912 <KRUD>

A.Cross-references: GB:X54133; NID:935789; PIDN:CA038068.1; PID:935790

A.Note: The sequence from Fig. 5B is inconsistent with that from Fig. 5A in having 56 RAdachi, M.; Sekiya, M.; Arimura, Y.; Takekawa, M.; Itoh, F.; Hnoda, Y.; Imai, K.; Cancer Res. 52, 737-740, 1992

A.Title: Protein-tyrosine phosphatase expression in pre-B cell NALM-6.

A.Reference number: A44929; MUID:92119637; PMID:1370651

A.Accession: B44929

A.Molecule type: mRNA

A.Residues: 1756-1804, 'C', 1806-1845 <ADA>

A.Cross-references: GB:ST8086; NID:9243545; PIDN:AA021147.1; PID:9243546

A.Experimental source: pre-B cell NALM-6

A.Note: Sequence extracted from NCBI backbone (NCBIN:78086, NCBIF:78087)

A.Note: The authors did not report the entire codon for residue 90

C.Genetics:

A.Gene: GDB:PTPRD

A.Cross-references: GDB:131384; OMIM:601598

A.Map position: 9p24-9p24

C.Superfamily: Leukocyte antigen-related protein; fibronectin type III repeat homolog

QY C:Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane
F:38-100/Domain: immunoglobulin homology <IMM1>
F:140-209/Domain: immunoglobulin homology <IMM2>
F:250-304/Domain: immunoglobulin homology <IMM3>
F:711-811/Domain: fibronectin type III repeat homology <3FR>
F:1293-1912/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F:1669-1692/Domain: protein-tyrosine-phosphatase homology <PTP>
F:1553/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1844/Binding site: Cys (phosphocysteine intermediate) #status predicted
F:1850/Binding site: substrate phosphate (Arg) #status predicted

Alignment Scores:
Pred. No.: 1,296-185 Length: 1912
Score: 2926.00 Matches: 538
Percent Similarity: 95.99% Conservative: 37
Best Local Similarity: 89.82% Mismatches: 24
Query Match: 45.41% Indels: 0
DB: 2 Gaps: 0

US-09-743-492-1 (1-3467) x A56178 (1-1912)

QY 30 CACTCCTGTGACCTGTGGAGATCGGAGGCTCACTACACAGACCCAGATGCGAGAC 89
||| :::
Db 1314 HisProThrAspProValGluLeuArgArgLeuAsnPhenGlnThrProGlyMetAlaSer 1333

QY 90 CACCCACCATCCCATACACCCAGCTGGCGGACACACATCGAGCGCTCAAGCCAAAGAT 149
||||| :::
Db 1334 HisProProIleProIleuGlnAlaAspHisIleGluArgLeuAlaAsnAsp 1353

QY 150 GGGCTCAAGTCTCCAGAGGATGATGCATGACCCGTGAGAGAGATTCATCGTGGAG 209
||||| :::
Db 1354 AsnIleuLysPheSerIleuGlnIleuTyrGluSerIleAspProGlnGlnPheThrProGlu 1373

QY 210 AATTCAAACCTGAGAGTGAACAAGCCCAAGAACCCGTATCGAATGTCATCGCTGAGAC 269
:::| :::
Db 1374 HisSerAsnLeuGluValAsnLysProLysAsnArgTyrAlaAsnValIleAlaTyrAsp 1393

QY 270 CACTCTCGAGATCATCTTACCTTATTCATGATGGCGTCCCGGAGTGACTACATCAATGCC 329
||||| :::
Db 1394 HisSerArgValLeuLeuSerAlaIleGlnGlyIleProGlySerAspTyrValAsnAla 1413

QY 330 AACTACATGATGCTACCGCAGACGAAGTGCCTACATGCGCCAGGCGCCCGCTGCCCC 389
||||| :::
Db 1414 AsnTyrIleAspIleYrIleTyrGlnAsnAlaTyrIleAlaThrGlnGlySerLeuPro 1433

QY 390 GAGACCATGGCGCATTTCTGGAGAAATGTTGGAGACAGCGCAGCGCACTGTGTCATG 449
||||| :::
Db 1434 GluThrPheGlyAspPheThrArgMetIleTyrGlnArgSerAlaThrValValMet 1453

QY 450 ATGACACGGCTGGAGAGAAAGTCCCGGTTAAATGTGATCATAGTACGCGCCAGCGCTGCC 509
||||| :::
Db 1454 MetThrLysLeuGlnGluArgSerArgValLysCysAspIleuTyrTrpProSerArgGly 1473

QY 510 ACCGAGACCTGNGGCTTATTCAGTGGACCCGTGTGAGACAGTGGAGCGCGCACATAC 569
||||| :::
Db 1474 ThrGlnThrHisGlyLeuValGlnValThrLeuLeuAspThrValGluLeuAlaThrTyr 1493

QY 570 ACTGTGCGACCTTGCACATCCACAAGAGTGGCTCCAGTGAGAAAGCGTGAAGCTGCAC 629
||||| :::
Db 1494 CysValArgThrPheAlaLeuTyrLysAsnGlySerSerGlnLysArgIleValAlaArgGln 1513

QY 630 TTTCATTTATGAGCGCTGGCCAGACCATGGATTCCTGAGTACCACTCCCATCTGGCC 669
||||| :::
Db 1514 PheGlnPheThrAlaThrProAspHisGlyValAlaProGlnHisProThrProPheLeuAla 1533

QY 690 TTCTCTAGCAGCGGTCAAGGCTGCAACCCCTGACAGCAGAGCGCCATGGGGTGCACTGC 749
||||| :::
Db 1534 PheIleuArgArgValLysThrCysAsnProProAspAlaGlyTyrMetValValHisCys 1553

QY 750 AGCGCGGGGTGGCGCAGCCGCTCTCATGCTGATTGATGCCATGTTGGAGCGGATG 809
||||| :::
:::| :::

Db 1554 SerAlaGlyValGlyArgThrGlyCysPheIleValIleAsnAlaMetLeuGluArgIle 1573

QY 810 AACACAGACAAAGACGGTGGACATGTATGGCCACGTGACCTGCATGGCATGACAGAGAAC 869
||||| :::
Db 1574 LysHisGlnLysThrValAspIleTyrGlnHisValThrLeuMetArgIleAlaArgAsn 1593

QY 870 TATATGGTGAAGACGGGAGCAGATGCGTGTATCATGATGAGCGCGCTGGAGCGCTGCC 929
||||| :::
Db 1594 TyrMetValGlnThrGluAspGlnTyrIlePheIleHisAspAlaLeuGluValAla 1613

QY 930 ACCTGGGCCACACAGAGTGGCTTGCSCCAGACCTGTATGCCACATCCAGAACTGGGC 989
||||| :::
Db 1614 ThrCysGlyAsnThrGluValAlaProAlaArgAsnLeuTyrIleGlnLysLeuThr 1633

QY 990 CAAGTCTCCAGGGAGAGAGTGGACCCGATGAGCTGAGTTCAGATTGCTGGCCAGC 1049
||||| :::
Db 1634 GlnIleGluThrGlyGluAsnValThrGlyMetGlnLeuGluPheLysArgLeuAlaSer 1653

QY 1050 TCCAGAGCCCAACAGTCCCGCTTCATCAGCGCCACACCTGCCCGCAACAGTCCAGAAC 1109
||||| :::
Db 1654 SerLysAlaHisThrSerArgPheIleSerAlaAsnLeuProCysAsnLysPheLysAsn 1673

QY 1110 CGGCTGGTGAACATCATGCCCCCTAGCAATTGACCCGTGTGTGTGACGCCATCCGTGT 1169
||||| :::
Db 1674 ArgLeuValAsnIleMetProTyrGlnUserThrArgValCysLeuGlnProIleArgGly 1693

QY 1170 GTGAGAGGCTGTACTATCATCAATGCCAGCTTCTCGATGGATTATGACAGCAAGAGCC 1229
||||| :::
Db 1694 ValGlnGlySerAspTyrIleAsnAlaSerPheIleAspIleYrArgGlnGlnLysAla 1713

QY 1230 TACATGAGTACACAGGGGCTCTGGCAGAGACAGCCAGAGACTTCGGCCCATGCTATGC 1289
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Db 1714 TyrIleAlaThrGlnGlyProLeuAlaGluThrThrGlnLysPheThrArgMetLeuTyr 1733

QY 1290 GAGCACAATTCACACATCATGTCATGCTGACCAAGCTTCGGAGATGGCGAGAGAAA 1349
||||| :::
Db 1734 GluHisAsnSerThrIleValValMetLeuThrLysLeuArgGluMetGlyArgGlnLys 1753

QY 1350 TGGCACCAGTACTGGCCAGAGAGAGCGCTGCTGCGTACCAAGTACTTGTGTTGACCCG 1409
||||| :::
Db 1754 CysHisGlnTyrTrpProAlaGluArgSerAlaArgTyrGlnTyrPheValAlaAspPro 1773

QY 1410 ATGCGTAGTACAAATGCCCCAGTATATCTCGCGAGTTCAGAGTTCAGAGCGAGTCCCGG 1469
||||| :::
Db 1774 MetAlaGluTyrAsnMetProGlnTyrIleLeuArgGluPheLysValThrAspAlaArg 1793

QY 1470 GATGGCAGTCAAGACAAATCCGAGTTCCAGTTCAACAGATCGCCAGAGCGGCTG 1529
||||| :::
Db 1794 AspGlyGlnSerArgThrValAlaArgGlnPheGlnPheThrAspThrProGlnGlnGlyVal 1813

QY 1530 CCCAAGACAGCGCAGAGGATTCATTGACTTCATGCGGAGGTGCGATAAGACCAAGAGAC 1589
||||| :::
Db 1814 ProLysSerIleGlnGlyPheIleAspPheIleGlyValHisLysThrLysGlnGln 1833

QY 1590 TTGGAAGAGATGGCCTATACAGTGCAGTGCAGTGCCTGGCGCCAGCGGCGTGG 1649
||||| :::
Db 1834 PheGlyGlnAspGlyProIleSerValHisCysSerAlaIleValGlyArgThrGlyVal 1853

QY 1650 TTCATCACTCTGAGCATGCTCTGAGAGCGCATCGCTATGAGGCGGTGTGACATGTTT 1709
||||| :::
Db 1854 PheIleThrLeuSerIleValAlaGluArgMetArgTyrGlnGlyValAlaAspIlePhe 1873

QY 1710 CACACCGTGAAGACCTGCGCTACACAGCGTCTGCGCATGCTGCGACAGAGAGCAAGTAT 1769
||||| :::
Db 1874 GlnThrValLysMetLeuArgThrGlnArgProAlaMetValAlaIleThrGluAspGlnTyr 1893

QY 1770 CAGCTGTGACCGCTGCGCGCTGGAGTACCTGGCAGAGCTTTCACCACTTGAACG 1826
||||| :::
Db 1894 GlnPheSerTyrArgAlaAlaLeuGluTyrLeuGlySerPheAspHisTyrAlaIleThr 1912

RESULT 6
D54689
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta, splice form D precu

N:Alternate names: MPRP delta type D
N:Contains: protein tyrosine phosphatase, receptor type delta, splice form A
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: D54689; A54689
R:Miluno, K.; Hasegawa, K.; Katagiri, T.; Ogimoto, M.; Ichikawa, T.; Yakura, H.
MOL. Cell. Biol. 13, 5513-5523, 1993
A:Title: MPRP delta, a putative murine homolog of HPRP delta, is expressed in specialized
A:Reference number: A54689; MUID:93360986; PMID:8355697
A:Accession: D54689
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1691 <MT>
A:Experimental source: brain
A>Note: sequence inconsistent with nucleotide translation
A>Note: sequence extracted from NCBI backbone (NCBIN:136522, NCBI:P136524)
A:Accession: A54689
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-398,799-1691 <MT>
A:Experimental source: brain
A>Note: sequence inconsistent with nucleotide translation
C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
ogy
C:Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hyd
F:42-95/Domain: immunoglobulin homology <IM3>
F:114-196/Domain: fibronectin type III repeat homology <FNA3>
F:1075-1691/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F:1449-1671/Domain: protein-tyrosine-phosphatase homology <PP2>
F:1333/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1339/Binding site: substrate phosphate (Arg) #status predicted
F:1629/Binding site: Cys (phosphocysteine intermediate) #status predicted
F:1629/Binding site: substrate phosphate (Arg) #status predicted

Alignment Scores:
Pred. No.: 3 24e-182 Length: 1691
Score: 2874.50 Matches: 534
Percent Similarity: 95.16% Conservative: 36
Best Local Similarity: 89.15% Mismatches: 26
Query Match: 44.61% Indels: 3
DB: 1 Gaps: 3

US-09-743-492-1 (1-3467) x D54689 (1-1691)

QY 30 CACTCTCTGACCTGTGAGATGCGAGGCTCAACTACAGACCCAGATGCGAGAC 89
||| :::
Db 1096 HSPProthraspProvalGluLeuArgrgleuAsnphgInThrProGlyMetLaser 1115
QY 90 CACCACCCATCCCATCCAGCTGGGGGACAAACATCGAGCGCTCAAGCCACGAT 149
||||| :::
Db 1116 HSPProthraspProvalGluLeuArgrgleuAsnphgInThrProGlyMetLaser 1135
QY 150 GCGCTGCTGACCTGTGAGATGCGAGGCTCAACTACAGACCCAGATGCGAGAC 209
||||| :::
Db 1136 AsnLeuLysPheSerGlnGluInThrProGlyMetLaser 1155
QY 210 AATTCAACTGAGAGTGAACAGGCAAGACCGCTATGCGAATGTCAGCTACGAC 269
::: :::
Db 1156 HisSerAsnLeuGluValAsnLysProLysAsnArgTyrAlaAsnValIleLeuLysAsp 1175
QY 270 CACTCTGACGATCCTTACCTTATGATGCGCTCCCGGAGTACATCATGCC 329
||||| :::
Db 1176 HisSerAlaValLeuLeuSerValIleGluInThrProGlySerAspTyrValAsnAla 1195
QY 330 AACTTCATGATGCTTACCGAAGCAAGATGCTACATCGACGACGAGGCCCTGCC 389
||||| :::
Db 1196 AsnTyrIleAspGlyTyrArgLysGlnAsnAlaTyrIleAlaThrGlnGlySerLeuPro 1215
QY 390 GAGACCATGGCGATTTCTGAGATGCTGTGGAACAGCGACGCGCATGCTGTCATG 449
||||| :::
Db 1216 GluThrPheGlyAspPheThrArgMetIleThrProGluGlnGlu--AlaThrValValMet 1234

QY 450 ATGACAGCGCTGAGAGAGATGCCGGGTAAATGTATGATCACTAGCGCCACCGCTGCC 509
||||| :::
Db 1235 MetThrLysLeuGluGluValSerArgValLysCysAspGlnTyrThrProSerArgGly 1254
QY 510 ACCGAGACCTGAGCTTTCAGAGTACAGGACCTGTTGAGACAGAGTGGAGTGGCCATAC 569
||||| :::
Db 1255 ThrGluThrHisGlyLeuValGlnValIleThrLeuLeuAspThrValGluLeu---ThrTyr 1273
QY 570 ACTGTGCGACCTTGGCACTCCAGAGAGTGGCTCCAGTGAAGAGGTGAGTGGCTGAC 629
||||| :::
Db 1274 CysValArgThrPheAlaLeuTyrAsnGlnSerSerGlnLysArgValArgGln 1293
QY 630 TTTTCAGTTATGCTGCGGACAGACCATGAGTTCCTGATACCCAACTCCCTGCTGCC 689
||||| :::
Db 1294 PheGlnPheThrAlaThrProAspHisGlyValProGlnHisProThrProPheLeuAla 1313
QY 690 TTCCTACAGAGGAGTGAAGGCTGCAACCCCTGACAGCGAGGCGCCATGCTGCTGAC 749
||||| :::
Db 1314 PheLeuAlaArgValIleLysThrCysAsnProProAspAlaGlyProMetValValHisCys 1333
QY 750 ACCGCGGCGCTGCGCGGACCCGCTGCTTCATGCTGATGATGCGCATGTTGGAGCGATG 809
||||| :::
Db 1334 SerAlaGlyValGlyArgThrGlyCysPheIleValIleAspAlaMetLeuGluArgGly 1353
QY 810 AAGCAGAGAGAGAGTGAACATCTATGCGCACGCTGACCTGATGCGATCAGAGAGAAC 869
||||| :::
Db 1354 LysHisGlyLysThrValAspIleTyrGlnHisValIleThrLeuMetValArgAlaArgAsn 1373
QY 870 TGCATGTCACAGAGGAGGACCATGACGTCATGTCATGACGAGGCGCTGAGAGCTGCC 929
||||| :::
Db 1374 TyrMetValGlnThrGluAspGlnTyrIlePheIleHisAspAlaLeuLeuGluValVal 1393
QY 930 ACGTCGCGGACACAGAGGCTGCTGCCGCAACCTGTATGCCACATGCGAGAGCTGGCC 989
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Db 1394 ThrCysGlyAsnThrGluValProAlaArgAsnLeuTyrAlaTyrIleGlnLysLeuThr 1413
QY 990 CAAATGCTCCAGGAGGAGAGTGTGACCGCATGAGACCTGAGTCAAGTCTGCGGCAC 1049
||||| :::
Db 1414 GlnIleGluThrGlnLysValIleThrGlyMetGlnLeuGlnPheLysArgLeuLaser 1433
QY 1050 TCCAGAGCCACACAGTCCCGCTTCATGAGCGGCAACCTGCGCAACAGTTCAGAAC 1109
||||| :::
Db 1434 SerLysAlaHisThrSerArgPheIleSerAlaAsnLeuProCysAsnLysPheLysAsn 1453
QY 1110 CGGCTGCTGACATGCTGCTGACATGAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCT 1169
||||| :::
Db 1454 ArgLeuValAsnIleMetProThrGlnLysArgValCysLeuGlnProIleArgGly 1473
QY 1170 GTGAGAGGCTGCTGATCATCATGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1229
||||| :::
Db 1474 ValGluGlySerAspTyrIleAsnLaserPheLeuAspGlyTyrArgGlnGlnLysAla 1493
QY 1230 TACATGCTACACAGAGGCTGCTGCGAGAGCACCGAGGACTTTCGGGCTGCTATAGG 1289
||||| :::
Db 1494 TyrIleAlaThrGlnGlyProLeuAlaGlnThrGlnLysPheThrArgMetLeuTyr 1513
QY 1290 GAGCAATTCACCATCATGCTGCTGACCAAGCTTCGGAGATGGGAGGAGGAGAA 1349
||||| :::
Db 1514 GlnHisAsnSerThrIleValValMetLeuThrLysLeuArgGlnMetGlyArgGlnLys 1533
QY 1330 TGGCAGAGTACGCTGCGCAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1409
||||| :::
Db 1534 CysHisGlnTyrTyrProAlaGlnArgSerAlaArgTyrGlnTyrPheValValAspPro 1553
QY 1410 ATGCTGATGATACATGCGCCAGATATACCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1469
||||| :::
Db 1554 MetAlaGluTyrAsnMetProGlnTyrIleLeuArgGlnPheLysValIleThrAspAlaArg 1573
QY 1470 GATGGCAGTCAAGAGCAATCGCGCATGCTTCAGTTCACAGACTGCGCAGAGCGCGCTG 1529
||||| :::
Db 1574 Asp---GlnSerArgThrValArgGlnPheGlnPheThrAspTyrProGluGlnGlyVal 1592
QY 1530 CCCAAGACAGGCGAGGAGTTCATTCATTCGCGGACAGTGCATTAAGACAGAGAGCAG 1589

|||||.....
Db 1593 ProlyserGlyGluGlyPheIleAspPheIleGlyGlnValHisLysThrLysGluGln 1612
QY 1590 TTITGGACAGATGGGCTTATCACGGTGCACTGCATGCTGGCGCGCCAGCGGGGTC 1649
Db 1613 PheGlyGlnAspGlyProIleSerValHisCysSerAlaGlyValAlaGlyThrGlyVal 1632
QY 1650 TTCATACGCTGAGCATGCTCCGCGAGCGCATGCGCTATGAGGCGCGTGCAGATGTTT 1709
Db 1633 PheIleThrLeuSerIleValLeuGluArgMetArgTyrGluGlyValAlaSpIlePhe 1652
QY 1710 CAGACGGTGAAGACCTGGGTACACAGCGTCCATGCGTGGTGAGACAGACAGATAT 1769
Db 1653 GlnThrValLysMetLeuArgThrGlnArgProAlaMetValGlnThrGluAspGlnTyr 1672
QY 1770 CAGCTGTGTACCGTGGCGGCTTGAGTACCTGCGACGCTTTGACCATATGCAACG 1826
Db 1673 GlnPheCysTyrArgAlaIleAlaLeuGluTyrLeuGlySerPheAspHisTyrAlaThr 1691
RESULT 7
C54689
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta, splice form B precursor
N:Alternate names: Mppr delta type B/C
N:Contains: protein tyrosine phosphatase, receptor type delta, splice form C
C:Species: Mus musculus (house mouse)
C:Date: 25-Apr-1995 #sequence_revision 19-May-1995 #text_change 12-Feb-1999
C:Accession: C54689; B54689
R:Milzuno, K.; Hasegawa, K.; Katagiri, T.; Ogimoto, M.; Ichikawa, T.; Yakura, H.
MOL. Cell. Biol. 13, 5513-5533, 1993
A:Title: Mppr delta, a putative murine homolog of Hppr delta, is expressed in specialized
A:Reference number: A54689; MUID:93360986; PMID:8355697
A:Accession: C54689
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1894 <M12>
A:Experimental source: brain; splice form B
A:Note: sequence inconsistent with nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBIN:137486, NCBI:137487)
A:Accession: B54689
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-352, 'H', 354-535, 'S', 537-601, 1002-1894 <M12>
A:Experimental source: brain; splice form C
A:Note: sequence inconsistent with nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBIN:136527, NCBI:136530)
C:Superfamily: Leukocyte antigen-related protein; fibronectin type III repeat homology;
ogy
C:Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoprotein; phosphoric monoester hyd
F:45-107/Domain: immunoglobulin homology <IMM1>
F:245-299/Domain: immunoglobulin homology <IMM2>
F:317-399/Domain: fibronectin type III repeat homology <FN3A>
F:1278-1894/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F:1652-1874/Domain: protein-tyrosine-phosphatase homology <PTP>
F:1536/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1542/Binding site: substrate phosphate (Arg) #status predicted
F:1806/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1832/Binding site: substrate phosphate (Arg) #status predicted
Alignment Scores:
Pred. No.: 3.3e-182 Length: 1894
Score: 2874.50 Matches: 534
Percent Similarity: 95.168 Conservative: 36
Best Local Similarity: 89.158 Mismatches: 26
Query Match: 44.618 Indels: 3
DB: 2 Gaps: 3
US-09-743-492-1 (1-3467) x C54689 (1-1894)
QY 30 CACTCTGTGACCTGTGGAGATGCGAGGCTCACTACCAAGCCAGGATATGCGAGAC 89
Db 1299 HisProThrLeuProValGlnLeuArgArgLeuAsnPheGlnThrProGlyMetAlaSer 1318
QY 90 CAGCCAGCATGCCCATCCAGCAGCTGGCGAGCAACATGAGAGGCGCTCAAGCAACGAT 149

|||||.....
Db 1319 HisProThrLeuProIleLeuGluLeuAlaAspHisIleGluThrGluLeuAlaAsnAsp 1338
QY 150 GGCCTCAAGTTCTCCAGAGATATGATCCATGAGCCCTGGAGACAGATTCACGTGGAG 209
Db 1339 AsnLeuLysPheSerGlnGluTyrGluSerIleAspProGlyGlnGlnPheThrTyrGlu 1358
QY 210 AATTCAACTGTGAGGTGAACAGCCAGAACACCCGATATCCGAATGTCATCGGCTACGAC 269
Db 1359 HisSerAsnLeuGluValAsnLysProLysAsnArgTyrAlaAsnValIleAlaTyrAsp 1378
QY 270 CACTTCGATCACTACCTTACCTATGATGAGGCGGCCGAGATGACTACATCATGCC 329
Db 1379 HisSerArgValLeuLeuSerAlaIleGluGlyIleProGlySerAspTyrValAsnAla 1398
QY 330 AACTACATGATGGCTACCGCAGAGATGCTTACATGCGCCAGAGAGGCGCCCTGCC 389
Db 1399 AsnTyrIleAspGlyTyrArgLysGlnAsnAlaTyrIleAlaThrGlnGlySerLeuPro 1418
QY 390 GAGACCATGGCGCATTTCTGAGATATGTTGGGAACGGCGCACGGCCATGTGTCATG 449
Db 1419 GluThrPheGlyAspPheThrPargMetIleTyrGluGlnGlu--AlaThrValAlaMet 1437
QY 450 ATGACACGGCTGGAGAGAGATGCCGCGTAAATGTGATCATGATGCGCCAGCGCGG 509
Db 1438 MetThrLysLeuGluGluArgSerArgValLysCysAspGlnTyrTyrProSerArgGly 1457
QY 510 ACCGAGACCTGTGGCTTATTCAGTGAAGTACCGCTTGGACACAGTGCAGTGCACATAC 569
Db 1458 ThrGluThrHisGlyLeuValGlnValThrLeuLeuAspPheValGluLeu--ThrTyr 1476
QY 570 ACTGTGCGACCTTTCGCACCTCCACAGAGTGGCTCCAGTGAAGACGTGAGCTGCTCAG 629
Db 1477 CysValArgThrPheAlaLeuTyrAsnAsnGlySerSerLysArgLysValArgGln 1496
QY 630 TTTCAGTTTCATGCGCTGGCGCCAGACCATGAGTTCGTGAGTCAACATCCATCCTGGCC 689
Db 1497 PheGlnPheThrAlaThrProAspHisGlyValProGlnHisProThrProPheLeuAla 1516
QY 690 TTTCATGACGAGGTCAAGGCTGCAACCCCTGACAGCGAGCGCCATGTGTGCTGCTGC 749
Db 1517 PheLeuArgArgValLysThrCysAsnProProAspIleTyrPheMetValValHisCys 1536
QY 750 AGCGCGGCGTGGCGCCAGCGCGCTGCTATGCTGATTCATGCTGATGAGCGGATG 809
Db 1537 SerAlaGlyValGlyArgTyrGlyCysPheIleValIleAspAlaMetLeuGluArgIle 1556
QY 810 AAGCAGAGAGAGAGGAGCATCTATGGCCAGCTGACCTGACATGACATGACAGAGAAC 869
Db 1557 LysHisGluLysThrValAspIleTyrGlyHisValThrLeuMetArgAlaGlnArgAsn 1576
QY 870 TACATGGTGAGAGAGAGACACAGTACGTTTCATCATGAGCGCTGAGAGGCTGCC 929
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QY 930 ACTGTGGGCGCACACAGAGTGCCTGCCCGACACCTGTATGCCACATCCAGAGCTGGGC 989
Db 1597 ThrCysGlyAsnThrGluValProAlaArgAsnLeuTyrAlaTyrIleGlnLysLeuThr 1616
QY 990 CAGTGCCTTCAGGAGGATGTGACCGCATGAGCTCAGTTCAGATGTGGCGCAGC 1049
Db 1617 GlnIleGluThrGlyLysAsnValThrGlyMetGluLeuGluPheLysArgLeuAlaSer 1636
QY 1050 TCCAGAGCCACACAGTCCCGCTTCATCAGCGCCACACTGCGCCAGCAACATTCAGAAC 1109
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QY 1110 CGCGTGTGAACATCATGCCCTTACGAATTCACCCGTGTGTGTGACAGCCATCGTG 1169
Db 1657 ArgLeuValAsnIleMetProTyrGluSerGlyArgValCysLeuGlnProIleArgGly 1676
QY 1170 GTGAGAGGCTGTGACATCATGATGCGAGCTTCTGATGAGTATGACAGCAAGAGGCC 1229

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 Db 1737 CysHISGIuThrTPProILaGIuArgSerILaAlaGIyGIuThrPheValILaAspPro 1756
 QY 1410 ATGCTGATACACATGCGCCAGATATCTGCTGCTGAGTTCAGAGTTCACGAGTCCG 1469
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 QY 1530 CCCAGACAGGCGAGGAGTTCATGACTTCATGCGGCGAGCTGATTAAGCAAGACGAG 1589
 Db 1736 ProLysSerGIyGIuGIyPheILeAsPheILeGIyGIuValILaHISLysThrsGIuGIu 1815
 QY 1590 TTTGGACAGAGTGGCGCTATCAAGGTGCACTGCACTGCTGCGTGGCGGCGACCGGCTG 1649
 Db 1816 PheGIyGIuAspGIyProILeSerValILaCysSerILaGIyValGIyArgThrGIyVal 1835
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 QY 1710 CAGACCGAGAGACCTCGGTACACAGGCTCTGCGCATGCTGCGACAGAGACGATAT 1769
 Db 1856 GIuThrValILysMetLeuArgThrILaArgProILaMetValGIuThrsGIuAspGIuThr 1875
 QY 1770 CAGCTGTCTACCGTGGCGCTGAGTACCTCGGCGAGCTTTGACCATATCAACG 1826
 Db 1876 GIuPheCysTyTAArgALaILaLeuGIuThrILeGIySerPheAsPheILaThr 1894
 RESULT 8
 150212
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 C:Species: Gallus gallus (chicken)
 C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jan-2000
 C:Accession: 150212
 R:Stocker, A.W.
 Mech. Dev. 46, 201-217, 1994
 A:Title: Isoforms of a novel cell adhesion molecule-like protein tyrosine phosphatase at
 A:Reference number: 150212; MUID:95001563; PMID:7918104
 A:Accession: 150212
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1499 <STOV>
 A:Cross-references: GB:I32780; NID:g485746; PIDN:AAA64460.1; PID:g485747
 C:Genetics:
 A:Gene: CRYPalphal
 C:Superfamily: Leukocyte antigen-related protein; fibronectin type III repeat homology;
 ogy
 C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase
 F:148-208/Domain: immunoglobulin homology <IMM1>
 F:245-299/Domain: immunoglobulin homology <IMM2>
 F:317-399/Domain: fibronectin type III repeat homology <3FP>
 F:881-1499/Domain: leukocyte common antigen cytosolic domain homology <LAC>
 F:1257-1479/Domain: protein-tyrosine-phosphatase homology <PTP2>
 F:1141/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:1147/Binding site: substrate phosphate (Arg) #status predicted
 F:1432/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:1438/Binding site: substrate phosphate (Arg) #status predicted

Pred. No.: 9,21e-182 Length: 1499
 Score: 2867.50 Matches: 527
 Percent Similarity: 94.32% Conservative: 38
 Best Local Similarity: 87.98% Mismatches: 33
 Query Match: 44,508 Indels: 1
 Gaps: 2
 DB: 1
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 Db 902 HISPProILeProValSerGIuLeuAlaGIuHISThrGIuHISLeuLysAlaAsnAsp 921
 QY 90 CACCAACCCATCCCATCAACAGACCTGGCGGCAACATGCAAGCGCTCAACCAACGAT 149
 Db 922 HISPProILeProValSerGIuLeuAlaGIuHISThrGIuHISLeuLysAlaAsnAsp 941
 QY 150 GGCCTCAAGTCTCCAGAGATAGTACATGACCTGAGACAGCAGTTCACAGTGGAG 209
 Db 942 AsnLeuLysLeuSerGIuInGIuThrGIuSerILeAspProGIyGIuInGIuPheThrPrGIu 961
 QY 210 AATTCAACCTGAGGTGACACAGCCCAAGACCGCTATGCGAATGTCTATGCGCTACGAC 269
 Db 962 HISSerAsnLeuGIuValAsnLysProLysAsnArgTyTAAsnValILeAlaTyTAAsp 981
 QY 270 CACTCTGAGTACCTGAGTACATGAGCGTCCCGGAGAGTACATCAATGCG 329
 Db 982 HISSerArgValILeLeuLeuProILeGIuGIyILeValGIySerAspTyTAAsnAla 1001
 QY 330 AACTCATGATGAGTACCGCAAGCAAGATGCTATGATGATGAGTGGCCAGGCGCCCTGCGCC 389
 Db 1002 AsnTyTAAsnGIyTyTAArgLysGIuAsnAlaTyTAAsnAlaThrGIuInGIuProLeuPro 1021
 QY 390 GAGACCATGGGCGATTTCTGGAGAAATGGTGGGAAACAGCGACGCGCCACTGTGGCATG 449
 Db 1022 GIuThrPheGIyAsPheThrPrArgMetValTrpGIuInArgSerILaThrILeValILeMet 1041
 QY 450 ATGACAGGCTGGAGAGAGTCCGGGTAAATGTGATCACTAGTGGCCAGCCTGTGCG 509
 Db 1042 MetThrLysLeuGIuInGIuLysSerArgILeLysCysAspGIuTyTAAsnArgGIy 1061
 QY 510 ACCGAGACCTGTGGCTTATTCAGTGAACCTGTGGACACAGTGGAGCTGGCCACATAC 569
 Db 1062 ThrAspThrTyGIyMetILeGIuValILeThrLeuLysAspThrILeGIuLeuAlaThrPhe 1081
 QY 570 ACTGTGGCAGCTTGCACTCCACAAGAGTGGCTCAGAGAGAGGTCAGTGGCTGAC 629
 Db 1082 CysValArgThrPheSerILeHISLysAsnGIySerSerGIuLysArgGIuValArgGIu 1101
 QY 630 TTTCAATTCATGCGCTGGCCAGACCATGAGTTCCTGAGTACCAACTCCATCTCGTGGCC 689
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 QY 750 AGCGGGCGGTGGCGGCGACCGGTGCTCATGCGATGATGATGATGATGATGATGATGATGATG 809
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QY 990 CAAGTGCCTCCAGGGAGAGTGTGACCGCCATGAGACTGAGTTCAGTTGCTGCCAGC 1049
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Db 1222 GlnIleGlnValGlyGlnHisValThrGlyMetGlnLeuGlnPheLysArgLeuAlaAsn 1241
QY 1050 TCCAAAGGCCACAGCTCCCGCTTCATCAGCGCCACACCTCCCTGCAACAAGTTCAAGAAC 1109
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Db 1242 SerLysAlaHisThrSerArgPheIleSerAlaAsnLeuProCysAsnLysPheLysAsn 1261
QY 1110 CCGCTGGTGAACATGATGCGCTTACGAAATGACCCCGTGTGTCTGACGCCATCCGTG 1169
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Db 1262 ArgLeuValAsnHisLeuMetProGlyLeuThrArgValCysLeuGlnProIleArgGly 1281
QY 1170 GTGAGGGCTGTGACTGACTCATGTCATGCGACCTGCTCGTGCATGATGATATGACAGAGAGGCC 1229
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Db 1282 ValGlnGlySerAspPylrIleAsnAlaSerPheIleAspGlyTyrArgGlnGlnLysAla 1301
QY 1230 TACATAGCTACACAGAGGGCTGTGCGAGAGACACCGAGACTTGTGGCGCATGCTATGG 1289
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Db 1302 TyrIleAlaThrGlnGlyProLeuAlaGlnThrThrGlnLysPheThrArgMetLeuThr 1321
QY 1290 GAGCAACAATTCACCATCATCTGTCATGCTGACCAACACTCGGAGATGGGCGAGGAGAA 1349
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Db 1322 GlnAsnAsnSerThrIleValValMetLeuThrLysLeuArgGlnMetGlyArgGlnLys 1341
QY 1350 TGCACACAGTACTGGCCAGACAGCGCTGCTGCTGCTACAGTACTTGTGTGACCGC 1409
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Db 1342 CysHisGlnTyrTrpProAlaGlnArgSerAlaAlaArgTyrGlnTyrPheValValAspPro 1361
QY 1410 ATGCTGAGTACACACATGCGCCAGTATATCTGCGTGAAGTCAAGGTCAGGATCGCCG 1469
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Db 1362 MetAlaGlnTyrAsnMetProGlnTyrIleLeuArgGlnPheLysValThrAspAlaArg 1381
QY 1470 GATGGGCACTCAAGACATCCGCGAGTTCAGTTCACAGACTGGCCAGAGAGCGCGTG 1529
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Db 1382 AspGlyGlnSerArgThrValAlaArgGlnPheGlnPheThrAspTrpProGlnGlnGlyVal 1401
QY 1530 CCCAAGACAGCGAGGAGATTCATTGACTTCATCGGCGAGGCTGATTAAGCAAGAGGACG 1589
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Db 1402 ProLysSerGlyGlnGlyPheIleAsnPheIleGlyGlnValHisLysThrLysGlnGln 1421
QY 1590 TTTGACACAGATGGCGCTATACAGGTCGACTGAGTGGCGGTGGCCGACCGGGGTG 1649
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Db 1422 PheGlyGlnAspGlyProIleSerValHisCysSerAlaGlyValGlyLysArgThrGlyVal 1441
QY 1650 TTTCATCACTGTGAGCATGCTCTGAGAGCCATGCGCTATGAGAGCGGTGCTCATGTTT 1709
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Db 1442 PheIleThrLeuSerIleValLeuGlnArgMetArgTyrGlnGlyValValAspIlePhe 1461
QY 1710 CAGACCGTGAAGACCTGCTGACACAGCGTCTGCCATGCTGACAGACAGACAGAT 1769
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Db 1462 GlnThrValLysMetLeuArgThrGln---ProAlaMetValGlnThrGlnAspGlyTyr 1480
QY 1770 CAGCTGTGCTACCTGCGGCGCTGGAGTACTCGGCGAGCTTGACCACTATGCAAG 1826
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Db 1481 GlnPheCysTyrGlnAlaAlaLeuGlnTyrLeuGlnLysSerPheAspHisTyrAlaThr 1499

RESULT 9
158148
protein-tyrosine-phosphatase (EC 3.1.3.48) 2B, splice form IAR - rat
N:Alternate names: leukocyte common antigen-related phosphatase
C:Species: Rattus norvegicus (Norway rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 20-Jun-2000
C:Accession: J58148; S46218
R:Walton, K.M.; Martell, K.J.; Kwak, S.P.; Dixon, J.E.; Largent, B.L.
Neuron 11, 387-400, 1993
A:Title: A novel receptor-type protein tyrosine phosphatase is expressed during neurogen
A:Reference number: J58148; MUID:93357030; PMID:8352946
A:Accession: J58148
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1501 <RML>
A:Cross-references: GB:L19933; NID:9310242; PIDN:AAA42309.1; PID:9310243
A:Note: In Genbank entry RATTYRPHOS, release 113.0, the source is designated as Rattus r
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R:Zhang, W.R.; Hashimoto, N.; Ahmad, F.; Ding, W.; Goldstein, B.J.
Biochem. J. 302, 39-47, 1994
A:Title: Molecular cloning and expression of a unique receptor-like protein-tyrosine-
A:Reference number: S46216; MUID:94347119; PMID:8068021
A:Accession: S46218
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-1501 <ZNR>
A:Cross-references: EMBL:L12329; NID:9294573; PIDN:AAC37657.1; PID:9294574
C:Superfamily: Leukocyte antigen-related protein; fibronectin type III repeat homolog
QY
C:Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; tyr
F:47-109/Domain: immunoglobulin homology <ITIM1>
F:149-209/Domain: immunoglobulin homology <ITIM2>
F:246-300/Domain: immunoglobulin homology <ITIM3>
F:413-506/Domain: fibronectin type III repeat homology <3FR>
F:882-1501/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F:969-1190/Domain: protein-tyrosine-phosphatase homology <PTP1>
F:1258-1481/Domain: protein-tyrosine-phosphatase homology <PTP2>
F:1142/Active site: Cys (phosphocysteine intermediate) #link PTP1 #status predicted
F:1148/Binding site: substrate phosphate (Arg) #link PTP1 #status predicted
F:1433/Active site: Cys (phosphocysteine intermediate) #link PTP2 #status predicted
F:1439/Binding site: substrate phosphate (Arg) #link PTP2 #status predicted

Alignment Scores:
Pred. No.: 1 13e-180 Length: 1501
Score: 2850.00 Matches: 523
Percent Similarity: 93.99% Conservative: 40
Best Local Similarity: 87.31% Mismatches: 36
Query Match: 44.23% Indels: 0
DB: 2 Gaps: 0

US-09-743-492-1 (1-3467) x J58148 (1-1501)
QY 30 CACTCTCTGACCTGAGTGTGAGATGCGAGGCTCACTACAGACCCAGGATGCGAGAC 89
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Db 903 HisProLysAspProValGlnMetArgArgIleAsnPheGlnThrProGlyMetLeuSer 922
QY 90 CACCACCCATCCCATCAACAGCACTGCGGAGCAACATGAGCGCTCAAGCCAAAGCAT 149
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Db 923 HisProGlnLeuProIleThrAspMetAlaGlnHisMetGlnArgLeuLysAlaAsnAsp 942
QY 150 GGCCTCAACTTCTCCAGAGATGATGCTCATCGACCCCTGGACAGCATGTCACGCTGGAG 209
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QY 210 AATTCAAACCTGAGGTGAACAAGCCCAAGAACCGCTATGCAATGTCATCCCTGACGAC 269
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Db 963 HisSerAsnLeuGlnAlaAsnLysProLysAsnArgTyrAlaAsnValIleAlaTyrAsp 982
QY 270 CACTCTCGATCATCTTACTCTATCGATGAGCGCTCCCGGAGAGTACTACATCAATGCGC 329
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Db 983 HisSerArgValIleLeuGlnProLeuGlnGlyIleMetGlySerAspTyrIleAsnAla 1002
QY 330 AACTTACATGATGAGGTGACCGGACAGAGATGCTTACATGCGCACGAGGCGCCCTGCGCC 389
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Db 1003 AsnTyrValAspGlyTyrArgArgGlnAsnAlaTyrIleAlaThrGlnIleProLeuPro 1022
QY 390 GAGACCATGCGGATTTCTGAGAAATGTTGGGAAACAGCGACGCGCCACTGTGTCATG 449
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Db 1023 GlnThrPheGlyAspPheThrArgMetValTrpGlnGlnArgSerAlaThrValAlaMet 1042
QY 450 ATGACAGCGCTGAGAGAGAAAGTCCCGGTAAATGTGATGACTACTGGCCACCGGTGCG 509
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QY 510 ACCGAGACCTGTGCGCTTATTCAGGTGACCTGTTGGACAGGTGAGAGCTGCGCAATAC 569
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Db 1063 ThrGlnThrTyrGlyPheIleGlnValThrLeuLeuAspThrMetGlnIleValAlaThrPhe 1082
QY 570 ACTGTGCGACCTTGTGCACTCCACAAGAGTGCTCCAGTGAAGAAGCGAGAGCTGGTGCAG 629
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Db 1083 CysValArgThrPheSerLeuHisLysAsnGlySerSerGlnLysArgGlnValArgHis 1102
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D	b	1389	Hisserar	g	val	l	leu	leu	g	l	pro	leu	g	l	g	l	l	me	c	l	y	l	le	a	s	a	l	a	1408			
O	y	330	AACTAC	T	CGAT	G	AGT	G	CTA	ACG	CA	G	AG	A	G	CA	T	G	CC	T	T	A	C	G	C	T	T	A	389			
D	b	1409	Asn	l	l	l	l	l	l	l	l	l	l	l	l	l	l	l	l	l	l	l	l	l	l	l	l	1428				
O	y	390	GAG	A	CCAT	T	G	G	C	C	A	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	449				
D	b	1429	G	l	u	t	h	r	p	h	e	l	y	a	s	p	r	h	e	t	r	a	p	a	m	e	t	a	l	1448		
O	y	450	ATG	A	CC	G	G	G	G	G	G	A	G	A	G	T	C	C	C	C	C	C	C	C	C	C	C	509				
D	b	1449	Me	t	h	r	a	g	l	e	u	g	l	u	l	y	s	e	r	a	g	l	i	e	l	y	s	a	1468			
O	y	510	ACC	G	A	G	A	C	C	T	G	T	G	C	C	T	T	A	T	T	A	T	T	A	T	T	A	T	569			
D	b	1469	Th	r	g	l	u	t	h	r	g	l	y	r	g	e	l	g	i	n	a	l	l	h	r	e	u	a	l	1488		
O	y	570	ACT	G	T	G	G	C	A	C	T	T	G	C	A	C	T	T	C	A	A	A	G	A	G	T	G	C	629			
D	b	1489	C	y	s	a	l	a	r	g	r	h	e	s	e	r	l	e	u	s	a	n	g	i	l	y	s	e	r	1508		
O	y	630	T	T	T	A	G	T	T	A	G	T	T	G	C	C	C	A	A	C	A	A	C	T	G	C	T	G	689			
D	b	1509	P	h	e	l	u	t	h	r	a	t	r	a	t	r	p	r	o	a	s	p	h	i	s	g	l	y	a	l	1528	
O	y	690	T	T	T	C	T	A	C	A	G	G	G	G	C	T	C	A	A	C	C	C	C	C	C	C	C	C	749			
D	b	1529	P	h	e	u	a	r	g	a	r	y	a	l	l	y	s	t	h	r	c	y	s	a	n	p	r	o	p	1548		
O	y	750	A	G	C	G	G	G	C	G	T	G	G	C	C	A	C	C	G	G	T	C	T	T	C	A	T	G	809			
D	b	1549	S	e	r	a	l	a	c	i	g	y	a	l	g	i	a	r	g	t	h	r	g	i	y	s	p	h	e	l	1568	
O	y	810	A	A	G	C	A	G	A	A	G	A	G	G	T	G	A	C	T	A	T	T	A	T	T	G	C	C	869			
D	b	1569	L	y	s	t	h	r	l	u	l	y	s	t	h	r	a	l	a	s	p	a	r	y	a	l	l	y	r	g	l	1588
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D	b	1589	T	y	r	m	e	t	a	l	g	i	n	h	r	e	l	u	s	a	p	g	i	n	t	y	r	g	i	l	1608	
O	y	930	A	C	G	T	G	C	G	C	A	C	A	G	A	G	T	G	C	T	G	C	C	C	C	C	C	C	989			
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Db 1769 MetAlaGluTyrAspMetPrgOGlnTyrLlleuAlaArgGluPheLysValTThrAspAlaArg 1788
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Db 1869 GlnThrValLysValIleuArgTThrGlnArgProAlaMetValGlnThrGlnAspGluTyr 1888
QY 1770 CAGCTGTCTTACCGTGGCGCCCTGGAGTACTCTGGCAGACTTTCAGCACTATGCAACG 1826
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Db 1889 GlnPheCysPheGlnAlaIleuGlnIleuGlySerPheAspIlnhLysTyrAlaThr 1907
RESULT 11
S46217
protein-tyrosine-phosphatase (EC 3.1.3.48) type sigma precursor - rat
N/Alternate names: leukocyte common antigen-related phosphatase
C/Species: Rattus norvegicus (Norway rat)
C/Date: 07-May-1995 #sequence,revision 03-Nov-1995 #text_change 23-Jul-1999
C/Accession: S46217; S51174; A49104
R/Zhang, W.R.; Hashimoto, N.; Ahmad, F.; Ding, W.; Goldstein, B.J.
Biochem. J. 302, 39-47, 1994
A>Title: Molecular cloning and expression of a unique receptor-like protein-tyrosine-
A/Reference number: S46216; MUID:94347119; PMID:8068021
A/Accession: S46217
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-1863 <ZHA>
A/Cross-references: EMBL:L11587
submitted to the EMBL Data Library, February 1993
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A/Accession: S51174
A/Molecule type: mRNA
A/Residues: 1-1788, 'G', 1790-1863 <GOL>
A/Cross-references: EMBL:L11587; MID:9205134; PIDN:AC37656.1; PID:9205135
R/Yan, H.; Grossman, A.; Wang, H.; D'Eustachio, P.; Mossie, K.; Musacchio, J.M.; Silv
Biol. Chem. 268, 24880-24886, 1993
A>Title: A novel receptor tyrosine phosphatase-sigma that is highly expressed in the
A/Reference number: A49104; MUID:94043351; PMID:8227050
A/Accession: A49104
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: nucleic acid
A/Residues: 1-596, 'R', 598-603, 'T', 967-1788, 'G', 1790-1863 <YAN>
F:149-209/Domains: immunoglobulin homology <IMM1>
A/Note: sequence extracted from NCBI backbone (NCBIP:139669)
C/Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homolog
QY
C/Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester
F:1-26/Domains: signal sequence #status predicted <SIG>
F:27-1863/Product: protein-tyrosine-phosphatase #status predicted <MAT>
F:149-209/Domains: immunoglobulin homology <IMM1>
F:246-300/Domains: immunoglobulin homology <IMM2>
F:318-400/Domains: fibronectin type III repeat homology <FN3A>
F:413-489/Domains: fibronectin type III repeat homology <FN3B>
F:511-592/Domains: fibronectin type III repeat homology <FN3C>
F:1244-1863/Domains: leukocyte common antigen cytosolic domain homology <LAC>

F:1331-1552/Domain: protein-tyrosine-phosphatase homology <PPI>
F:1504/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1510/Binding site: substrate phosphate (Arg) #status predicted
F:1795/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1801/Binding site: substrate phosphate (Arg) #status predicted

Alignment Scores:

Pred. No.:	3,44e-180	Length:	1863
Score:	2844.00	Matches:	522
Percent Similarity:	93.82%	Conservative:	40
Best local Similarity:	87.15%	Mismatches:	37
Query Match:	44.13%	Indels:	0
DB:	2	Gaps:	0

US-09-743-492-1 (1-3467) x S46217 (1-1863)

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QY 30 CACCTCTGTCACCTGAGGATGCGGAGCTCACTACGACCCGAGTATGCGAGAC 89
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1265 HisProlysaSprProvalGImetcarGArGIlleasnPhelnThrProGlyMetleuSer 1284

QY 90 CACCCACCATCCCATCCAGCAGCTGGCGGAGACACATCGAGCGCTCAAGCCAGCAT 149
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1285 HisProProIleProIleThrAspMetValaGluHisMetGluArgLeuValaAsnAsp 1304

QY 150 GCGCTCAAGTCTCCAGAGATGATGTCATCGACCTGGACAGCAGTTCAGCTGGAG 209
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1305 SerLeuIysLeuSerGlnGluTyrGluSerIleAspProGlyGlnGlnPheThrTrpGlu 1324

QY 210 AATCAACCTGGAGGTGAGACAGCCCAAGAACGCTATGCGAATGTCATGCGCTAGAC 269
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1325 HisSerAsnLeuGlnAlaAsnLysProLysAsnArgTyrAlaAsnValIleAlaTyrAsp 1344

QY 270 CACTCTGAGTACCTCTTACCTATGATGAGCGCTCCCGGAGTACTATCATATGCC 329
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1345 HisSerArgValIleLeuGlnProLeuGlnGlyIleMetGlySerAspTyrIleAsnAla 1364

QY 330 AACATACATGATGGCTACCCGACAGAAATGCTACATCGCGACGAGGCCCTGCC 389
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1365 AsnTyrValaLysArgGlyTyrArgGlnAsnAlaTyrIleAlaThrGlnGlyProLeuPro 1384

QY 390 GAGACCATGGCGATTTCTGAGATGGTGGGAGACGCGACGCGCCACTGTGTCATG 449
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1385 GluThrPheGlyAspPheThrPargMetValaTrrProGlnAlaGlySerAlaThrValaMet 1404

QY 450 ATGACAGCGGTGAGAGAAATCCCGGTAAATGTATGATGACTGCGCCAGCCCTGGC 509
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1405 MethTrArgLeuGlnGluLysSerArgValaLysCysAspGlnTyrTrpProAsnArgGly 1424

QY 510 ACCGAGACCTGGCTTATTCAGAGTACCTGTGGACACAGTGGAGCTGGCCACATAC 569
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1425 ThrGluThrTyrGlyPheIleGlnValaThrLeuLeuAspTrpMetGluLeuAlaThrPhe 1444

QY 570 ACTGTGGACACTCGACATCCACAGAGTGGCTCCAGTGGAGCGAGACTCGGTGAG 629
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1445 CysValaLysThrPheSerLeuHisLysAsnGlySerGlnLysArgGlnValaArgHis 1464

QY 630 TTTTCAGTTCAGCTGGCGCCAGACCATGAGTTCCTGAGTACCCCAACTCCCATCTGGCC 689
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1465 PheGlnPheThrAlaTrrProAspHisGlyValaProGluTyrTrpThrProPheLeuAla 1484

QY 690 TTTCTACGAGCGGTCAAGGCTGCAACCCCTTAAGCAGAGGCGCCATGGTGGTGCATGC 749
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1485 PheLeuArgArgValaLysThrCysAsnProProAspArgGlyProValaValaHisCys 1504

QY 750 AGCGCGGCGTGGCGCGACCGGCTGCTCATGCTGATGTGATGTCATGTCATGTCGAGTGC 809
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1505 SerIleArgValaGlyArgThrGlyCysPheIleValaIleAspAlaMetLeuGlnArgGly 1524

QY 810 AAGCAGCAGAGAGCGTGAATATGAGCAGCTGACCTGACATGCGATCAGACAGAGAC 869
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1525 ArgThrGluLysThrValaLysValaTyrGlyHisValaThrLeuMetArgSerGlnArgAsn 1544

QY 870 TACAATGGTGCAGACGAGACCACTACGCTTTCATCCATGAGGCGCTGCTGGAGCTGCC 929
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Db 1545 TyrMetValaGlnThrGluAspGlnTyrSerPheIleHisGlnAlaLeuLeuGlnAlaVal 1564
QY 930 ACGTGGCGCCACAGAGAGTCTGTCGCCCAACCGTATGTCGCCACATCCAGAGCTGGCC 989
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1565 GlyCysGlyAsnThrGluValaProAlaLysSerLeuTyrThrTyrIleGlnLysLeuAla 1584

QY 990 CAAGTCCCTCCAGGAGGAGAGTGTGAACCGCCATGAGAGCTGAGTTCAGTCTGGCCAGC 1049
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1585 GlnValaGluProGlyGlnHisValaThrGlyMetGluLeuGlnPheLysArgLeuAlaSer 1604

QY 1050 TCCAAAGGCCACAGCTCCCGCTTCATCAGCCCAACCTGCCCCCTGCACAACTTCAAGAC 1109
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1605 SerLysAlaHisThrSerArgPheIleThrAlaSerLeuProCysAsnLysPheLysAsn 1624

QY 1110 CGGCTGGTGAACATCATCTCCCTACCAATTCAGCCGCTGTGTGTGTCAGCCCATCCGTGGT 1169
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1625 ArgLeuValaAsnIleLeuProTyrGluSerSerArgValaCysLeuGlnProIleArgGly 1644

QY 1170 GTGAGGCGCTGACTACATCATATGCGACCTTCCTGATGGTTATGACAGCAGAGGCC 1229
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1645 ValGlnGlySerAspTyrIleAsnAlaSerPheIleAspGlyTyrArgGlnGlnLysAla 1664

QY 1230 TACATAGCTACAGAGGGGCTCTGGCAGAGACACCGAGACTTCTGGCGCATGCTATGG 1289
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1665 TyrIleAlaThrGlnGlyProLeuAlaGluThrThrGluAspPheTrpArgAlaLeuTrrp 1684

QY 1290 GAGCACAATTCACCATCATCTGTCATGCTGACCAAGCTTCGGAGATGCGAGGAGAGAA 1349
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1685 GluAsnAsnSerThrIleValaValaMetLeuThrLysLeuAlaGluMetGlyArgGlnLys 1704

QY 1350 TGCCACAGTACTGGCCGACGAGCGCTGCTGCTGCTACAGACTTGTGTTGACCGG 1409
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1705 CysHisGlnTyrTrpProAlaGluArgSerAlaArgTyrGlnTyrPheValaValaAspPro 1724

QY 1410 ATGGCTGATGACACATGCCCATATATCTCGGTGATGTTCAAGGTACGAGATGCCGG 1469
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1725 MetAlaGlnTyrAsnMetProGlnTyrIleLeuArgGlnPheLysValaThrAspAlaArg 1744

QY 1470 GATGGGCGATCAAGAGACATCCGCGAGTTCAGATTCAAGACTGGCCGACGAGCGCGTG 1529
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1745 AspGlyGlnSerArgThrValaArgGlnPheGlnPheThrAspTrpProGlnGlnGlyAla 1764

QY 1530 CCCAAGACAGCGGAGGATTCATTGACTTCATCGGGCAGGTGCATTAAGCCAGAGACAG 1589
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1765 ProLysSerGlyGlnGlyPheIleAspPheIleGlyGlnValaHisLysThrLysGlnGln 1784

QY 1590 TTTGGACAGGATGGCGCTATCAGCGTGCATGTCAGTGTGGCGTGGCGCCAGCGGGTG 1649
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1785 PheGlyGlnAspAlaProIleSerValaHisCysSerAlaGlyValaGlyArgThrGlyVal 1804

QY 1650 TTTCACTACTGAGCATGCTGCTGGAGCGCATGGCGTATGAGGGGCGTGGCATGTTT 1709
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1805 PheIleThrLeuSerIleValaLeuGlnLysArgMetArgTyrGlnGlyValaValaAspIlePhe 1824

QY 1710 CAGACCGTGAAGACCTGCTGCTACACAGCGTCTCCATGCTGCACAGACAGACAGATAT 1769
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1825 GlnThrValaLysValaLeuArgThrGlnArgProAlaMetValaGlnThrGluAspGluTyr 1844

QY 1770 CAGCTGTGCTACCGTGGCGCGCTGGAGTACTGGCGACCTTTGACACACTATGCAAG 1826
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1845 GlnPheCysPheGlnAlaAlaLeuGluTyrLeuGlnLysSerPheAspHisTyrAlaThr 1863

RESULT 12
A48758
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor-linked form pI precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence-revision 10-Sep-1999 #text-change 10-Sep-1999
R:Pan, M.G.; Rim, C.; Lu, R.P.; Florio, T.; Stork, P.J.S.
J. Biol. Chem. 268, 19284-19291, 1993
A:Title: Cloning and expression of two structurally distinct receptor-linked protein-
A:Reference number: A48758; MUID:93374907; PMID:8396131
```

A:Accession: A48758
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1496 <PAN>
 A:Cross-references: GB:LI19180
 A:Note: authors translated the codon TGC for residue 27 as Gly, GAG for residue 79 as Glu as Phe
 C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
 Oxy
 C:Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; transmembrane
 F:149-209/Domain: immunoglobulin homology <IMM1>
 F:149-209/Domain: immunoglobulin homology <IMM2>
 F:318-405/Domain: fibronectin type III repeat homology <FN3A>
 F:411-504/Domain: fibronectin type III repeat homology <FN3B>
 F:509-599/Domain: fibronectin type III repeat homology <FN3C>
 F:600-684/Domain: fibronectin type III repeat homology <FN3D>
 F:880-1496/Domain: leukocyte common antigen cytosolic domain homology <LAC>
 F:1256-1477/Domain: protein-tyrosine-phosphatase homology <PTP2>
 F:1140/Active site: Cys (phosphotyrosine intermediate) #status predicted
 F:1146/Binding site: substrate phosphate (Arg) #status predicted
 F:1428/Active site: Cys (phosphotyrosine intermediate) #status predicted
 F:1435/Binding site: substrate phosphate (Arg) #status predicted

Alignment Scores:

Pred. No.:	3,236-174	Length:	1496
Score:	2753-50	Matches:	512
Percent Similarity:	92.50%	Conservative:	43
Best Local Similarity:	85.33%	Mismatches:	40
Query Match:	42.73%	Indels:	5
DB:	1	Gaps:	4

US-09-743-492-1 (1-3467) x A48758 (1-1496)

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OY 30 CACTCTCTGACCCCTTGAGATGCGAGGCTCACTACAGCCAGGATGCGAGAC 89
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 901 HISPRQLYASPRVALGIMETARGARGILEASNPHEGLNTHRPROGLMETLEUSER 920
OY 90 CACCCACCATCCCATCCATCCCGCCGCGGAGAACATGAGCGGCTCAAGCCACGAT 149
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 921 HISPRQLIETPROILETHRSPMELALAGLNIHMETLUNRGLYEUYSALAASASP 940
OY 150 GGCCTCAAGTCTCCAGAGATGATGATCATGACCTGAGACAGATTCACGTGGAG 209
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 941 SETLEULYLSERLNGIUTYRGILUSERLLEASPROGLYGLNINPHEHTTRPGIL 960
OY 210 AATTCAAACCTGGAGGTGAACAAGCCCAAGACCGGTATGCAATGTCATGCGCTAC 269
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 961 HISSEKASNLNGLIUNLALASNLSPOLYSASNAIRGTALASNAVALLIETATYRASP 980
OY 270 CACTCTCGAGTACTCTTACTCTTATCGATGGCGTCCCGGAGTACATACATATGCC 329
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 981 HISSEKARVALILELLEUNLPROLEUNGILYILEMETLISERISPRYRIIEASNAL 1000
OY 330 AACTACATGATGCTACGACGACGAAGATGCTTACATGCGCCAGAGGCGCCCTGCC 389
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1001 ASNTTYVALASPLIYTRIRGARGILNASHALATYRIIEALATHRLNGLYPROLEUPRO 1020
OY 390 GAGACCATGGCGATTCTTGAGAAATGTTGGGAACGCGACGCGCCACTGTGTCATG 449
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1021 GLUTHRPHEGLYASPRPHEPTRARGMETVALTRPGILNARGSERALATHRIVALMET 1040
OY 450 ATGACACGGCTGAGAGAGAGATCCCGGSTRMAATGTGATCAGTACAGTGGCCAGCC 509
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1041 METTHARLEUNGLIUNLUSSEKARVALIYSCYASPLINTRYTRPROASNAARGIL 1060
OY 510 ACCGAGACCTGTGCTTATTCAGTACGCTGTTGACACAGTGGAGGCTGGACATAC 569
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1061 THNGILTHRTYRGLYRHELEGLNVALTHRLLEUNASPRHMETGLUENALATHRPH 1080
OY 570 ACTGTCGACCTTGGCACTCCACAAGAGTGGCTCCAGTGAAGCGTGAAGCTGCTGAC 629
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1081 CYSVALARGTHRPHESERLEUNHISLYSASNGILSERSERCLUNYRARGILVALARGHIS 1100

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OY 630 TTTCAGTTCATGGCTGGCCAGACCATGAGTTCTTGAGTACCCATCCATCTGGCC 689
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1101 PHEGLNPHEHTRALTRPROASPHISGLYVALTRPGILTRYTRPROTHRPROPHLEUAL 1120
OY 690 TTTCAGACAGGGGTCAAGGCTCCCAACCCCTTGAGACGAGGCGCCATGTTGTCAC 749
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1121 PHELEUARGLYVALIYSTRYRHCYSASNPROPOASPLAELIYPROVALVALHISCYS 1140
OY 750 AGCGCGGCTGGCGCCAGCCGCTGCTTCATGTCGTATGATTCATGTTGAGCGGATG 809
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1141 SERALAGLYALGLYRGLYRHCYSPHEILEVALILEASPLAMETLEUNGILUAYGLE 1160
OY 810 AACACAGAGAGAGCGGTGACATCTATGCGCAGCTGACCTGCGATCGATCCAGAGAAC 869
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1161 ARGTHGLYSTRVALASPRVALTYRGLYHISVALTHRLLEUNETARGSERGLNARGASN 1180
OY 870 TACATGTCGACAGGAGACGACAGTACGTTGATCCATGAGCGGCTGGAGCGCTGCC 929
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1181 TYRMEVALGLNTHRGLASPRGLNTRYRSPHEILEHISGLNALALEUNGLIUALVAL 1200
OY 930 ACGTGGCCACACAGAGTGCCTGCCGACACCTGTATGCCACATCCAGAGCTGGC 989
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1201 GLYCYSGLYASNTHRGILVALPROALARGSERLEUTYRTHRYRILEGLNYSLEUAL 1220
OY 990 CAAGTGCCTCCAGGAGAGAGTGTGACCCGACATGAGCTGAGTTCAGTTGCGGCCAGC 1049
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1221 GLNVALGLUPRODLYGLNHSVALTHRGLYMEGLIUNGLIUNHESARGLUEALALA 1240
OY 1050 TCCAGGCCACACAGCTGCCGCGC--TTCAATCCAGCCACCTGGCCCAACAAGTTCAAG 1106
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1241 PROARG--HISTHRLLEUNARGASPRPHEHTHALSERLEUNPROCYASNLSPHELYS 1259
OY 1107 AACCGCTGTGTAACATCATGCTTACGAATTGACCCGTGTGTCTGACGCCATTCGT 1166
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1260 ASNARGLEUNVALSNLLEUNPROTYRGLUSERSERARGVALIYLSLEUNGILNPROILEARG 1279
OY 1167 GGTGTGAGGCGCTGACTCATCATGATGCCAGCTTCTGATGAGTATAGACAGCAAG 1226
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1280 GLYVALGLIUNYSEKSPRYRIIEASNALASERPHLELSPOLYTRARGINGLNL 1299
OY 1227 GCCTACATGACTCACAGGCGCTTGGCAGAGACCGAGGACTTGGCCATGCTA 1286
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1300 ALATYRIIEALATHRGLNGLYPROLEUALAGLTHRTHRLIUNSPHERPTRARGALALEU 1319
OY 1287 TGGGACACAAATTCACACATCATGCTCATGCTGACCAAGCTTGGAGATGGCCAGGAG 1346
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1320 TRPGILASNASNSERTHRLIIEVALIEMETLUTHRYSLEUNARGILUMETGLYARGIL 1339
OY 1347 AATGSCACAGTACATGCGCAGAGAGCGGTGCTGCTACCAAGTACTTGTGTGAC 1406
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1340 LYSCHISGLINTYRTRPROALAGLUNARGSERIALARGTYRGLINTYRPHENVALASP 1359
OY 1407 CCGATGGCTGAGTAAACATGCCCAATATCTCGTGAAGTTCAGGACGAGTGGC 1466
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1360 PROMETALAGLUNYRHSNMETPROGLIYRIIELEUNARGILUNHESVALTHRSPALA 1379
OY 1467 CGGATGGCGAGTCAAGAGACATCCGAGATCCAGTTCACAGATGGCCAGAGCGC 1526
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1380 ARGASPLIYGLINSEKARGTHRIVALARG-----GLNPHERTHRSAPTRPROGLINGILY 1397
OY 1527 GTGCCCAAGACGAGCGGAGTATCATGACTTATGCGGAGGTGATAGACCAAGAGAG 1586
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1398 ALARPLYSEKLYGLNGLYRHEILEASPRHEILEYGLNVALHISLYSTRNLSGL 1417
OY 1587 CAGTTTGCAGAGATGGCTTATCAGGCTGACATGAGTCTGCGCTGGCGCCAGCCAG 1646
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1418 GLNPHGLYGLNASPRGLYRPROLIESERVALHISCYSEKRLAELIYALGLYRGLNGLY 1437
OY 1647 GTGTTATCATCTGAGCATGCTCTGAGAGCGCATGCGCTATAGAGGCGTGTGCATAG 1706
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1438 VALPHEILETHRLEUNSERILEVALLEUNGILUNRGMETARGTYRGLIUNGLYVALASP 1457
OY 1707 TTTCAGACCGTGAAGACCTTGGCTACACAGCGTCTGCCATGTGTCAGACAGAGAC 1766

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Db 1458 PhegIntHrValLysValLeuArGrThrGlnAArgProAlaMetValGlnThrGlnuSpGlu 1477
1767 TATCAGCTGTACCGCTGCGCGCCCTGGAGTACCTCGCGAGCTTGACACATATCAACG 1826
1478 TyrGlnPheCysPheGlnAlaAlaLeuGlu---LeuGlySerPheAspHisTyrAlaThr 1496

RESULT 13
S53089
protein-tyrosine-phosphatase (EC 3.1.3.48) AnLAR - African malaria mosquito (fragment)
N:Alternate names: leukocyte antigen-related protein
C:Species: Anopheles gambiae (African malaria mosquito)
C>Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C:Accession: S53089
R:Spiers, S.
Submitted to the EMBL Data Library, March 1995
A:Description: Anlar-a transmembrane, receptor-like protein tyrosine phosphatase from th
A:Reference number: S53089
A:Accession: S53089
A:Molecule type: DNA
A:Residues: 1-1231 <SPI>
A:Cross-references: EMBL:X85217; NID:g732549; PIDN:CAAS9483.1; PID:g732550
C:Genetics:
A:Introns: 1026/3; 1209/3
C:Superfamily: Leukocyte antigen-related protein; fibronectin type III repeat homology;
ogy
C:Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane
F:208-293/Domain: fibronectin type III repeat homology <3PR>
F:619-1231/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F:988-1211/Domain: protein-tyrosine-phosphatase homology <PTP>
F:872/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1163/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1169/Binding site: substrate phosphate (Arg) #status predicted

Alignment Scores:
Pred. No.: 4.74e-158 Length: 1231
Score: 2509.00 Matches: 448
Percent Similarity: 87.94% Conservative: 77
Best Local Similarity: 75.04% Mismatches: 72
Query Match: 38.94% Indels: 0
DB: Gaps: 0

US-09-743-492-1 (1-3467) x S53089 (1-1231)
QY 36 TCTGACCCCTGTGAGATGCGGAGGCTCACTACAGACCCAGTATGCGAGCCACCA 95
:::|||||
Db 635 ThrAspProValAspMetArgArgIleAsnPheGlnThrProGlyMetIleSerHisPro 654
QY 96 CCCATCCCCATCACCGACCTGGCGGACAAACATCGAGCGCTCAAAAGCAGAGGCGCTC 155
|||||
Db 655 ProIleSerIleAlaGlnLeuProAsnHisValGlnProLeuLysAlaAsnAspAsnLeu 674
QY 156 AAGTCTCCCGAGGATGATGAGTCCATGCACTGAGACCGTTCAGAGTTCAGTGGGAGAAATCA 215
|||||
Db 675 LysPheSerGlnGlnIleGlnSerIleGlnProGlyGlnGlnPheThrTyrPheHisSer 694
QY 216 AACGTGAGGTGAACAGACCCAGAACCCGCTATGCGAATGTCATGCTAGCGACACATCT 275
|||||
Db 695 AsnMetGlnValAsnLysProLysAsnArgTyrAlaAsnValThrSerTyrAspHisSer 714
QY 276 CGAGTACCTCTTACCTATGATGAGTGGCGTCCCGGAGTGACTATCATCAATGCCAAGTAC 335
|||||
Db 715 ArgValIleLeuProGlnIleGlnIleValProGlySerAspTyrIleAsnAlaAsnTyr 734
QY 336 ATCGATGCTACCGCAGACAGCAAAATGCCAATCGCCAGCGAGGCCCTCGCCGACAGCC 395
|||||
Db 735 CysAspGlyTyrArgLysHisAsnAlaTyrValAlaThrGlnGlyProLeuGlnIleThr 754
QY 396 ATGGCGCAATTTCTGGAGATGCTGTGGAGACAGCGACGCGACATGCTGATCATGACGA 455
|||||
Db 755 PheGlyAspPheThrPheArgMetCysTyrProLysSerSerThrIleValMetMetThr 774
QY 456 CGGCTGGAGGAGAAATCCCGGGTAATAATGTATCATGTAAGTGGCAGCCCGTGGACCGAG 515

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|||||
Db 775 ArgLeuGlnGluArgSerArgIleLysCysThrMetTyrTyrProSerArgGlnThrGlu 794
QY 516 ACCTGGCGCTTATCAGATGACCCGTTGGACAGAGAGGAGGAGGAGCCACATACAGCTGG 575
|||
Db 795 ValTyrGlnAlaMetThrValThrIleThrGlnThrGlnIleValAlaThrTyrSerIle 814
QY 576 GCGACCTTGCGACCTCCAGCAAGAGTGGCTCCAGTGAAGACCTGAGCTGCTGCTTTCAG 635
|||||
Db 815 ArgThrPheGlnIleValThrGlnArgSerGlnSerAsnGlnIleArgGlnIleLysGlnLeuGln 834
QY 636 TTTCATGGCTGGCGGACAGACCTTGGAGTCTCTGAGTACCCAACTCCCATCTGCGCTTCTCA 695
|||
Db 835 PheThrAlaTyrProAspHisGlnValProAspHisProAlaProPheLeuGlnPheLeu 854
QY 696 CGACGGTCAAGAGCCCTGCAACCCCTAGACGAGGAGGCCATGCTGGTGCATGCGACGCGG 755
|||||
Db 855 ArgArgThrLysValAlaThrProSerGlnSerGlnProIleIleValHisCysSerAla 874
QY 756 GCGTGGGCGCGACCGGCTCTTCATCGTATGATGCGCATGTTGAGCGGATGAAGCAC 815
|||||
Db 875 GlnValGlnValThrGlnLysPheIleValIleAspSerMetLeuGlnArgMetLysTyr 894
QY 816 GAGAAAGCGGTGCGATCTATGCGCCAGTGAAGCTGCAATGCGCATCAAGAGACATACATG 875
|||||
Db 895 GlnLysThrIleAspIleTyrGlnLysValThrCysLeuArgAlaHisArgAsnTyrMet 914
QY 876 GTCGAGCGAGGAGGACAGTACAGTTCATCCATGAGAGGGCTCTGGAGGCTCCAGCGTG 935
|||||
Db 915 ValGlnThrGlnAspGlnTyrIlePheIleHisAspAlaLeuLeuGlnAlaValIleCys 934
QY 936 GCCCAGACAGAGTGCCTGCGCCGCAACCTGTATGCGCCACATCCAGAACGCTGGCCCAAGTG 995
|||||
Db 935 GlySerThrGlnValProAlaArgSerLeuHisAsnHisIleGlnLysLeuMetGlnThr 954
QY 996 CCTCCAGGAGAGTGTGACCGCCATGAGAGCTCGAGTTCAAGTTGCTGCGCCAGCTCCAG 1055
|||
Db 955 GlnProHisGlnAsnIleThrGlnLysMetGlnMetGlnPheLysLysLeuSerAsnValLys 974
QY 1056 GCCCAGAGGTCGCGCTTATGATGAGCGGCAACGCTGCGCCAGCAACATGTAAGAACCGGCTG 1115
|||
Db 975 AlaAspSerThrArgPheValThrAlaAsnLeuProCysAsnLysHisLysThrArgVal 994
QY 1116 GTGAACATCATGCCCTAGCAATGACCCGCTGTGTGTGCAAGCCATCCGCTGTGTGAG 1175
:::|||||
Db 995 ProHisIleLeuProTyrGlnSerSerArgValCysLeuThrProIleArgGlnValGln 1014
QY 1176 GCGTGTGACTATCATATGACAGCTTCTCGATGGTATATACAGACAGAGAGCCATACATA 1235
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Db 1015 GlySerAspTyrIleAsnAlaSerLeuValAspGlnTyrArgTyrArgLysArgTyrIle 1034
QY 1236 GCTACACAGGCGCTCGGACAGAGCACCGGAGCTTCTGGCGCATGCTATGGAGAGCAC 1295
|||||
Db 1035 AlaAlaGlnGlnLysProLeuGlnIleThrAlaGlnAspPheThrPheArgMetLeuThrLys 1054
QY 1296 AATTCACCATCATGCTGATGCTGACCAAGCTTCGGAGATGCGGAGAGCAAAATGCCAC 1355
|||||
Db 1055 AsnSerThrIleValValMetLeuThrLysLeuLysGlnMetGlnArgGlnLysCysSche 1074
QY 1356 CAGTACTGGCCAGACAGACGCTGCTGCTACCAAGTACTTGTGTTGTTGACCCGATGCT 1415
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Db 1075 GlnTyrTyrProHisGlnArgSerValArgTyrGlnCysTyrValValAspProIleAla 1094
QY 1416 GAGTCAACATGCCCCCATATATCTCGTGTGAGTCAAGGTCAGAGGATGCGCGGATGGG 1475
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Db 1095 GlnTyrAsnMetProGlnTyrLysLeuArgGlnPheLysValThrAspAlaArgAspLys 1114
QY 1476 CAGTCAAGGACAATCCGCAATTCAGTTCACAGACTGCGCAGAGCAGGCGTGGCCCAAG 1535
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QY 1536 ACAGCGAGGATTCATGACTTCATGCGGACGAGTGCATTAAGACCAAGACGACGTTTGA 1595
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Db 1155 SerGlyGlnGlyPheIleAspPheIleGlyGlnValHisIleGlyThrIleGlnGlnPheGly 1154
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 Db 1155 GlnAspGlyProIleThrValHisCysSerIleGlyValGlyArgThrIleValPheIle 1174
 QY 1656 ACTGAGACATGCTGCTGAGCGGACATGCGCTATGAGAGGGGCTGACATGTTTGACACC 1715
 Db 1175 ThrIleSerIleValIleuGlnIleuArgMetGlnIleuGlnIleValIleuAspValPheGlnThr 1194
 QY 1716 GTGAGACCCCTGCTACAGCGCTCTGCGCATGTCAGACAGAGGACCATATCAGCTG 1775
 Db 1195 ValArgIleLeuArgSerGlnArgProAlaMetValGlnThrGlnAspIleuIleuArgPhe 1214
 QY 1776 TGTATACCGTGGCGCCCTGGAGTACTGGCGACCTTGACCACTATGCAACG 1826
 Db 1215 CysTyrArgIleAlaIleuGlnIleuIleuGlySerIleuAspHisTyrAlaThr 1231

RESULT 14

TDPRFLK
 protein-tyrosine-phosphatase (EC 3.1.3.48) DLAR precursor - fruit fly (Drosophila melanogaster)
 N:Alternate names: leukocyte antigen-related protein
 C:Species: Drosophila melanogaster
 C:Date: 14-Dec-1990 #sequence_revision 02-May-1994 #text_change 22-Jun-1999
 C:Accession: A36182
 R:Streuli, M.; Krueger, N.X.; Tsai, A.Y.M.; Saito, H.
 Proc. Natl. Acad. Sci. U.S.A. 86, 8698-8702, 1989
 A:Title: A family of receptor-linked protein tyrosine phosphatases in humans and Drosophila
 A:Reference number: A36182; MUID:90046860; PMID:2554325
 A:Accession: A36182
 A:Molecule type: mRNA
 A:Residues: 1-2029 <STR>
 A:Cross-references: GB:M27700; NID:9157811; PIDN:AAA28668.1; PID:9157812
 C:Gene: FlyBase:lar
 C:GeneID:5
 A:Superfamily: Leukocyte antigen-related protein; fibronectin type III repeat homology;
 C:Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane
 F:1-32/Domain: signal sequence #status predicted <SIG>
 F:33-2029/Product: leukocyte antigen-related protein #status predicted <MAT>
 F:33-1377/Domain: extracellular #status predicted <EXT>
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 F:154-211/Domain: immunoglobulin homology <IMM2>
 F:249-303/Domain: immunoglobulin homology <IMM3>
 F:321-401/Domain: fibronectin type III repeat homology <FN3A>
 F:416-502/Domain: fibronectin type III repeat homology <FN3B>
 F:514-592/Domain: fibronectin type III repeat homology <FN3C>
 F:610-699/Domain: fibronectin type III repeat homology <FN3D>
 F:708-802/Domain: fibronectin type III repeat homology <FN3E>
 F:811-896/Domain: fibronectin type III repeat homology <FN3F>
 F:909-936/Domain: fibronectin type III repeat homology <FN3G>
 F:1006-1091/Domain: fibronectin type III repeat homology <FN3H>
 F:1101-1198/Domain: fibronectin type III repeat homology <FN3I>
 F:1378-1402/Domain: transmembrane #status predicted <TM>
 F:1403-2029/Domain: intracellular #status predicted <INT>
 F:1417-2029/Domain: leukocyte common antigen cytosolic domain homology <LAC>
 F:1476-1718/Domain: protein-tyrosine-phosphatase homology <PTP>
 F:1766-2009/Domain: protein-tyrosine-phosphatase homology <PTP2>
 F:57-111,161-209,256-301/Disulfide bonds: #status predicted
 F:176/Binding site: carbohydrate (asn) (covalent) #status predicted
 F:1670/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:1676/Binding site: substrate phosphate (Arg) #status predicted
 F:1961/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:1967/Binding site: substrate phosphate (Arg) #status predicted

Alignment Scores:

Align. No.: 1,29e-157 Length: 2029
 Score: 2503.00 Matches: 447
 Percent Similarity: 88.24% Conservative: 78
 Best Local Similarity: 75.13% Mismatches: 70
 Query Match: 38.84% Indels: 0
 DB: 1 Gaps: 0

US-09-743-492-1 (1-3467) x TDPRFLK (1-2029)

QY 36 TGTGACCTGTGTGAGATGCGGAGGTCATCAATCAAGACCCAGATGTGGAGACACCA 95
 Db 1433 SerAspProValAspMetArgIleuAsnPheGlnThrProGlyMetIleSerHisPro 1452
 QY 96 CCCATCCCATATCAGGACCTGGCGGACAAATGTGAGCGGCTCAAAAGCCAAAGATGGCC 155
 Db 1453 ProIleProIleSerGlnPheAlaAsnHisIleGlnIleuGlySerAsnAspGln 1472
 QY 156 AAGTTTCCAGAGATGATGATGTCATGCAAGCCCTGGACAGCATGTCAGGGAGAAATCA 215
 Db 1473 LysPheSerGlnIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 1492
 QY 216 AACCTGAGATGACAAAGCCCAAGAACCCCTATGCAATGTCAATGCTCAAGACCACTCT 275
 Db 1493 AsnIleuGlnHisAsnLysSerLysAsnArgTyrAlaAsnValThrAlaThrAspHisSer 1512
 QY 276 CGAGTCATCTTACCTCTATGCGATGCGCTCCCGGAGTGAATCAATGCAATGCAATGCA 335
 Db 1513 ArgValGlnIleuProAlaValGlnIleuValIleuIleuIleuIleuIleuIleuIleu 1532
 QY 336 ATGATGGCTATCCGCAAGCAAGATGCTCATGCGCCAGCGAGGCCCTGGCCCGAGACC 395
 Db 1533 CysAspGlyTyrArgLysHisAsnAlaTyrValAlaThrIleuIleuIleuIleuIleuIleu 1552
 QY 396 ATGGCGATTTGTGAGATGTGTGGAACAGCGACGCGACGCGCATGTGTGATGATGACA 455
 Db 1553 PheValAspPheThrArgMetCysTrpGlnIleuIleuIleuIleuIleuIleuIleuIleu 1572
 QY 456 CGGCTGAGAGACAGATCCCGGTAATAATGATCACTAGTGGCAGCCGCTGGACACCGAG 515
 Db 1573 ArgIleuGlnIleuArgThrArgIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 1592
 QY 516 ACCTGAGGCTTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATG 575
 Db 1593 ThrTyrGlnGlnIleuPheValThrIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 1612
 QY 576 CGCAGCTTGCATCCCAAGAGTGGCTCAGTGAAGAGCTGAGCTGAGCTGAGCTGAGCTGAG 635
 Db 1613 ArgThrPheGlnIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 1632
 QY 636 TTTCATGCTGCGCAGACCATGAGTGTCTGAGTATGAGTATGAGTATGAGTATGAGTATGAGT 695
 Db 1633 PheThrAlaThrProAspHisGlyValProAspHisProAlaThrPheIleuIleuIleuIleu 1652
 QY 696 CGAGGCTGCAAGGCTGCAAGGCTGCAAGGCTGCAAGGCTGCAAGGCTGCAAGGCTGCAAGG 755
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 QY 756 GCGGTGGGCGGACCGGCTGCTCATGATGATGATGATGATGATGATGATGATGATGATGATG 815
 Db 1673 GlyValGlyArgThrIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 1692
 QY 816 GAGAGAGGCTGAGATCTATGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 875
 Db 1693 GlnLysIleIleAspIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 1712
 QY 876 GTGCACAGGAGAGACAGTACGATGATGATGATGATGATGATGATGATGATGATGATGATG 935
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 QY 936 GGCACACAGAGATGCTGCTGCGCAACCTGATGCGCCACATCCAGACCAAGCTGGGCGCAAGTG 995
 Db 1733 GlyValThrGlnValProAlaThrAsnIleuHisThrHisIleuGlnIleuIleuIleuIleu 1752
 QY 996 CCTCCAGGGAGAGCTGACCGGCATGAGCTGAGTGAATGATGCTGGCAGCTCAAG 1055
 Db 1753 GlnProGlyGlnThrIleSerGlyMetGlnValGlnPheLysLysSerAsnValLys 1772
 QY 1056 GCCACACGCTCCCGCTTATCAGCGCCACCTGCGCCCTGCAACAAGTTCAAGAACCGGCTG 1115

Db 1773 MetAspSerSerLysePhValhAlhrlAlasnlEuProGysAsnLysHnIsLysAsnArgLeu 1792

QY 1116 GTGAACATCATGCGCCCTACGAAATTGACCCGCTGTGTCTGTGACCCCATCCGTCGTGGAG 1175

Db 1793 ValHnIsLLeuLeuProGylCtLuserSerArgValTYrLeuThrProIleHnIsLgLeuG 1812

QY 1176 GGCCTGACTACATGAAAGCCGAGCTTCCGAGTGGTATAGACACAGAGCCCTACATA 1235

Db 1813 GlysSerAspTYrValAsnAlaSerPheIleAspGlyTYrArgTYrArgSerAlaTYrIle 1832

QY 1236 GTTACACAGAGGCGCTCTGGCAGAGACCCGAGCACTTCTGGCGCATCTTACGAGAGAC 1295

Db 1833 AlaAlaGlnGlnTYrProValGlnAspAlaAlaGlnAspPheTrpArgMetLeuTrpLntHs 1852

QY 1296 AATTCACCATCATGCTATGCTGACCAAGCTTCCGGAGAGATGGGACGAGAAATGCCAC 1355

Db 1853 AsnSerThrIleValAlaIleMetLeuThrLysLeuLysGlnMetGlyArgGlnLysCysPhe 1872

QY 1356 CAGTACTGGCCACGAGAGCGCTCTGCTGCCATCCAGTACTTTGTGTGTGACCCCATGGCT 1415

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QY 1416 GAGTACACATGCCCCAGTATATCTCGCTGAGTTCACAGGTACGAGATGCCGGAGATGGG 1475

Db 1893 GluTYrAsnMetProGlnTYrLysLeuArgGlnPheLysValThlAspAlaArgAspGly 1912

QY 1476 CAGTCAAGACAAATCGGACAGTTCACAGTTCACAGACTGGCCAGACAGCGCTGCCCAAG 1535

Db 1913 SerSerArgThlValArgGlnPheGlnPheIleAspTrpProGlnGlnGlyAlaProLys 1932

QY 1536 ACAGCGCAGAGGATTTATTTGACTTTCATCCGGGACAGGTGCATTAAGACCAAGAGCAGTTTGA 1595

Db 1933 SerGlyGlnGlyPheIleAspPheIleGlyGlnValHnIsLysThlLysGlnIlePheGly 1952

QY 1596 CAGGATGGGCCCATACAGGATGACATGCAGTGCCTGGCTGGGCGCAGCCGGGGTGTTCATC 1655

Db 1953 GlnAspGlyProIleThrValHnIsCysSerAlaGlyAlaGlyArgSerGlyAlaPheIle 1972

QY 1656 ACTGTGACATCGTCTGTGAGCGCATGCGCTATGAGAGCGCTGGTGCAGATGTTTCAGACC 1715

Db 1973 ThrLeuSerIleValIleGlnGlnArgMetGlnTYrGlnGlyValIleuAspValPheGlnThr 1992

QY 1716 GTGAAGACCCCTGCTGACAGCGCTCTGCCATGTGTGCAGACAGAGAGCAGTATGACGTC 1775

Db 1993 ValArgIleLeuArgSerGlnArgProAlaMetValGlnThlGlnAspGlnTYrHnIsPhe 2012

QY 1776 TGCTACCGGCGGCGCCCTGGAGTACCTGGCAGACTTTCAGCCACTAT 1820

Db 2013 CysTYrArgAlaAlaLeuGlnTYrLeuGlnLysSerPheAspAsnTYr 2027

RESULT 15

T31093

N:Alternate names: receptor tyrosine phosphatase

C:Species: Hnudo medicinalis (medicinal leech)

C:Date: 22-Oct-1999 #sequence revision 22-Oct-1999 #text change 31-Jan-2000

C:Accession: T31093

R:Gershon, T.R.; Baker, M.; Nitabach, M.; Wu, P.; Macagno, E.R.
submitted to the EMBL Data Library, December 1997

A:Description: Two receptor tyrosine phosphatases expressed by neurons and muscle cells c

A:Reference number: Z20976

A:Accession: T31093

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1437 <GBR>

A:Cross-references: EMBL:AF017084; NID:g2695656; PID:g2695657; PIDN:AA891461.1

C:Gene: LARI

C:Genetics:

C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;

C:Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane

Alignment Scores:

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Query Match:	38.03%	Indels:	9
DB:	2	Gaps:	3

US-09-743-492-1 (1-3467) x T31093 (1-1437)

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QY	81	ATGGGAGACACCCACCCATCCCATCCAGCCAGCTGGCGGACACATCGAGCGCTCAAA	140
DB	849	MetaIacYshISProSerIleProIleSerGIuPhelaIaIaHisValGIuIlnleuYS	868
QY	141	GCCAAAGATGGCCGTCAGTTCTCCAGAGATATGATGTCATGCACTCCGTCAGACAGATT	200
DB	869	AlacYsaasngIyAlaIaArgPheSerGIuIynrIuSerIleGIuProIylInIlnIlnPhe	888
QY	201	ACGTGGGAGATTTCAAACTGGAGAGTGAACAACCCCAAGAACCGGCTATGCAATGCATC	260
DB	889	ThrTrpGIuAlaSerSerIleAsPheCysAsnIlyProIyAsnArgIyTrIaIaSnValIle	908
QY	261	GCTTAGGACACATCTGCACTCATCTTAACTCTATGCAATGGCCGTCGGGAGTACTAC	320
DB	909	AlaTyTrAspHisSerArgValIaIeGIuIlnSerIleuGIuIylIleSerGIySerAspYr	928
QY	321	ATCAATGGCAACTGATCATCGATGGCTACCCGACACAAATGGCTCATCATGCCACGAGGCG	380
DB	929	IleAsnAlaAsnPrhMetAsPheGIyTyArgIySerAsnAlaTyTrIleAlaIhTrGIuIln	948
QY	381	CCCTGGCCCGGACCATGGCGGATTTCTGGAGAATGCTGGGACACAGCGCACGGCCACT	440
DB	949	ProIeuPrroGIuIlnPrhPheValAsPheTrArgIuMetValIlnProIyIlnArgIyAlnThr	968
QY	441	GTGGTCATGATGACACGGCTGGAGAGAAATCCCGGATAAATGTGATCATGATCGGCA	500
DB	969	IleValMetMetThrIlySleuGIuIlnArgGIyAlnGIleIyScysAspIlnIynrIlnPro	988
QY	501	GCCGCTGGCACCGGACACTGTGGCTTATTCAGAGTGAACCTGTGGACACAACTGGAGCTG	560
DB	989	AsnArgGIuIlnPrhGIuValIyTrGIyProMetHisValIlnThrIleuValAsPheValIleu	1008
QY	561	GCCACATGACTGTGGGACCTTGGCACTGCCAACAGAGTGGCCGCTGATGAGAAAGGCTGAG	620
DB	1009	AlaIleTyTrIlnPrhIleuArgIlnPrhIleValIlnIySerIlnIyGIuIlnIyGIuIlnIleGIu	1028
QY	621	CTGGCTGAGTTTCAATTGATGGCTGGCCGACCAATGGAATTCCTGATGCCAACTCCG	680
DB	1029	ValIlySlnPrhGIuIlnPrhIlnIlnAlaTrPrroAsPheIyValIlnPrroIlnIlnPrhIlnAla	1048
QY	661	ATCTGGGCTTTCTTACAGACGGGTGTAAGGCTGACACCCCTTAAGACAGAGGCGGCTGGTG	740
DB	1049	LeuIeuMetPrhHisArgArgValIaIlnSerPrhIlnIlnValAsPheSerGIyProMetValI	1068
QY	741	GTGGACTGACCGGGGCGGTGGGCGGACCGGCTGATGATGGATGTATGATGCTGCTGTG	800
DB	1069	ValHisCysSerIaIaGIyValIaGIyArgTrGIyAlnPrhIleValIaIaIAsPArgMetIeu	1088
QY	801	GAGCGAGTAAAGACACGAGAGACAGCTGTGATGATGGCCACAGCTGACATCGATGGCATCA	860
DB	1089	GIuArgIaIaIeHisIaGIuIlySlnIlnIleAsPheValIyGIuIlnIlnIlnIlnIlnIlnIlnIln	1108
QY	861	CAGAGGAATPACATGCTGTGACAGACGGAGGACCACTAGCTGTTCATCCATGAGGCGCTGGTG	920
DB	1109	GIuArgAsenTyTrMetValIaGIuIlnPrhGIuAsPheGIuIlnIlnIlnIlnIlnIlnIlnIlnIln	1128
QY	921	GAGGCTGGCAAGTGGCGGCGACACAGAGGTGCTGGCCGCAACCTGTATGGCCATCCAG	980
DB	1129	GIuGIyValIlnThrSerGIyCysTrhGIuValIlnProIaIaArgAsnIleuTyTrAlaHisMetGIu	1148

Oy	381	AAATGGGCGCAAGTGCCTCCAGGGGAGAGTGTCACCGGCATGTGGACTGAGTTCAAAGTGG	1040
Db	1149	LysLeuMetSerLeuLgUserGlySerAsnLeuThrLeuMetGluValGlnPheIleuLys	1168
Oy	1041	CTGGCCACGCTTCACAAGGCCACCAGTCCCGCCTTCATGAGCGCCAACCTCCCTGCACAAG	1100
Db	1169	LeuAlaAsnIleLysThrSerSerSerGlnPheAlaSerLeuProSerAsnLys	1188
Oy	1101	TTCAGAAGCCGGGTGTGAACATCATGCCCCCTACGAATTGACCCGCTGTGTCTGCAGCCC	1160
Db	1189	PheLysAsnArgLeuValAsnIleLeuProTyGlnUseterArgValThrLeuGlnLeu	1208
Oy	1161	ATCCGTGTGTGGAGGGCTGTACTACATCAATAATGCCAGCTTCCTGGATGGTTATAGACAG	1220
Db	1209	IleArgGlyValAspGlySerAspTyrIleAsnAlaAsnPheIleAspGlyTyrAlaGlyr	1228
Oy	1221	CAGAAGGCTACATAGCTATACAGAGGGGCGCTGGCGCAGAGAGCACCGAGACTTCGGCGC	1280
Db	1229	LysLysAlaTyrIleAlaThrGlnGlyProLeuAlaSerThrThrGlnAspHeTrpArg	1248
Oy	1281	ATGCTAATGGGAGCACAATTCACCAATCAATCGTCATGCTACCAACCTTCGGAGATGGAC	1340
Db	1249	MetLeuTrpGlnUhisAsnSerThrIleValValMetLeuValLysLeuAlaGlnUcetyl	1268
Oy	1341	AGGAGAAATGCCACCAGTACTGGCCAGCAGAACCGCTGTGCTGCATCCAGTACTTGGT	1400
Db	1269	ArgGlnLysScyLeuGlnTyrTrpProserGluArgSerAlaArgTylGlnTyPheVal	1288
Oy	1401	GTTGATCCCGATGGCTGAGTACACATGCCCCAGTAATCTCTCGTAGATTCAAGTCAAG	1460
Db	1289	ValAspPrometValGlnTyrAsnMetProGlnTyrIleLeuAlaGlnPheLysValThr	1308
Oy	1461	GATCCCGGGGATGGGCGAGTAAAGAACAAATCCGCACTTCAGTTCAACAGCTGGCCAGAG	1520
Db	1309	AspAlaArgAspGlyGlnSerAlaGlyThrIleArgGlnPheGlnPheThrAspTrpProGln	1328
Oy	1521	CAGGGCTGCCCAAGACAGGCGGAGGATTCATTGACTTCATCGGCGAGTGCATAAAGC	1580
Db	1329	GlnGlyValProLysSerGlyGlnGlyPheValAspPheIleGlyGlnValHisLysThr	1348
Oy	1581	AAGGACGATTTGGACAGCATGGGCGCTATACAGGTCACATGCAGTGTGGCGTGGCGCC	1640
Db	1349	LysGlnGlnPheGlyGlnAspGlyProIleThrValHisScyGlyAlaGlyValSerArg	1368
Oy	1641	ACCGGGGGTTCATCACTGTGACGATCGTCGTCGAGACCGATCGCTATAGAGGGCGTGC	1700
Db	1369	ThrIleValPheIleAlaLeuSerValValLeuGlnArgMetArgTyrGlnGlyValVal	1388
Oy	1701	GACATGTTTCAGACCGCTGAGACCGCTCGCTACACAGCGCTCGCC-----	1745
Db	1389	AspLeuArgHeGlnThrValAlaLeuLeuAlaGlyThrGlnArgProCyScyValLysLeuArg	1408
Oy	1746	--ATGCTGCAGACA--GAGGACCAAGTATCAAGCTGTGCTACCGTGGCGCCCTGGAGTAC	1799
Db	1409	LeuGlnValGlnThrProGlnAspHisTylAlaPheCysTylArgAlaIleuGlnUtyr	1428
Oy	1800	CTGGCAGACTTTCACCACTATGCA	1823
Db	1429	LeuGlySerPheArgHisTylAla	1436

Search completed: January 17, 2003, 10:15:51
Job time : 182.5 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: January 17, 2003, 09:54:14 ; Search time 45.5 Seconds

(without alignments)
6320.810 Million cell updates/sec

Title: US-09-743-492-1

Perfect score: 6444

Sequence: 1 gatccgactgaagactcc.....attgataatcagattctt 3467

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 225784

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DOCLIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTWT=plco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09743492_@CGN.1.1.72.@runat.17012003_093835_11506 -NCPU=6 -ICPU=3
-NO_XLPRX -NO_MMAR -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV.TIMEOUT=120
-WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Swissprot_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3236	50.2	1897	1	PTP9_HUMAN
2	2826	45.4	1912	1	PTPD_HUMAN
3	2503	38.8	2029	1	LAR_DROME
4	1551	24.1	802	1	PTP6_HUMAN
5	1522	23.6	796	1	PTP6_HUMAN
6	1518	23.6	829	1	PTP6_HUMAN
7	1429	22.2	700	1	PTP6_HUMAN
8	1421	22.1	699	1	PTP6_HUMAN
9	1307	20.3	1452	1	PTP6_HUMAN
10	1306	20.3	1452	1	PTP6_HUMAN
11	1255	19.5	1439	1	PTP6_HUMAN
12	1243	19.3	1457	1	PTP6_HUMAN
13	1168	18.1	1445	1	PTP6_HUMAN
14	1162	18.0	1442	1	PTP6_HUMAN
15	1153.5	17.9	1430	1	PTP6_HUMAN
16	1142	17.7	1422	1	PTP6_HUMAN
17	1125.5	17.5	2316	1	PTP6_HUMAN
18	1117.5	17.3	2314	1	PTP6_HUMAN

19	1089.5	16.9	1301	1	PTP9_DROME	P35832 drosophila
20	1038	16.1	1255	1	CD45_RAT	P04157 rattus norv
21	1035.5	16.1	1304	1	CD45_HUMAN	P08575 homo sapien
22	1011.5	15.7	1462	1	PTP6_DROME	P16620 drosophila
23	1004	15.6	1152	1	CD45_MOUSE	P06600 mus musculu
24	702	10.9	1711	1	PTP6_RAT	P06612 rattus norv
25	678.5	10.5	1705	1	PTP6_MOUSE	P70289 mus musculu
26	603.5	9.4	1631	1	PTP1_DROME	P35992 drosophila
27	596	9.2	1114	1	PTP1_STYPL	P28205 styela plic
28	588	9.1	1238	1	PTP1_MOUSE	P04455 mus musculu
29	586	9.1	1997	1	PTP1_HUMAN	P23467 homo sapien
30	585	9.1	1337	1	PTP1_HUMAN	P12913 homo sapien
31	547.5	8.5	593	1	PTP9_HUMAN	P43378 homo sapien
32	526	8.2	593	1	PTN6_HUMAN	P06124 homo sapien
33	523	8.1	593	1	PTN6_RAT	P4199 rattus norv
34	522.5	8.1	595	1	PTN6_MOUSE	P29351 mus musculu
35	513	8.0	585	1	PTN6_MOUSE	P35235 mus musculu
36	502	7.8	595	1	PTN6_HUMAN	P29350 homo sapien
37	496.5	7.7	432	1	PTN1_RAT	P20417 rattus norv
38	496.5	7.7	845	1	CSR_DROME	P29349 drosophila
39	490.5	7.6	363	1	PTN2_RAT	P35233 rattus norv
40	490.5	7.6	415	1	PTN2_HUMAN	P17706 homo sapien
41	490	7.6	360	1	PTN7_HUMAN	P35236 homo sapien
42	489	7.6	432	1	PTN1_MOUSE	P35821 mus musculu
43	489	7.6	434	1	PTN1_CHICK	O13016 gallus gall
44	486.5	7.5	435	1	PTN1_HUMAN	P18031 homo sapien
45	485	7.5	2485	1	PTN2_HUMAN	O12923 homo sapien

ALIGNMENTS

RESULT 1
PTP6_HUMAN
ID PTP6_HUMAN STANDARD; PRT; 1897 AA.
AC P10586;
DT 01-JUL-1989 (rel. 11, Created)
DT 01-JUN-1989 (rel. 11, Last sequence update)
DT 15-JUN-2002 (rel. 41, Last annotation update)
DE LAR protein precursor (leukocyte antigen related) (EC 3.1.3.48).
GN PTP6 OR LAR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Tonsil;
RX MEDLINE=89035978; PubMed=2972792;
RA Streuli M., Krueger N.X., Hall L.R., Schlossman S.F., Saito H.;
RT "A new member of the immunoglobulin superfamily that has a
RT cytoplasmic region homologous to the leukocyte common antigen.";
RT J. Exp. Med. 168:1523-1530(1988).
RN [2]
RP MUTAGENESIS.
RX MEDLINE=90046860; PubMed=254325;
RA Streuli M., Krueger N.X., Tsai A.Y.M., Saito H.;
RT "A family of receptor-linked protein tyrosine phosphatases in humans
RT and Drosophila.";
RT Proc. Natl. Acad. Sci. U.S.A. 86:8698-8702(1989).
RN [3]
RP MUTAGENESIS.
RX MEDLINE=90316093; PubMed=1695146;
RA Streuli M., Krueger N.X., Tsai A.Y.M., Saito H.;
RT "Distinct functional roles of the two intracellular phosphatase like
RT domains of the receptor-linked protein tyrosine phosphatases LCA and
RT LAR.";
RT EMBO J. 9:2399-2407(1990).
CC -!- FUNCTION: IT IS POSSIBLE THAT LAR IS A CELL ADHESION RECEPTOR.
CC IT POSSESSES AN INTRINSIC PROTEIN TYROSINE PHOSPHATASE ACTIVITY
CC (PTPASE).
CC -!- FUNCTION: THE FIRST PTPASE DOMAIN HAS ENZYMIC ACTIVITY, WHILE
CC THE SECOND ONE SEEMS TO AFFECT THE SUBSTRATE SPECIFICITY OF THE
CC FIRST ONE.

```

CC -I- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC -I- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -I- SIMILARITY: CONTAINS 8 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -I- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: Y00815; CA68754.1; -.
DR PIR: S03841; TDHULK.
DR HSSP: P18052; TYRO.
DR Genew; HGNC:3670; PTPRF.
DR MIM: 179590; -.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003962; FNIII_repeat.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003598; Ig_C2.
DR InterPro: IPR003587; TYR_phosphatase.
DR InterPro: IPR000242; TYR_Pp.
DR Pfam: PF00041; Fn3; 7.
DR Pfam: PF00047; Ig; 3.
DR Pfam: PF00102; Y_phosphatase; 2.
DR PRINTS: PRO0014; ENTPEPITI.
DR PRINTS: PRO0700; PRTYPHPHASE.
DR SMART: SM00060; FN3; 5.
DR SMART: SM00408; IGC2; 3.
DR SMART: SM00194; PTPC; 2.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE: PS00556; TYR_PHOSPHATASE_2; 2.
DR PROSITE: PS50053; TYR_PHOSPHATASE_PTP; 2.
DR PROSITE: PS50053; TYR_PHOSPHATASE_PTP; 2.
KW Hydroxylase, Receptor, Glycoprotein, Signal, Transmembrane;
KW Cell adhesion; Immunoglobulin domain; Repeat.
FT SIGNAL 1 16
FT CHAIN 17 1897
FT DOMAIN 17 1250
FT TRANSMEM 1251 1274
FT DOMAIN 1275 1897
FT DOMAIN 1360 1606
FT DOMAIN 1649 1897
FT ACT_SITE 1538 1538
FT ACT_SITE 1829 1829
FT CARBOHYD 107 107
FT CARBOHYD 240 240
FT CARBOHYD 285 285
FT CARBOHYD 711 711
FT CARBOHYD 956 956
FT MUTAGEN 1538 1538
SQ SEQUENCE 1897 AA; 211844 MW; 439850F1D5C031FF CRC64;

Alignment Scores:
Pred. No.: 1,48e-186 Length: 1897
Score: 3236.00 Matches: 607
Percent Similarity: 100.00% Conservative: 0
Best local Similarity: 100.00% Mismatches: 0
Query Match: 50.22% Indels: 0
DB: 1 Gaps: 0

US-09-743-492-1 (1-3467) x PTPF_HUMAN (1-1897)
QY 6 GGACTGAGGAGCTCCTTGCTGAGCCACATCCCTGACCTGGAGATGCGGAGGCTCAAC 65
Db 1291, GlyleuynsAspsetleuAlahisrsetersAspprovalGluMeArGArgleuasn 1310
Yy 66 TACCAGACCCCGAGGTATGCGAGACCCACCCACCCATCCCATACCGAGCTGCGGACAAAC 125
Db 1311 TyrgnntirProglYMeArGAsphisProProlleProllethAspleuAlaaspasn 1330

```

[illegible]

OY 1206 GATGGTATAGACAGACAGAGCCCTACATAGCTACACAGAGCGCTCTGACAGACAGC 1265
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1691 ASPGLYTYRARGINGLINSALATYRILEALATHGINGLYPROLEUALAGLUSERTHR 1710
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 1266 GAGGACTTCTGGCGCATGCTATGGAGACAAATTCACCATCATGCTCATGCTGACCAAG 1325
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1711 GLUASPHETPRARGMETLEUTRPGIUNHISASNSETRHILELVALMETLEUTHRLYS 1730
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 1326 CTTCGGGAGATGGCGAGGAGAAATGCCACCACTACTGGCCAGACAGAGCGCTCTGCTGC 1385
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1731 LEUAARGGLUMETGLYARGGLULYSCHSHISGLINTYTRPRALAGLARGSERALAARG 1750
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 1386 TACCACTACTTGTGTGTTACCCGAGTGGCTGATACATGATGCCACAGATATCCGCGGT 1445
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1751 TYRGINTYRPHVEALVALASPROMETALAGLUTYRASHMETPROGLINTYRILEUALAG 1770
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 1446 GAGTTCAGAGTCACGAGATGCCGGGATGGGACATGACGACGACCAATCCGGCAGTTCCAGTTC 1505
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1771 GLUPHETYSVALTHRASPLAARGASPGIYGLNSERARGTHRILEARGLINPHEGINPHE 1790
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 1506 ACAGACTGGCCAGACAGCGCGCTGCCACAGACAGAGGAGGATTCATTGACTTCATCGCGG 1565
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1791 THRASPTTPRPGGLUGLNLGLYVALPROLYSTHNGLYGILYPHELLEASPHETILEGLY 1810
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 1566 CAGGTGATTAAGACCAAGACAGCATGTTGGACAGATGCGCTATCAGCGTGCATCGACT 1625
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1811 GLNVALHLSLYSTHRLYSGLINLNPHEGLYGLINASPGLYPROLLETHRYALHISGLYSER 1830
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 1636 GCTGGCGTGGGCGGACCGCGGGTGTTCATCACTGTGACATCGTCCCTGGAGCGCATCGCC 1685
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1831 ALAAGLYVALGLYARGTHRGILYVALPHELETHRLHUSERILEVALLEUGLUARGLMETARG 1850
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 1666 TATGAGGCGGTGTGACATGTTTCAGACCCGTGAGAACCCCTGCTACACAGCTCTGCTGCC 1745
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1851 TYRGINGLYVALVALASPMETPHEGLINTHRYALVLYSTHLEAARGTHRLINARGPROALA 1870
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 1746 ATGGTGACAGACAGACAGCATGATCACTGTGCTACCGCGCGCCCTGGAGTACCTCGCGG 1805
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1871 METVALGINTHRLGLASPGIINTYRGLINLEUCYSTYRARGALALALEUGLINTYRILEUGLY 1890
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 1806 AGCTTTGACCACTATGCAACG 1826
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1891 SERPHEASPHISTYRALATHR 1897
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 RESULT 2
 PTPD_HUMAN STANDARD: PRT; 1912 AA.
 ID PTPD_HUMAN STANDARD: PRT; 1912 AA.
 AC P23468;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Protein-tyrosine phosphatase delta precursor (EC 3.1.3.48) (R-PTP-
 delta).
 GN PTPRD.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 CC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND MUTAGENESIS OF ARG-1178.
 RX MEDLINE=95204468; PubMed=7896816;
 RA Pulido R., Krueger N.X., Serra-Pages C., Saito H., Streuli M.;
 RT "Molecular characterization of the human transmembrane protein-
 tyrosine phosphatase delta. Evidence for tissue-specific expression of
 alternative human transmembrane protein-tyrosine phosphatase delta
 isoforms".
 RT J. Biol. Chem. 270:6722-6728(1995).
 RL [2]
 RN SEQUENCE OF 390-1912 FROM N.A.
 RP TISSUE=Placenta;
 RC MEDLINE=91006018; PubMed=2170109;
 RA Krueger N.X., Streuli M., Saito H.;
 RT "Structural diversity and evolution of human receptor-like protein

RT tyrosine phosphatases".
 RL EMBL J. 9:3241-33252(1990).
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
 CC tyrosine + phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: A number of isoforms are produced by
 CC alternative splicing.
 CC -1- PTM: A CLEAVAGE OCCURS THAT SEPARATES THE EXTRACELLULAR DOMAIN
 CC FROM THE TRANSMEMBRANE SEGMENT.
 CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 8 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.
 CC -----
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 DR EMBL: L38929; AAC1749.1; -
 DR EMBL: X54133; CAA38068.1; -
 DR PIR: S12052; S12052.
 DR HSSP: P18052; TYPO.
 DR Genew: HGNC:9668; PTPRD.
 DR MIM: 601598;
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003962; FNIII_repeat.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003598; Ig_C2.
 DR InterPro: IPR000387; TYR_phosphatase.
 DR InterPro: IPR000242; Tyr_PP.
 DR Pfam: PF00041; fn3; 8.
 DR Pfam: PF00102; Y_phosphatase; 2.
 DR PRINTS: PR00014; ENTYPETII.
 DR PRINTS: PR00700; PRTPHPTASE.
 DR SMART: SM0060; FN3; 8.
 DR SMART: SM00408; IGC2; 3.
 DR SMART: SM00194; PTPC; 2.
 DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 2.
 DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 2.
 DR PROSITE: PS50055; TYR_PHOSPHATASE_ptp; 2.
 DR Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane; Repeat;
 KW Immunoglobulin domain; Alternative splicing.
 KW SIGNAL.
 FT CHAIN 21 1912
 FT DOMAIN 21 1265
 FT TRANSMEM 1266 1290
 FT DOMAIN 1281 1912
 FT DOMAIN 23 115
 FT DOMAIN 118 225
 FT DOMAIN 232 318
 FT DOMAIN 320 414
 FT DOMAIN 417 513
 FT DOMAIN 516 606
 FT DOMAIN 609 708
 FT DOMAIN 711 822
 FT DOMAIN 825 916
 FT DOMAIN 918 1017
 FT DOMAIN 1020 1137
 FT DOMAIN 1375 1618
 FT DOMAIN 1619 1912
 FT ACT_SITE 1553 1553
 FT ACT_SITE 1844 1844
 FT SITE 1175 1178
 FT CARBOHYD 254 254
 FT CARBOHYD 289 289
 FT CARBOHYD 724 724
 FT CARBOHYD 832 832
 FT VARSPPLIC 181 189
 FT VARSPPLIC 226 229

 N-TERMINAL.
 PROTEIN-TYROSINE PHOSPHATASE DELTA.
 EXTRACELLULAR (POTENTIAL).
 POTENTIAL.
 CYTOPLASMIC (POTENTIAL).
 IG-LIKE C2-TYPE DOMAIN 1.
 IG-LIKE C2-TYPE DOMAIN 2.
 IG-LIKE C2-TYPE DOMAIN 3.
 FIBRONECTIN TYPE-III 1.
 FIBRONECTIN TYPE-III 2.
 FIBRONECTIN TYPE-III 3.
 FIBRONECTIN TYPE-III 4.
 FIBRONECTIN TYPE-III 5.
 FIBRONECTIN TYPE-III 6.
 FIBRONECTIN TYPE-III 7.
 FIBRONECTIN TYPE-III 8.
 PROTEIN-TYROSINE PHOSPHATASE 1.
 PROTEIN-TYROSINE PHOSPHATASE 2.
 BY SIMILARITY.
 CLEAVAGE (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 MISSING (IN KIDNEY ISOFORM).
 MISSING (IN KIDNEY ISOFORM).

FT VARSPLIC 775 783 MISSING (IN KIDNEY ISOFORM)
 FT VARSPLIC 609 1137 MISSING (IN FETAL BRAIN ISOFORM).
 FT MUTAGEN 1178 1178 R->A: 2.5-FOLD REDUCTION IN CLEAVAGE.
 SQ SEQUENCE 1912 AA: 214759 MW: 3AE8BCBD32182E26 CRC64:

Alignment Scores:

Pred. No.: 5.63e-168 Length: 1912
 Score: 2926.00 Matches: 538
 Percent Similarity: 95.99% Conservative: 37
 Best Local Similarity: 89.82% Mismatches: 24
 Query Match: 45.41% Indels: 0
 DB: 1 Gaps: 0

US-09-743-492-1 (1-3467) x PTPD_HUMAN (1-1912)

QY 30 CACTCTCTGACCCCTGTGAGATGCGAGCGCTCACTACAGACCCCAAGTATGCGAGAC 89
 DB 1314 Hisprothraaprovallgluenuargyleuasnphneglnthrproglymetlaser 1333
 QY 90 CACCCACCCATCCCATACCGACCTGGCGGACAACATCGAGCGCTCAAAACCAACGAT 149
 DB 1334 Hisprothraaprovallgluenuargyleuasnphneglnthrproglymetlaser 1333
 QY 150 GGCCTCAAGTCTCCAGAGATGATGTCATGCTGACCTGGACACAGCTACGCTGGAG 209
 DB 1354 Asnleuylspieserlglnlutyrglnserlleaspproglyglnlphnethrtrp 1373
 QY 210 AATTCAAACCTGAGAGTGAACAGACCCCAAGAACCCCTATGCGAATGTCATGCTGAC 269
 DB 1374 HisseraenleugluvalasnllyspnarytyrAlaasnlvalllelatyrsp 1393
 QY 270 CACTCTGAGTACCTCTTACCTATGATGAGCGCTGCCCGGAGTACTATCAATGCC 329
 DB 1394 HisseraenleugluvalasnllyspnarytyrAlaasnlvalllelatyrsp 1393
 QY 330 AACTACATGATGGGTACCGAGAGCAAGTACCTATGCGAATGTCATGCTGAC 389
 DB 1414 AsnlyrllasplgyltyrAlaasnlvalllelatyrAlaasnlvalllelatyrsp 1433
 QY 390 GAGACGATGCGATGTTGTGAGATGCTGAGAACGCGACGCGACCTGTGCTCATG 449
 DB 1434 GluthrphnegllyasprphetrparymetllettrpoglunlaryserAlaThrValMet 1453
 QY 450 ATGACACGCGTGAAGAGAACCTCCGGTAAATGTATGATGATGCTGCGACCCGCTG 509
 DB 1454 MetllyrllasplgyltyrAlaasnlvalllelatyrAlaasnlvalllelatyrsp 1473
 QY 510 ACCGACCTGTGCGCTTATGATGAGCGCTGTCGACAGTACGAGTACCTGCGACATAC 569
 DB 1474 ThrGluthrllasplgyltyrAlaasnlvalllelatyrAlaasnlvalllelatyrsp 1493
 QY 570 ACTGTGCGACCTTGCACCTCCACAGAGTGTGCTGACAGTACGAGTACCTGCGACATAC 629
 DB 1494 CysValaArgThrphnegllyasprphetrparymetllettrpoglunlaryserAlaThrValMet 1513
 QY 630 TTTCAGTTCATGCGCTGCGACAGTACGAGTACCTGAGTACCTGAGTACCTGCGACATAC 689
 DB 1514 PheGlnThrllasplgyltyrAlaasnlvalllelatyrAlaasnlvalllelatyrsp 1533
 QY 690 TTTCAGTTCATGCGCTGCGACAGTACGAGTACCTGAGTACCTGAGTACCTGCGACATAC 749
 DB 1534 PheGlnThrllasplgyltyrAlaasnlvalllelatyrAlaasnlvalllelatyrsp 1553
 QY 750 AGCGCGGCGTGTGCGACGCGCTGCTTCACTGATGATGATGATGATGATGATGATGATG 809
 DB 1554 SerAlaGlyValGlyArgThrGlyCysPheThrValIleAspAlaMetLeuGlnArgIle 1573
 QY 810 AAGACAGAAAGAGCGTGAATCATGATGATGATGATGATGATGATGATGATGATGATG 869
 DB 1574 LysThrGlnThrllasplgyltyrAlaasnlvalllelatyrAlaasnlvalllelatyrsp 1593
 QY 870 TACATGGTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 929

DB 1594 TyrMetValGlnThrGluAspGlnTyrIlePheIleHisAspAlaLeuGlnAlaVal 1613
 QY 930 AGCTGCGGACACAGAGAGTGCCTGCCCAACTGTATGCCACATCCAGAGCTGGCG 989
 DB 1614 ThrCysGlyAsnThrGluValProAlaArgAsnLeuTyrAlaTyrIleGlnIlyserThr 1633
 QY 990 CAAGTCCCTCCAGGGGAGAGAGTGTACCCCATGAGACAGTCTGAGTCAAGTCTGGCCAC 1049
 DB 1634 GlnIleGluThrGlyGluAsnValThrGlyMetGluLeuGluPheLysArgLeuAlaSer 1653
 QY 1050 TCCAGGCGCCACAGCTCCCGCTTCATACGCGGCAACCTGCCCTGCAACAGTTCAGAAC 1109
 DB 1654 SerLysAlaHisThrSerArgPheIleSerAlaAsnLeuProCysAsnLysPheLysAsn 1673
 QY 1110 CGGCTGTGAACATGATGCGCTTACGAATTCAGCCCTGTGTCTGCTACAGCCATCCGTGAT 1169
 DB 1674 ArgLeuValAsnIleMetProTyrGlnSerThrArgValCysLeuGlnProIleArgGly 1693
 QY 1170 GTGAGGCGCTGACTATCATATGACAGCTTCTGTGATGTTATAGACAGCAAGGCC 1229
 DB 1694 ValGluGlySerAspTyrIleAsnAlaSerPheIleAspGlyTyrArgGlnGlnLysAla 1713
 QY 1230 TACATAGCTACACAGGCGCTGTGCGACAGAGACCGAGAGTCTTGCGCATGCTATAG 1289
 DB 1714 TyrIleAlaThrGlnGlyProleuAlaGluThrThrGluAspPheThrArgMetLeuThr 1733
 QY 1290 GAGCACAATTCACCATCATGCTCATGCTGACCAAGCTTCGGAGATGGAGGAGAGAA 1349
 DB 1734 GluHisAsnSerThrIleValValMetLeuThrLysLeuArgGluMetGlyArgGlnLys 1753
 QY 1350 TGCACACGATGCTGCGACAGAGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1409
 DB 1754 CysHisGlnTyrTyrProAlaGluArgSerAlaArgTyrGlnTyrPheValAlaAspPro 1773
 QY 1410 ATGCTGATACAAATGATGCGCGCATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1469
 DB 1774 MetAlaGluTyrAsnMetProGlnTyrIleLeuAspGluPheLysValThrAspAlaArg 1793
 QY 1470 GATGGCGATCAAGAGACATCCGCGAGTTCAGTTCACAGATGCGCCAGAGCGCGCTG 1529
 DB 1794 AspGlyGlnAspGlyProIleSerValHisCysSerAlaGlyValGlyArgThrGlyVal 1813
 QY 1530 CCCAAGACGCGAGGAGTTCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1589
 DB 1814 ProLysSerGlyGlnGlyPheIleAspPheIleGlyGlnValHisLysThrLysGln 1833
 QY 1590 TTTCAGACAGATGCGCTTATGATGAGCGTGCATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1649
 DB 1834 PheGlyGlnAspGlyProIleSerValHisCysSerAlaGlyValGlyArgThrGlyVal 1853
 QY 1650 TTTCATGCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1709
 DB 1854 PheIleThrIleSerIleValLeuGlnArgMetArgTyrGlnGlyValValAlaIlePhe 1873
 QY 1710 CAGACCTGAGAACCTTGCCTGACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1769
 DB 1874 GlnThrValLysMetLeuArgThrGlnArgProAlaMetValGlnThrGlnLysPheIle 1893
 QY 1770 CAGCTGTGCTACCGTGGCGCGCTGAGTACCTGCGACGCTTGCACATGATGATGAT 1826
 DB 1894 GlnPheSerTyrArgAlaAlaLeuGlnTyrLeuGlnLysPheAspHisTyrAlaThr 1912

RESULT 3
 LAR_DROME STANDARD: PRT: 2029 AA.
 AC P16621:
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Protein-tyrosine phosphatase Lar precursor (EC 3.1.3.48) (Protein-tyrosine-phosphate phosphohydrolase) (DLAR).
 GN Lar.
 OS Drosophila melanogaster (Fruit fly).

Db 1553 PheValAspPheThrArgMetCysTrpLeuLysThrAlaThrIleValMetMetThr 1572
 QY 456 CGGGTGGAGAGAAATCCCGGGTAAATGTATGATCAGTACTGGCCAGCCCTGGACCCAG 515
 Db 1573 ArgLeuGluGluArgThrArgIleLysCysAspGlnTyrTrpProThrArgIleGlu 1592
 QY 516 ACCTGTGGCCCTTATTCAGAGTACCCCTGTGGACACAGTGGACCTGGCCACATACACTGTG 575
 Db 1593 ThrTyrGlnGlnIlePheValThrIleThrGlnGlnIleValAlaThrTyrSerIle 1612
 QY 576 CGCACCTCGAGCCACCAAGAGTGGCTCCAGTGGAGAGCCAGTGGACCTGGCAGTTTGA 635
 Db 1613 ArgThrPheGlnIleCysArgGlnIlePheAsnAspArgGluIleLysGlnLeuGln 1632
 QY 636 TTCATGGCTGGCCAGACCATGAGTTCTGTAGTACCCACATCCCATCTGGCTTCTCTTA 695
 Db 1693 PheThrAlaTrpProAspHisGlyAlaProAsnHisProAlaProPheLeuGlnPheLeu 1652
 QY 696 CGAGCGGTCAAGGCCCTGACACCCCTAGACCGAGGCCCATGTGGTGCACCTGACGCGC 755
 Db 1653 ArgArgCysArgAlaLeuThrProProGlnSerGlyProValIleValHisCysSerAla 1672
 QY 756 GGGCGGGGGCCGACCGGCTGTCATCGTATGATGGCATGGTGGAGCGGATGAAGCAC 815
 Db 1673 GlyValGlyArgThrGlnGlyCysTyrIleValIleAspSerMetLeuGluArgMetLysHis 1692
 QY 816 GAGAAGAGCGTGGACATGTATGGCCACGTGACCTGCATGCATGCATGCACAGAGAACTACATG 875
 Db 1693 GluLysIleIleAspIleTyrGlyHisValThrCysLeuArgAlaGlnArgAsnTyrMet 1712
 QY 876 GTGCAGAGCGAGGACCACTAGCTGTTCATCCATGAGCGGCTGCTGGAGCGTCCACGTCG 935
 Db 1713 ValGlnThrGluAspGlnTyrIlePheIleHisAspAlaIleLeuGlnAlaIleIleLys 1732
 QY 936 GGGCACACAGAGGTGCTGGCCGACCTGTATGCCACATGCACAGACAGCTGACCAAGTG 995
 Db 1733 GlyValThrGluValProAlaArgAsnLeuHisThrHisLeuGlnLysLeuLeuIleThr 1752
 QY 996 CCTCCAGGGAGAGTGTAGCCGACATGGAGCTCGAGTTCAAGTTGCTGGCCAGCTCCAG 1055
 Db 1753 GluProGlyGluThrIleSerGlyMetGluValGluPheLysLysLeuSerAsnValLys 1772
 QY 1056 GCCCACAGTCCCGCTTATAGCGCCCACTGCCCTGCACACAGTTCAAGACCGGCTG 1115
 Db 1773 MetAspSerSerLysPheValThrAlaAsnLeuProCysAsnLysHisLysAsnTrpLeu 1792
 QY 1116 GTGACATCATGACCCCTACGAAATTCACCGCTGTGCTGACGCCACCGAGGCTGAG 1175
 Db 1793 ValHisIleLeuProTyrGluSerSerArgValTyrLeuThrProIleHisGlyIleGlu 1812
 QY 1176 GGCTGTGACTATCATATGACAGCTTCTGTGATGGTATAGACAGACAGAGGCTTACATA 1235
 Db 1813 GlySerAspTyrValAlaAsnIleSerPheIleAspGlyTyrArgTyrArgSerAlaTyrIle 1832
 QY 1236 CCTACACAGGGGCTGTGGACAGACACGACGACTTCTGGCCGATCTTATGGAGACAC 1295
 Db 1833 AlaIaGlnGlnGlyProValGlnAspAlaIaGlnAspThrPargMetLeuTrpGlnHis 1852
 QY 1296 AATTCACACATCATGCTGCTGACCAAGCTGGAGGATGGGAGGAGAGAATATGCCAC 1355
 Db 1853 AsnSerThrIleValIleValMetLeuThrLysLeuLysGluMetGlyArgGlnLysCysPhe 1872
 QY 1356 CAGTACTGGCCAGACAGCGCTGCTGCTGCTACAGTACTTGTGTGTGACCCGATGGCT 1415
 Db 1873 GlnTyrTrpProHisGlnArgSerValArgTyrGlnTyrValValAspProIleAla 1892
 QY 1416 GAGTACAAATGCCCCAGTATATCTGCGTGAAGTTCAAGTACACGAGATGCCGGGATGG 1475
 Db 1893 GlnTyrAsnMetProGlnTyrLysLeuArgGlnPheLysValIleAspAlaArgAspLys 1912
 QY 1476 CAGTCAAGGAAATCCGGCAATTCAGTTCACAGACTGGCCAGAGCAGCGGTGCCACAG 1535
 Db 1913 SerSerArgThrValArgGlnPheGlnPheIleAspTrpProGlnGlnGlyValProLys 1932

QY 1536 ACAGCGAGGGATTCATTGACTTCATCGGCGAGTGCATTAAGACCAAGAGCACTTTGGA 1595
 Db 1993 SerGlyGluGlyPheIleAspPheIleGlyGlnValHisLysThrLysGluGlnPheGly 1952
 QY 1596 CAGCATGGCCCTATCAGCGTGCATGCACTGCACTGCTGGCGTGGCCGACCGGGGTTCATC 1655
 Db 1953 GlnAspGlyProIleThrValHisCysSerAlaGlyValGlyArgSerGlyValPheIle 1972
 QY 1656 ACTGTGACATCGTCTGTGAGGCGCATGCGCTATGAGGGCGTGGTGCATGTTTCAGACC 1715
 Db 1973 ThrLeuSerIleValIleGluGluTrpMetGlnTyrGlnGlyValLeuAspValPheGlnThr 1992
 QY 1716 GTGAAGACCTGCGGTACAGACAGCGTCTCCATGTCAGTGCACAGACAGACAGTACAGCTG 1775
 Db 1993 ValArgIleLeuArgSerGlnArgProAlaMetValGlnThrGlnAspGlnTyrHisPhe 2012
 QY 1776 TGCTACCGTGGCGGCTTGAGTACTCGGACGCTTGACCACTAT 1820
 Db 2013 CysTyrArgAlaAlaIleGluGluTyrIleGluLysSerPheAspAsnTyr 2027
 RESULT 4
 PTR_A_HUMAN STANDARD: PRT: 802 AA.
 AC P18433; Q14513;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Protein-tyrosine phosphatase alpha precursor (EC 3.1.3.48) (R-PTP-
 alpha)
 CN pTPRA OR pTPRA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90349565; PubMed=2166945;
 RA Sap J., D'Eustachio P., Givol D., Schlessinger J.;
 RT "Cloning and expression of a widely expressed receptor tyrosine
 RT phosphatase";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:6112-6116(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90384936; PubMed=2169617;
 RA Kaplan R., Morse B., Huebner K., Croce C., Hawk R., Ravera M.,
 RA Ricca G., Jaye M., Schlessinger J.;
 RT "Cloning of three human tyrosine phosphatases reveals a multigene
 RT family of receptor-linked protein-tyrosine-phosphatases expressed in
 RT brain.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:7000-7004(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91006016; PubMed=2170109;
 RA Krueger N.X., Streuli W., Saito H.;
 RT "Structural diversity and evolution of human receptor-like protein
 RT tyrosine phosphatases";
 RL EMBO J. 9:3241-3252(1990).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Kidney;
 RX MEDLINE=91088320; PubMed=2175890;
 RA Ohagi S., Nishi M., Steiner D.F.;
 RT "Sequence of a cDNA encoding human LRP (Leukocyte common antigen-
 RT related peptide).";
 RL Nucleic Acids Res. 18:7159-7159(1990).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91032191; PubMed=2172030;
 RA Jirik F.R., Janzen N.M., Melhado I.G., Harder K.W.;
 RT "Cloning and chromosomal assignment of a widely expressed human
 RT receptor-like protein-tyrosine phosphatase.";
 RL FEBS Lett. 273:239-242(1990).

Percent Similarity:	66.84%	Conservative:	97
Best Local Similarity:	50.26%	Mismatches:	188
Query Match:	23.62%	Indels:	6
DB:	1	Gaps:	3

US-09-743-492-1 (1-3467) x PTRR_RAT (1-796)

OY	84	CGAAGACCCACCCACCCATCCCATCCAGACCTGGGGGACACATCGAGGCGCTCCAAAGCC	143
Db	210	ArgLysTyrProProIleuProValAspLysLseGluGluGlnIleAsnIleAsnIleVal	229
OY	144	AACATGAGCCCAAGTCTCTCCAGAGGTATGATGATCCATCGACCTGGACAG---CAGTTC	200
Db	230	AspAspAsnLysIleuPheValGluGluIlePheAsnIleValLeuProAlaCysProIleGlnIle	249
OY	201	ACGTGGGAGATTTAAACCTGGAGGTGACAAAGCCCAAGAACCCGTATGCGAATGTCATC	260
Db	250	ThyrGluAlaIleAserLysGluGluAsnLysGluLysAsnArgTyrAlaAsnIleu	269
OY	261	GCTCAACGACACTTCGACATCCATCCATCCATGAGGGGTGCCGAGGACTATC	320
Db	270	ProTyrAspHisSerArgValHisIleuThrProValGluGluValProAspSerAspTyr	289
OY	321	ATCAATGCCAATACATCATGATGGCTACCCGACAGACAGAAATGCTACATCGCCACGAGGC	380
Db	290	IleAsnIleSerPheIleAsnGluTyrGluGlnIulLysAsnLysPheIleAlaIleGlnIly	309
OY	381	CCCCGGCCGAGACCATGGGCGATTCCTGGAGAAATGGTGGGAAACGCGCAGGCGCACT	440
Db	310	ProLysGluGluThrValAsnAspPheThrPargMetIleIlePdlGlnIleAsnThr	329
OY	441	GTGGTCATGATGACGAGCGCTGGAGAGAAATCCCGGGTAAATGTGATCAGTACAGCCCA	500
Db	330	IleValMetValThrAsnIleuLysGluArgLysGluCysLysCysAlaIleTyrTrpPro	349
OY	501	GCCCGTGGCACCGAGACCTGGCGCTTATTCACAGTACCTGTGGACACAGTGGAGCTG	560
Db	350	AspGlnIlyCysTrpProTyrGluAsnValArgValSerValGluAspAlaThrValIleu	369
OY	561	GCCACATACACTGTGGCCACCTCGCATCCACAAAGAGGCTCCAGTAGAGAGCGTAG	620
Db	370	ValAspTyrThrValArgLysPheCysIleGlnGlnValGlyAspValThrAsnArgLys	389
OY	621	-----CTGGCTCAAGTTCAAGTTCATGCGCTGGCCACAGACCATGGAGTTCTCGAG	668
Db	390	ProGlnArgIleuIleThrGlnPheHisPheThrSerTyrProAspPheIlyValProPhe	409
OY	669	TACCAACTCCATCGAGGCTCTCTCAACGAGGGTCAAGAGCTCGCAACCCCTTAGACCA	728
Db	410	ThrProIleGluMetIleuLysPheIleuLysValIlyAlaCysAsnProGlnIlyAla	429
OY	729	GGGCGCATGGTGGTCATCGTCACTGACGCGGGCGTGGGCGCACCGGCTTCATCGTAGT	788
Db	430	GlyAlaIleValValHisCysSerIleArgIlyValGlyArgThrGlyThrPheValIalle	449
OY	789	GATCCCATGTGGGCGGAGGAAGACGACGAACAGCTGCATCGATCGAGCCACGTGACC	848
Db	450	AspIleMetIleuAspMetIleHisSerGluArgLysValAspAlaTyrGlyPheValSer	469
OY	849	TGCATGCGATCACAGAGAACTACATGTGTCAGACGAGGAGGACTACGTGTTCTATCATC	908
Db	470	ArgIleArgAlaGlnArgCysGlnMetValGlnThrAspMetGlnTyrAlaPheIleIlyr	489
OY	909	GAGGCGCTGCTGGAGGCTGCCACGTGCGGCGCACACAGAGAGTGCCTCCCGCAACTGTAT	968
Db	490	GlnAlaIleuIleuGlnIlyIlyrIleuTyrGlyAspThrGluIleuGlnValThrSerIleuAsp	509
OY	969	GCCCAACATCCAGAGCTGGGCGCAAGTGGCCCAAGGGAGAGTGTACAGCCCATGGAGCTC	1028
Db	510	ThrHisIleuGlnIlyrIleTyrAsnLysIleProGluThrSerAsnAsnGlyIleuGlnIly	529
OY	1029	GAGTTCAAGTTGCTGGCCAGCTCCAAAGCCCAACAGCTCCCGCTTATCATCAGGCCAAGCTG	1088

Db	530	GIUPHELYSLYSLEUTHINSETLLELYSLIEGLHNSHSPULYSMEKARTRHCLYLYRLEU	543
Qy	1089	CCCTCCACAAAGTTCCAGAAACCGGCTGCTGTAACATCATGCGCTACGAATTGACCGCTG	1148
Db	550	PROIALASMETLYSLYASNAARGVALLEUGHLEILEPROTYCLUPHNSHARGVAL	569
Qy	1149	TGTCGCAGCCCATCCGTGGTGTGAGGGCTCTGCATACATCATATGCCAGTTCCTGGAT	1208
		::: :: :: :: :: :: ::	
Db	570	ILEILEPROVALYLSARGGLYGLUGLNSHNTHRASPTLYVALASNAHSERPHLEIASP	589
Qy	1209	GGTTATACAGCAGCAAGAGCCCTCATATGCTACACAGGGGCTCTGGCAGAGACAGCCAG	1268
		::	
Db	590	PROTYRARGGLNLYSASPSETYRLLLEALASERCLNGLYPROLEUENHISHTHRGLU	609
Qy	1269	GACTCTTGCCCATGCTATGGGAGACAAATCCACATCATGCTCATGCTGACCAAGCT	1328
Db	610	ASPHETTRPATGMETILEETRPGILNTRPLYSSERCYSSERILEVALMETHEUTHRGLU	629
Qy	1329	CGGGAGATGGCCAGGAGAAATGCCACCACTACTGGCCCAAGACAGCCCTCTGCTGCTAC	1388
		::	
Db	630	GLUGLARGGLYGLINGLILYSCYSLAGLNTYTRPROSEHASPGLYLEUVALSERTYR	649
Qy	1389	CAGTACTTGTGTTGTGACCCGATGGCGCTGAGTACAAATGCCCAATGCTCTGCTGCTAG	1448
Db	650	GLYASPIETHRVALIGLLEULYSLYSGLUGLUGLUCYSLUSERYTRHRYVALRASP	669
Qy	1449	TTCAAGTGCACGAGATGCCCGGATGGGCTCAAGAGCAATCCGCGAGTTCACAGTTACA	1508
Db	670	LEULEUVALTHIRASNTHRARGLUNASLYSSERARGLNLLEARGLNPHEHISPHENS	689
Qy	1509	GACTGCCCCAGACGGCCGTGCCCAACACAGCGGAGGATTCATGACTTCACTCGGGCAG	1568
Db	690	GLYTRPROGLUNVALIGLYLEPROSEHASPGLYGLYMETILEANSILLELEALALA	709
Qy	1569	GTGCATAGACCAAGAGACAGATTGGACAGAGATGGGCTCATACGGTGCATGTCAGTGT	1628
		:: :: :: ::	
Db	710	VALGLNLYSGLINGLNGLNSERGL--ASNHISPROILETHRVALHISCYSERIALA	728
Qy	1629	GCGCGGGCCACCCACCGGGGATGTCATCTAGACATGCTGCTGGAGCGCATGGCGCTAT	1688
Db	729	GLYALAGLYARGTHRGLYTHRPHECYSALALEUSERTHVALLEUGLUCYSVALYSLALA	748
Qy	1689	GAGGCGTGTGCAGATGTTTCAGACCCTGAGAAACCTGCTGACAGCGCTCCATG	1748
Db	749	GLUGLYLEULEUASPVALPHEGLNTHRYALLYSTRHLEUARGLEUGLNARGPROHISMET	768
Qy	1749	GTCCAGACAGAGACCACTATCAGCTGTGTAACCGTGGCGCCCTGAGTACTCGGCAGC	1808
Db	769	VALGLNLEUGLNGLNTYRGLUPHECYSTYLYSVALVALGLNLTUTYRILEASPLA	788
Qy	1809	TTTGCACCATWCCA 1823	
Db	789	PHESERASPTYRALA 793	
RESULT 6			
PTRA_MOUSE			
ID	PTRA_MOUSE	STANDARD;	PRT; 829 AA.
AC	P18052; 061808;		
DT	01-NOV-1990 (Rel. 16, Created)		
DT	01-FEB-1996 (Rel. 33, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	protein-tyrosine phosphatase alpha precursor (BC 3.1.3.48) (R-PTP-alpha) (ICA-related phosphatase).		
GN	PTPRA OR LRP OR PTPA.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.		
OX	NCBI_Taxid=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.		
RC	STRAIN=C57BL/6 X DBA/2;		
RX	MEDLINE=90280391; PubMed=2162042;		
RA	Matthews R.J., Cahir E.D., Thomas M.T.;		


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QY 801 GAGGCGATGAAGCAGACAGAGCGGTGACATCTATGGCCAGCGTGCATGGCATCA 860
Db 487 AspmethcHissergluArgLysValAlaSpValTyrGlyPheValSerArgLLeuAla 506
QY 861 CAGAGAACTCATGTCAGACGAGGAGCATGTCGTTCATCCATGAGGCGCTGCTG 920
Db 507 GlnArgGysGlnMetValGlnThrAspMetGlnTyrValPheLleTyrGlnAlaLeu 526
QY 921 GAGCGTCCAGCGTCCAGACAGAGTCCGCGCCAGCATGTATGCCCATTCAG 980
Db 527 GlnHisTyrLeuTyrGlyAspThrGlnLeuGlnValThrSerLeuGlnThrHisLeuGln 546
QY 981 AAGCGGGCCCAAGTCCCTCCAGGGAGAGTGTGACCGGCATGAGACTCGAGTCAAGTTG 1040
Db 547 LysLleTyrAsnLysLleProGlyThrSerAsnAsnGlyLeuGlnGlnPheLysLys 566
QY 1041 CTGCGCCAGCTCCAGGCGCCACACGCTCCGTCATCATCGCCCATCCCTCCCAACAG 1100
Db 567 LeuThrSerLleLysLleGlnAsnAspLysMetArgThrGlyAsnLeuProAlaAsnMet 586
QY 1101 TTCAGAACCGCGCTGGTGAACATCATGCGCTACGAAATTCACCGCTGTCTGTCAGGCC 1160
Db 587 LysLysAsnArgValLeuGlnLleLleProTyrGlnPheAsnArgValLleLleProVal 606
QY 1161 ATCGGTGTGTGAGGCGCTGACTACATCATGCGCTTCCTGGATGGTTATGACAG 1220
Db 607 LysArgGlyGlnGlnAsnThrAspTyrValAsnAlaSerPheLleAspLleTyrArgLys 626
QY 1221 CAGAGAGCGCTCATATGATACATGAGGCGCTGCGAGAGACACCGAGACTTCTGAGCGC 1280
Db 627 LysAspSerTyrLleAlaSerGlnGlyProLeuLeuHisThrLleGlnAspPheThrArg 646
QY 1281 ATGCTATGAGACACAAATTCACATCATGCTCATGCTGACCAAGCTTGGAGATGGGC 1340
Db 647 MetLleArgLysTyrLysSerCysSerLleValMetLeuThrGlnLeuGlnGlyLys 666
QY 1341 AGGGAAGATGCCACACCTACTGAGGCGACAGCGCTGCTGCTGCTACAGACTTGT 1400
Db 667 GlnGlnLysCysAlaGlnTyrTTrProSerAspLysLeuValSerTyrGlyAspLleThr 686
QY 1401 GTTGACCCGATGGCTGATACATGAGCGCCAGTATATCTGCGTGAAGTTCAAGTGCAG 1460
Db 687 ValGlnLeuLysLysGlnGlnGlnCysLysSerTyrThrValArgAspLeuValThr 706
QY 1461 GATGCCCGGATGGGCACTCAAGACAAATCCGCGACATTCCAGTTCAAGACTGGCCAGAG 1520
Db 707 AsnThrArgGlnAsnLysSerArgGlnLleArgGlnPheHisPheHisGlyTTrProGln 726
QY 1521 CAGGGCGTGGCCCAAGACAGGAGGAGTTCATGTACTTCATCGGCGAGTGCATGAAGAC 1580
Db 727 ValGlyLleProSerAspLysGlyMetLleAsnLleLleAlaAlaValGlnLysGln 746
QY 1581 AAGGAGCAGTTTGGACAGATGGGCTATATCAGCGTCACTGACAGTGCAGTGGGCGCGC 1640
Db 747 GlnGlnGlnInsery---AsnHisProLleThrValHisCysSerAlaGlyAlaGlyArg 765
QY 1641 ACCGGGGTTCATCATCACTCATGACATGCTGCTGAGCGCCATGAGCGCGCTGCTG 1700
Db 766 ThrLysThrPheCysAlaLeuSerThrValLeuGlnArgValLysAlaGlnGlyLleLeu 785
QY 1701 GACATGTTTGAAGCGGAGACAGCGTGGTATACAGCGCTGCTGCGCATGAGACAGAG 1760
Db 786 AspValPheGlnThrValLysSerLeuArgGlnArgGlnProHisMetValGlnThrLeu 805
QY 1761 GACCAAGTATCAGCTGTGCTACCGTGGCGCGCTGAGTACCTGCGGACCTTTCACCATAT 1820
Db 806 GlnGlnTyrGlnPheCysTyrLysValValGlnGlnTyrTTrLeaAspAlaPheSerAspTyr 825
QY 1821 GCA 1823
Db 826 Ala 826

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RESULT 7

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PRTPE_HUMAN
ID PRTPE_HUMAN STANDARD: PRT: 700 AA.
AC P23469.
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Protein-tyrosine phosphatase epsilon precursor (EC 3.1.3.48) (R-PTP-
  epsilon).
DE PRTPE.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=91006018; PubMed=2170109;
RA Krueger N.X., Streuli M., Saito H.;
RT "Structural diversity and evolution of human receptor-like protein
  tyrosine phosphatases."
RL EMBL J. 9:3241-3252(1990).
CC -I CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
  tyrosine + phosphate.
CC -I SUBCELLULAR LOCATION: Type I membrane protein.
CC -I SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL outstation -
  the European Bioinformatics Institute. There are no restrictions on its
  use by non-profit institutions as long as its content is in no way
  modified and this statement is not removed. Usage by and for commercial
  entities requires a license agreement (see http://www.isb-sib.ch/announce/
  or send an email to license@isb-sib.ch).
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DR EMBL: X54134; CAA38069.1; -.
DR PIR: S12053; S12053.
DR HSSP: P18052; 1YPO.
DR Genew: HGNC:9669; PTPRE.
DR MIM: 600926; -.
DR InterPro: IPR000387; TYR_phosphatase.
DR InterPro: IPR000242; TYR_PP.
DR Pfam: PF00102; Y_phosphatase.
DR PRINTS: PR00700; PRTYPHPTASE.
DR SMART: SM00194; PTPc: 2.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 2.
KW Glycoprotein; Transmembrane; Hydrolase; Phosphorylation; Repeat;
  signal.
FT SIGNAL 1
FT CHAIN 20..700 POTENTIAL.
FT DOMAIN 20..46 PROTEIN-TYROSINE PHOSPHATASE EPSILON.
FT TRANSMEM 47..69 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 70..700 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 154..393 PROTEIN-TYROSINE PHOSPHATASE 1.
FT DOMAIN 394..700 PROTEIN-TYROSINE PHOSPHATASE 2.
FT ACT_SITE 335..335 BY SIMILARITY.
FT ACT_SITE 630..630 BY SIMILARITY.
FT CARBOHD 23..23 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 30..30 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO SEQUENCE 700 AA; 80641 MW; D096BDADEA5708 CnC64;

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Alignment Scores:

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Pred. No.: 2,44e-78 Length: 700
Score: 1429.00 Matches: 284
Percent Similarity: 64.82% Conservative: 103
Best Local Similarity: 47.57% Mismatches: 200
Query Match: 22.18% Indels: 10
DB: 1 Gaps: 5

```

US-09-743-492-1 (1-3467) x PRTPE_HUMAN (1-700)

QY 60 CTCACTACACAGCCAGGTATGCGAGACCCACCCATCCCATCCAGCTG6GC 119
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 102 LeuSerArgSerProSerGlyProLysLysTyrPheProIleProValGluHisLysGlu 121
QY 120 GACACATCTCAGGGCCCTCAAGGCCAAGCATGGCTCAAGTTCTCCAGAGTATGATCC 179
: : : : : ||| :
Db 122 GluGluIleArgIleArgSerAlaAspAspCysLysGlnPheArgGluGluPheAsnSer 141
QY 180 ATCGACCTGGAGAG--CAGTTTCACGTGGAGAAATTCAAACTGGAGGTGACAGACCC 236
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 142 LeuProSerGlyHisIleGlnGlyThrPheGluIleuAlaAsnLysGluGluAsnArgGlu 161
QY 237 AAGACCGCTATGCGAATGTATCGCTACAGCACCTCTGAGTCATCTTACTCTATC 296
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 162 LysAsnArgTyrProAsnIleLeuProAsnAspHisSerArgValIleLeuSerGluLeu 181
QY 297 GATGGGCTCCCGGAGTGTACTACATACGCGACATACATGCTGAGCTCCGACAGCAG 356
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 182 AspGlyIleProCysSerAspTyrIleAsnAlaSerTyrIleAspGlyTyrLysGluLys 201
QY 357 AATGCTACATCGCCACGACGAGGCCCTGCGGACGACATGGGCGATTCTTGAGATG 416
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 202 AsnLysPheIleAlaIleGlnGlyProLysGlnGluThrValAsnAspPheTrpArgMet 221
QY 417 GTGTGGACACGCGACGCGCTGTGTGTCATGATGACAGCGCTGAGAGAGAGTCCCGG 476
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 222 ValTyrPheGluIleLysSerAlaThrIleValIleMetLeuThrAsnLeuLysGluArgGlu 241
QY 477 GTAAATGTATGATGTCATGTCGCGCGCGGCGACGACGCTGCGCTTATGACGTG 536
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 242 GluLysCysHisGlnTyrTrpProAspGlnGlyCysTrpThrTyrGluAsnIleArgVal 261
QY 537 ACCCTGTGGACACAGTGGAGCTGGCCACATACACTGTGGCACTTCCGACCTCCAG-- 593
: : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 262 CysValGluAspCysValValLeuValAspTyrThrIleArgLysPheCysIleGlnPro 281
QY 594 -----AAGAGTGGCTCACTGAGAGACCGTGAAGCTGCTCACTTTCATGCTCG 647
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 282 GlnLeuProAspGlyCysLysAlaProArgLeuValSerGlnLeuHisPheThrSerThr 301
QY 648 CCAAGCATGAGAGTCTCTGATGATCCCAACTCCCATCGGCTTCCATACGAGGCTCAAG 707
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 302 ProAspPheGlyValProPheThrProIleGlyMetLeuLysPheLeuLysValLys 321
QY 708 GCTGTCAACCCCTAGACGAGGCGCCATGCTGTGTCATGTCACAGCGGCGCTGAGCGC 767
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 322 ThrLeuAsnProValHisAlaGlyProIleValValHisCysSerAlaGlyValGlyArg 341
QY 768 ACCGGCTGCTTCATCGTATGATGATGATGATGATGATGATGATGATGATGATGATG 827
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 342 ThrGlyThrPheIleValIleAspAlaMetMetAlaMetMetHisAlaGluGlnLysVal 361
QY 828 GACATCATATGGCCACGCTGATGATGATGATGATGATGATGATGATGATGATGATG 887
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 362 AspAlaPheIleuPheValSerArgIleArgAsnIleArgProGlnMetValGlnThrAsp 381
QY 888 GACAGTACGTGTTTCATCGATGATGATGATGATGATGATGATGATGATGATGATG 947
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 382 MetGlnTyrThrPheIleTyrGlnAlaLeuLeuGlnTyrTyrLeuTyrGlyAspThrGlu 401
QY 948 GTGCTGCGCCGCAACTGTATGCCACATCCAGAGAGTGGGCCAAGTGCCTCCAGGGGAG 1007
: : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 402 LeuAspValSerSerLeuGluLysHisLeuGlnThrMetHisGlyThrThrHisPhe 421
QY 1008 AGGTGACCCGCAATGAGCTCGAGTCAAGTGTGTCGCGACGCTCCAGAGGCCACAGCTCC 1067
: : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 422 AspLysIleGlyLeuGluGluGluPheArgLysLeuThrAsnValArgIleMetLysGlu 441
QY 1068 CGCTTTCACAGCCGCACTGCTCCGCAAGATTCAGAGACCGGCTGTGATCATATG 1127
: : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 442 AsnMetArgThrGlyAsnLeuProAlaAsnMetLysLysAlaArgValIleGlnIleIle 461
QY 1128 CCTACGAATTGACCCGTGTGTGTCTGACAGCCATCCGTGTGTGTGAGGGCTGTGACTAC 1187

Db 462 ProTyrAspPheAsnAlaArgValIleLeuSerMetLysArgGlyGlnGlyTyrThrAspTyr 481
QY 1188 ATCAATGCCAGCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1247
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 482 IleAsnAlaSerPheIleAspGlyTyrArgGlnLysAspTyrPheIleAlaThrGlnGly 501
QY 1248 CCTGTGCGACAGACACCGAGAGCTTGTGGCGCATGCTATGGAGACAAATCCACATC 1307
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Db 502 ProLeuAlaHisThrValGlnAspPheTrpArgMetIleTrpGluTyrLysSerHisThr 521
QY 1308 ATGCTCATGCTGACCAAGCTTCGCGAGATGGGAGGAGAAATGCCACGACTACTGGCA 1367
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Db 522 IleValMetLeuThrGluValGlnGluArgGluGlnAspLysCysTyrGlnTyrTrpPro 541
QY 1368 GCAAGCGCTGTCTGCTCCCTACCACTACTTGTGTGACCCGAGAGCTGATACAGATG 1427
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Db 542 ThrGluGlySerValThrHisGlyGluIleThrIleGluIleLysAsnAspThrLeuSer 561
QY 1428 CCCCAGTATATCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1472
: : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 562 GluAlaIleSerIleArgAspPheLeuValThrLeuAsnGlnProGlnAlaArgGlnGlu 581
QY 1473 GCGCAGTCAGAGACAAATCCGCGACCTTCCAGTTCACAGACTGCCAGAGCAGGCGTCCC 1532
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 582 GluGlnValArgValValArgGlnPheHisPheHisGlyTyrProGluIleGlyLeuPro 601
QY 1533 AAGACAGCGGAGGATTCATGATGATGATGATGATGATGATGATGATGATGATGATG 1592
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 602 AlaGluGlySerGlyMetIleAspLeuIleAlaValGlnGlyGlnGlnGlnThr 621
QY 1593 GGACAGATGGGCTATACAGGCTGCTGATGATGATGATGATGATGATGATGATGATG 1652
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 622 Gly---AsnHisProIleThrValHisCysSerAlaGlyAlaGlyThrGlyThrPhe 640
QY 1653 ATCACTGTGACATGCTCTGAGAGCGCATGGCGCATGATGAGGCGGTGTCATGTTTCAG 1712
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 641 IleAlaLeuSerAsnIleLeuGluArgValLysAlaGluGlyLeuAspValPheGln 660
QY 1713 ACCCTGAGACCCCTGCTATACAGCGTCTCCATGCTGATGATGATGATGATGATGATG 1772
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 661 AlaValLysSerLeuArgLeuGlnArgProHisMetValGlnThrLeuGlnGlyGlu 680
QY 1773 CTGTGCTACCGTGGCGCTGAGTACCTCGGACGCTTTCACCACTATGCA 1823
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 681 PheCysTyrLysValValGlnAspPheIleAspIlePheSerAspTyrAla 697
RESULT 8
PRT: 699 AA.
ID PRT: 699 AA.
AC P49446; Q62134; Q62444; Q64496;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Protein-tyrosine phosphatase epsilon precursor (EC 3.1.3.48) (R-PRT-
epsilon)
GN PTPRE OR PTPPE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI-TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N.
RX MEDLINE=96064677; PubMed=7592814;
RA Elson A., Leder P.,
RT "Protein-tyrosine phosphatase epsilon. An isoform specifically
expressed in mouse mammary tumors initiated by v-Ha-ras OR neu.",
RL J. Biol. Chem. 270:26116-26122(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=DBA/2.
RA Muroyama Y.,

Oy	1068	CGCTTCATCACGGCCAGCCTGCTGCCCTGCAGAACTTCAACAGCCGGTGTAACATCAAG	1127
Db	441	Asmethylgthrlylgaasnleuprolalasnmetlllysalaargvalilleelillelle	460
Oy	1128	CCGTACGAATTGACCSCGTGTGTCTTGACGCCCATCCGTTGTGTGGAGGGCTGTGACTAC	1187
Db	461	Protylasprpheasnaadvalilleusermetllysargylglngluiphehriaspury	480
Oy	1188	ATCAATGCCAGCTTCCTGGATGGTTATAGACACACAGAAGCCTACATACTACACAGGG	1247
Db	481	IleasnalaserrhellleasrglytYArglnLlysasptyrPheMetIathrlndily	500
Oy	1248	CSTGTGCAGACAGACACCCGAGCACTTGGCGCATCTGTATGGAGACACAATCCASCATC	1307
Db	501	Proteulanlanshtyrlygluasaprhetrphgmetylatrtreldutrpysentiastr	520
Oy	1308	ATGCTCATGTGACCAAGCTTCTGGGAGADATGGCAGGAGAAAATGCCACCACTATGGCCA	1367
Db	521	IleValmetLeuthrGluaValGlnGlnatrgSglnglnalspylsctytlntntrypro	540
Oy	1368	GCAAGAGGCGCTGTGCTGCCCTACCCAGTACTTGTGTGTGGACCCGATGGCTGAGTACAATG	1427
Db	541	ThrludlyserValThrnlsglyasrpilethrlileglullelyseserphrleuser	560
Oy	1428	CCCCAGTATATCCCTGCGTAGTTCAAGGTCACG-----GATCCCGGAGT	1472
Db	561	GlualalleaserValAtargasprhellevatlThrPhelysGlnProleualaarglnidu	580
Oy	1473	GGGAGATGACAGCAATCCGCGACATTCGACTTCACAGACTGGCCACAGCAGGGCTGCC	1532
Db	581	GlueInValArjmetValAarglnPrhenIsGlytTPRoglUwAlIdyllero	600
Oy	1533	AAGACGGCGGGATTCATTGACTTCATCGGGCAGGTGCATAAAGCSAAGAGGAGTTT	1592
Db	601	AlaetuglylsgetlmectlleaspleulllealalavalaglnlysdmlnmImlnlthr	620
Oy	1593	GGACAGAGTGGCCCTATACACAGGTGCATCGTAGTCTGGCGTGGGCCGACCGGGGTCTT	1652
Db	621	Gly---AsnhIsProllthrValInsycyserAlaglYalaglYarghcnlythrPhe	639
Oy	1653	ATCAGCTGTAGACATCGCTCGTGGAGCCGATGCGCTATAGAGGGCTGTGCATGTTTGA	1712
Db	640	IlealaleSerAsnIlleuleuglnatrgValylsalglnglylLendleuaspvalPhebln	659
Oy	1713	ACCGTGAAGACCCGCTGATACACAGCGCCGCCATGCTGCACAGCAGAGGACAGATGAG	1772
Db	660	AlaValylsserleuAlglyleuGlnatrgProhIsMeValGlnThlleuIndustnytleu	679
Oy	1773	CTGTGCTACCGTGGCGCCCTGGAGTACCTCGCAGCCTTTGACCCTACTATGCA	1823
Db	680	PhecystyrylsvallValalnaspheilleasrpillePheserAsptylala	696

RESULT 9

ID	PTPM_MOUSE	STANDARD:	PRT:	1452 AA.
AC	p28828;			
DT	01-DEC-1992 (Rel. 24, Created)			
DT	01-DEC-1992 (Rel. 24, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Protein-Tyrosine phosphatase W0 precursor (BC 3.1.3.48) (R-PTP-MU).			
GN	pppM.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Lung;			
RX	MEDLINE=92008644; PubMed=1655529;			
RA	Geibnik M.F.B.G., van Etten I., Hebeero G., Suijterhuijk R.,			
RA	Beijersbergen R., Geurts van Kessel A., Mooleenaar W.H.;			
RT	"Cloning," expression and chromosomal localization of a new putative			

RT		receptor-like protein tyrosine phosphatase.";	
RL	FEB8 Lett.	290:123-130(1991).	
CC	-I-	FUNCTION: MAY PLAY A KEY ROLE IN SIGNAL TRANSDUCTION AND GROWTH CONTROL.	
CC	-I-	CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein tyrosine + phosphate.	
CC	-I-	SUBCELLULAR LOCATION: Type I membrane protein.	
CC	-I-	TISSUE SPECIFICITY: MOST ABUNDANT IN LUNG, LESS IN BRAIN AND HEART.	
CC	-I-	SIMILARITY: CONTAINS 1 MAM DOMAIN.	
CC	-I-	SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.	
CC	-I-	SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.	
CC		This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb.ch/announce/or_send_an_email_to_license@isb-sib.ch).	
CC	EMBL:	X58287; CAA41225.1; -.-----	
DR	PfR:	S16701, S16701.	
DR	HSP:	P28627; IRP.	
DR	MGD:	MG1:102694; PCPrm.	
DR	InterPro:	IPR003961; FN_III.	
DR	InterPro:	IPR003962; FNIII_repeat.	
DR	InterPro:	IPR003599; Ig.	
DR	InterPro:	IPR003006; IG_MHC.	
DR	InterPro:	IPR000998; MAM_domain.	
DR	InterPro:	IPR000387; TYR_Phosphatase.	
DR	pfam:	PF00044; fn3; 3.	
DR	pfam:	PF00047; Ig; 1.	
DR	pfam:	PF00102; Y-phosphatase; 2.	
DR	pfam:	PF00629; MAM; 1.	
DR	PRINTS:	PR00014; ENTPEIT.	
DR	PRINTS:	PR00020; MAMDMAIN.	
DR	PRINTS:	PR00700; PRYPHPTASE.	
DR	SMART:	SM00409; FN3; 2.	
DR	SMART:	SM00409; IG; 1.	
DR	SMART:	SM00137; MAM; 1.	
DR	SMART:	SM00194; PTPC; 2.	
DR	PROSITE:	PS00383; TYR_PHOSPATASE_1; 2.	
DR	PROSITE:	PS00036; TYR_PHOSPATASE_2; 2.	
DR	PROSITE:	PS00055; TYR_PHOSPATASE_PNP; 2.	
DR	PROSITE:	PS00740; MAM_1; 1.	
DR	PROSITE:	PS0060; MAM_2; 1.	
KW	Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane; Immunoglobulin domain; Repeat.		
FT	SIGNAL	1..20	POTENTIAL.
FT	CHAIN	21..1452	PROTEIN-TYROSINE PHOSPHATASE MU.
FT	DOMAIN	21..742	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	743..764	POTENTIAL.
FT	DOMAIN	765..1452	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	22..184	MAM.
FT	DOMAIN	199..267	IG-LIKE C2-TYPE DOMAIN.
FT	DOMAIN	287..374	FIBRONECTIN TYPE-III 1.
FT	DOMAIN	383..466	FIBRONECTIN TYPE-III 2.
FT	DOMAIN	486..571	FIBRONECTIN TYPE-III 3.
FT	DOMAIN	589..671	FIBRONECTIN TYPE-III 4.
FT	DOMAIN	923..1153	PROTEIN-TYROSINE PHOSPHATASE 1.
FT	DOMAIN	1213..1447	PROTEIN-TYROSINE PHOSPHATASE 2.
FT	ACT_SITE	1095..1095	BY SIMILARITY.
FT	ACT_SITE	1389..1389	BY SIMILARITY.
FT	DISULFID	206..260	POTENTIAL.
FT	CARBOHYD	72..72	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	92..92	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	131..131	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	249..249	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	406..406	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	414..414	N-LINKED (GLCNAC. .) (POTENTIAL).


```

DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein-tyrosine phosphatase mu precursor (EC 3.1.3.48) (R-PTP-mu).
GN PTPRM OR PTPRL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=92008644; PubMed=1655529;
RA Gebbink M.F.B.G., van Etten I., Hateboer G., Suijverduijk R.,
RA Beijersbergen R., Geurts van Kessel A., Mooleenaar W.H.;
RA "Cloning, expression and chromosomal localization of a new putative
RA receptor-like protein tyrosine phosphatase.";
RL FEBS Lett. 290:123-130(1991).
RN (2)
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 879-1156.
RX MEDLINE=96010572; PubMed=9346878;
RA Hofmann K.M., Tonks N.K., Barford D.;
RA "The crystal structure of domain 1 of receptor protein-tyrosine
RA phosphatase mu.";
RL J. Biol. Chem. 272:27505-27508(1997).
CC -1- FUNCTION: MAY PLAY A KEY ROLE IN SIGNAL TRANSDUCTION AND GROWTH
CC CONTROL.
CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2O) -> protein
CC tyrosine + phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: CONTAINS 1 MAM DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.
CC -----
CC CC THE SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL, X58288, CAA41226.1; -.
DR PIR, S17669, S17669.
DR PDB, IRPM; 01-APR-98.
DR Genew; HGNC:9675; PPRM.
DR MIM; 176888; -.
DR InterPro: IPR0033961; FN_III.
DR InterPro: IPR0033962; FN_III_repeat.
DR InterPro: IPR003599; I9.
DR InterPro: IPR003006; I9_MHC.
DR InterPro: IPR000998; MAM_domain.
DR InterPro: IPR000387; TYR_phosphatase.
DR InterPro: IPR000242; Tyr_PP.
DR Pfam; PF00041; fn3; 3.
DR Pfam; PF00047; I9; 1.
DR Pfam; PF00102; Y_phosphatase; 2.
DR Pfam; PF00629; MAM; 1.
DR PRINTS; PR00014; ENTPEPIL1.
DR PRINTS; PR00020; MAMDOMAIN.
DR PRINTS; PR00700; PRTYPPHASE.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00409; IG; 1.
DR SMART; SM00137; PTPc; 2.
DR SMART; SM0194; PTPc; 2.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
DR PROSITE; PS00740; MAM_1; 1.
DR PROSITE; PS50060; MAM_2; 1.
DR Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane;
DR Immunoglobulin domain; Repeat; 3D-structure.
DR SIGNAL * 1 20 POTENTIAL.

```

FT	CHAIN	21	1452	PROTEIN-TYROSINE PHOSPHATASE MU.
FT	DOMAIN	21	742	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	743	764	POTENTIAL.
FT	DOMAIN	765	1452	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	22	184	MAM.
FT	DOMAIN	199	267	IG-LIKE C2-TYPE DOMAIN.
FT	DOMAIN	287	374	FIBRONECTIN TYPE-III 1.
FT	DOMAIN	383	466	FIBRONECTIN TYPE-III 2.
FT	DOMAIN	486	571	FIBRONECTIN TYPE-III 3.
FT	DOMAIN	589	671	FIBRONECTIN TYPE-III 4.
FT	DOMAIN	923	1153	PROTEIN-TYROSINE PHOSPHATASE 1.
FT	DOMAIN	1213	1447	PROTEIN-TYROSINE PHOSPHATASE 2.
FT	ACT_SITE	1095	1095	BY SIMILARITY.
FT	ACT_SITE	1389	1389	BY SIMILARITY.
FT	DISULFID	206	260	POTENTIAL.
FT	CARBOHD	72	72	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHD	92	92	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHD	131	131	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHD	249	249	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHD	406	406	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHD	414	414	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHD	454	454	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHD	534	534	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHD	544	544	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHD	598	598	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHD	651	651	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHD	681	681	N-LINKED (GLCNAC. . .) (POTENTIAL).
SO	SEQUENCE	1452 AA:	163633 MW; 081750359CA6C7E0 CRC64.	

Alignment Scores:			
Pred. No.:	6,55e-71	Length:	1452
Score:	1306.00	Matches:	277
Percent Similarity:	61.59%	Conservative:	95
Best Local Similarity:	45.86%	Mismatches:	212
Query Match:	20.27%	Indels:	20
DB:	1	Gaps:	11
US-09-743-492-1 (1-3467) x PTPM_HUMAN (1-1452)			
QY	27	GCCACCTCCTGTGACCCCTGGAGATCGGAGCTCAACTACCAAGCCCGAGTATGCCA	86
DB	858	SeRHsIRhYrLYsLYsALrGluPrAlAspAlrPrGrYGLnThrLYGLnLeu---	876
QY	87	GACCACCCACCCATCCCATATCCATATCCAGCGATGCGGAGCAACATGACGGCCCAAGCCAC	146
DB	877	---HsPrAlAlIleALrGVALAlAspLeuLcUlnIsIleHrGlnMeLYsCYsAlA	895
QY	147	GATGCCCTCAAGTTCTCCACGAGATATGATCCATGCACCCCTGGACAGCAAGTTACAGCTG	206
DB	896	GInGLYrLYrGLyPheLYsGInGLYrGLuLYsErPhehGInGLYnSerAlrPrOTrP	915
QY	207	GAGATTTCAACCTGGAGAGTGAACAACCCCAAGACCGCATGCAGATGCATCGGCTAC	266
DB	916	AspSerAlAlsLYsAspGluAsnAlrGlyMetLYsAsnAlrGlyrGLnIleAlrLY	935
QY	267	GACCATCTGCAGTCATCCTTAACTCTATGCATGGCGCTCCCGGAGTCACTACATCAT	326
DB	936	AspHisSerArGVALArGLcGInThrILeGInGLYAspHrAsnSerAspTYrILeAsn	955
QY	327	GCCAACTCATCGATGGTGTACCGGACAGACAGATCCCTACATCGCCAGCGAGGCCCTG	386
DB	956	GLYsAsnTYrILeAspGLYrLYrHIsArGPrAsnHIsTYrILeAlrHrGInGLYrPrOMeT	975
QY	387	CCCGAGACCATGGCGATTTCTGGAGANTGGTGGGACAGCGCCACGGCCACTGTGTGTC	446
DB	976	GInGLYrHrILeTYrAspPheTrPArGMeTVALrPrILsGInAsnThrAlAsrILeAlr	995
QY	447	ATGATGACACGGCGTGGAGAGCAAAATCCCGGGTAAATGTGATAGTACAGTCCGACGCCCT	506
DB	996	MeTVALrHrAsnLeuVALrGLVALrGLYrVALrLYsCYsLYsTYrTrPrO---Asp	101
QY	507	GGCACCGAGACCTGTGGCTTATTCCTATTCAGTACAGCTGTGTGGACAGTGGAGCTGGCCACA	566

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Db 1015 AsptHgluiletyrLysaspIleLysValThrLeuIleGluThrGluLeuLeuAlaGlu 1034
Oy 567 TACACGTGGCGACCTGGACATCCACAAGACTGGCTCCAGTGAAGAGCTGAGCTGGT 626
Db 1035 TyrValIleArgThrPheAlaValAluLysArgValHisGluIleArgGluIleArg 1054
Oy 627 CAGTTTCATTCATGGCTGGCCAGACCATGGATGCTTCATGATCCACCACTCCATCCG 686
Db 1055 GluPheHisPheThrGlyTyrProAspHisGlyValProTyrHisAlaThrGlyLeuLeu 1074
Oy 687 GCCTTCACAGAGGGGTGAAGGCTGCACCCCTAGACGAGGGCCCATGGTGGTGCAC 746
Db 1075 GlyPheValArgGluValLysSerLysSerProPheSerAlaGlyProLeuValAlaHis 1094
Oy 747 TGCACCGGGGGGTGGGGCCGACCGGCTTCATCGTGTGATTCATGATCCATGTCGACGG 806
Db 1095 CysSerAlaGlyAlaGlyArgThrGlyCysPheIleValIleAspIleMetLeuAspMet 1114
Oy 807 ATGAGACGACGAGAGAGCATGTGACATGTGACGACCTGCATCGATGCACACAGAG 866
Db 1115 AlaGluArgGluGlyValAlaAspIleTyrAsnCysValArgGluLeuArgSerArgArg 1134
Oy 867 AACTACATGATGTCACAGCAGGAGCCAGTACGTTCATCCATGAGCGCTGCTGGAGGCT 926
Db 1135 ValAsnMetValGlnThrGluGluGlnIleTyrValPheIleHisAspAlaIleLeuGluAla 1154
Oy 927 GCCACGTCCGGCCACACAGAGGTGCTGCC-----CGCACCTGTATGCCACATC 977
Db 1155 CysLeuCysGlyAspThrSerValProAlaSerGlnValArgSerLeuTyrArgAspMet 1174
Oy 978 CAGAAAGCTGGGGCAGAGTCCCTCCAGGGAGAGTGTGAGCGGCATGAGACTGACGTCAAG 1037
Db 1175 AsnLysLeu-----AspProGlnThrAsnSerSerGlnIleLeuGluIleHisArg 1191
Oy 1038 TTGCTG-----GCCAGCTCCAGAGCCACAGTCCCGCTTCATGAGGCGCAACCTGGCC 1091
Db 1192 ThrLeuAsnMetValThrProThrLeuArgValGluAspCysSerIleAlaLeuLeuPro 1211
Oy 1092 TGCACAGAGTTCACAGACCGGCTGTGTACATCATGCCCCCTACAGATTCGACCCGTGTGT 1151
Db 1212 ArgAsnHisGluLysAsnArgCysMetAspIleLeuProProAspArgCysLeuProPhe 1231
Oy 1152 CTGCAGCCCATCCGGTGGTGGAGGGCTGTGACTACATCATGCCCCCGCTCCGTGGATGGT 1211
Db 1232 LeuIleThrIleAspGly---GluSerSerAsnTyrIleAsnAlaIleLeuMetLysPhe 1250
Oy 1212 TATAGACAGCAGAAAGCCTACATGCTACACAGGGGCTGTGCAGAGAGCAGCAGAGAC 1271
Db 1251 TyrLysGlnProSerAlaPheIleValThrGlnHisProLeuProAsnThrValLysAsp 1270
Oy 1272 TTTCGGCCCATGCTATGGGAGACACATTCACCATCATCGTCATGCTCAACAGCTTGGG 1331
Db 1271 PheThrPArgLeuValLeuAspTyrHisCysThrSerValIleMetLeuAsnAspValAsp 1290
Oy 1332 GAGATGGCGAGGAGAAATGCACACACTGAGTGGCA-----GCAGAGGGCTCTGCT 1382
Db 1291 Pro-----AlaGlnLeuCysProGlnTyrTrpProGluAsnGlyValHisIleHisGly 1308
Oy 1383 CGTACACAGTACTTGTGTGTGACCCGATGGCTGATGATCAACATGCCAGATATTCCTG 1442
Db 1309 ProIleGlnValGluPheValSerAlaAspLeuGluGluAlaIleSerArgIlePhe 1328
Oy 1443 CGTGAAGTTCAGAGGTACCGATGCCGGATGGGAGTCAAGAGACATCCGGCAGTTCCAG 1502
Db 1329 ArgIleTyrAsnAlaAlaArgProGlnAspGlyTyr---ArgMetValGlnGlnPheGln 1347
Oy 1503 TTCACAGAGTGGCA---GAGCAGGGGCTGCCCAAGACGAGCGAGGATTCATGACTTC 1559
Db 1348 PheLeuGlyTrpPrometTyrArgAspThrProValSerLysArgSerPheLeuLysLeu 1367
Oy 1560 ATCGGGCAGGTGATACAGACCAAGAGCAGT---GGACAGCAGATGGCTATACAGGTG 1616
Db 1368 IleArgGlnValAlaAspLysTyrPheGlnGluIleTyrAsnGlyGlyGlyProThrValVal 1387

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Oy 1617 CACTGCAGTGTGGGCTGGGCGCCGACCGGGGCTTCATCATCTGACATGCTCTGGAG 1676
Db 1388 HisCysLeuAsnGlyGlyValArgSerGlyThrPheCysAlaIleSerIleValCysGlu 1407
Oy 1677 CGCATGCGGTATGAGGGCGCTGCAGCATGTTCAGACCGTGAAGACCCCTGGCTACAG 1736
Db 1408 MetLeuAlaGlnHisGlnArgThrValAspValPheHisAlaValLysThrLeuArgAsnAsn 1427
Oy 1737 CGTCTGCCATGTCACAGACAGAGCAAGTACATGAGCTGTGCTACCGTGGCCCTGGAG 1796
Db 1428 LysProAsnMetValAspLeuLeuAspGlnTyrLysPheCysTyrGlyValAlaLeuGlu 1447
Oy 1797 TACCTGGCGACG 1808
Db 1448 TyrLeuAsnSer 1451

RESULT 11
PTPK_HUMAN
ID PTPK_HUMAN STANDARD: PRT: 1439 AA.
AC Q15262; Q14763;
DT 01-NOV-1997 (Rel. 35, Created)
DR 01-NOV-1997 (Rel. 35, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein-tyrosine phosphatase kappa precursor (EC 3.1.3.48) (R-PTP-
DE kappa).
GN PTPRK OR PTPK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=96279245; PubMed=8663237;
RX Fuchs M., Mueller T., Lerch M., Ullrich A.;
RT "Association of human protein-tyrosine phosphatase kappa with members
RT of the armadillo family.";
RL J. Biol. Chem. 271:16712-16719(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA TISSUE=ForeSkin;
RX MEDLINE=97199372; PubMed=9047348;
RA Yang Y., Gil M.C., Choi E.Y., Park S.H., Pyun K.H., Ha H.;
RT "Molecular cloning and chromosomal localization of a human gene
RT homologous to the murine R-PTP-kappa, a receptor-type protein
RT tyrosine phosphatase.";
RL Gene 186:77-82(1997).
CC -!- FUNCTION: REGULATION OF PROCESSES INVOLVING CELL CONTACT AND
CC ADHESION SUCH AS GROWTH CONTROL, TUMOR INVASION, AND METASTASIS.
CC FORMS COMPLEXES WITH BETA-CATENIN AND GAMMA-CATENIN/PLAKOGLOBIN.
CC BETA-CATENIN MAY BE A SUBSTRATE FOR THE CATALYTIC ACTIVITY OF PTP-
CC KAPPA.
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN; AT ADHERENS
CC JUNCTIONS.
CC -!- TISSUE SPECIFICITY: HIGH LEVELS IN LUNG, BRAIN AND COLON; LESS IN
CC LIVER, PANCREAS, STOMACH, KIDNEY, PLACENTA AND MAMMARY CARCINOMA.
CC -!- PTM: THIS PROTEIN UNDERGOES PROTEOLYTIC PROCESSING.
CC -!- SIMILARITY: CONTAINS 1 MAM DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -!- SIMILARITY: CONTAINS 4 FIBROBLASTIN TYPE III-LIKE DOMAINS.
CC -!- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.
CC -!- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; 270660; CAA94519.1; -.

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DR	EMBL; U7786; AAC37599.1; -	
DR	HSSP; P28827; 1RPM.	
DR	Genew; HGNC:9674; PTPRK.	
DR	MIM; 602545; .	
DR	InterPro; IPRO003961; FN_III.	
DR	InterPro; IPRO03962; FnIII_repeat.	
DR	InterPro; IPRO03599; Ig.	
DR	InterPro; IPRO003006; Ig_MHC.	
DR	InterPro; IPRO00998; MAM_domain.	
DR	InterPro; IPRO00387; Tyr_phosphatase.	
DR	Pfam; PF00041; fn3; 2.	
DR	Pfam; PF00047; igf; 1.	
DR	Pfam; PF00102; Xphosphatase; 2.	
DR	Pfam; PF00629; MAM; 1.	
DR	PRINTS; PR00014; ENTYEIII.	
DR	PRINTS; PR00020; MAMDMAIN.	
DR	PRINTS; PRO0700; PTYPHPTASB.	
DR	SMART; SM00060; FN3; 2.	
DR	SMART; SM00409; IG; 1.	
DR	SMART; SM00137; MAM; 1.	
DR	SMART; SM00194; PTPC; 2.	
DR	PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.	
DR	PROSITE; PSS0056; TYR_PHOSPHATASE_2; 2.	
DR	PROSITE; PSS0055; TYR_PHOSPHATASE_PTP; 2.	
DR	PROSITE; PS00740; MAM_1; 1.	
DR	PROSITE; PSS0060; MAM_2; 1.	
KM	Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane; Immunoglobulin domain; Repeat.	
FT	SIGNAL	1
FT	CHAIN	27
FT	DOMAIN	27
FT	TRANSLEM	753
FT	DOMAIN	775
FT	DOMAIN	31
FT	DOMAIN	209
FT	DOMAIN	297
FT	DOMAIN	393
FT	DOMAIN	494
FT	DOMAIN	597
FT	DOMAIN	910
FT	DOMAIN	1200
FT	ACT_SITE	1082
FT	ACT_SITE	1376
FT	DISULFID	216
FT	SITE	641
FT	CARBOHYD	101
FT	CARBOHYD	140
FT	CARBOXYD	211
FT	CARBOXYD	416
FT	CARBOXYD	424
FT	CARBOXYD	436
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FT	CARBOXYD	552
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FT	CONFLICT	9
FT	CONFLICT	158
FT	CONFLICT	284
FT	CONFLICT	422
FT	CONFLICT	672
FT	CONFLICT	715
FT	CONFLICT	732
FT	CONFLICT	1366
SO	SEQUENCE	1439 AA; 162087 MW;
Alignment Scores:		
Pred. No.:	7,45e-68	Length: 1439
Score:	1255.00	Matches: 260
Percent Similarity:	62.59%	Conservative: 108
Best Local Similarity:	44.22%	Mismatches: 206

Query Match:	19.48%	IndeIs:	14
DB:	1	Gaps:	9
US-09-743-492-1 (1-3467) x PTPK_HUMAN (1-1439)			
OY	66	TACAGACCCGAGGTATGCAGAGACCACCCACCCCATCCCATCCAGCAGCTGGCGGCAAC	125
Db	858	TyrGlnThrGlyGlnLeu-----HisProAlaIleArgValAlaLaspPheLeuGlnHis	875
OY	126	ATCGAGCGCCCTCAAAGCCAAAGATGGCCCTCAAGTCTCCAGAGATGATGTCATGCAC	185
Db	876	IleAsnLeuMetLysThrSerAspSerTygIlyPheLysGluGlnIlyrGlnSerPhephe	895
OY	186	CCTGACACGACGCTCACGTGGAGGAATTCAACTGGAGTGTAACAAGCCCAAGAAGCCG	245
Db	896	GluGlyInserAlaSerTrpAspValAlaLysLysPoliAsnSnArGAlaLysAsnArg	915
OY	246	TATCGCATGTCTCATCGGCTCCAGACACCTCGAGTATCATCTTACCTTATCGATGGCGTC	305
Db	916	TyrGlyAsnIleIleAlaTyrrAspHisSerArgValIleLeuGlnProValGluAsp	935
OY	306	CCCCGAGTACTCATCATTCATGCCAATAATATGATGGCTACCGCAACAGATGCTTAC	365
Db	936	ProSerSerAspTyrIleAsnAlaAsnTyrIleAspIlyrGlnIlnArgProSerHnIlyr	955
OY	366	ATCCGACGACGAGGCGCCCTGCCGACACCATGGAGATTTCTGGAGATGTGGGAA	425
Db	956	IleAlaThrGlnGlyProValHisGluThrValTyrrAspHetrArgmetIleTrpGln	975
OY	426	CAGGCGACGCGCACTGTGTATGATGATGACAGGCTGGAGAGAAAGTCCCGGTAATGT	485
Db	976	GluGlnSerAlaCysIleValMetValThrAsnLeuValGluValAlaLyrrArgValLysCys	995
OY	486	GATGATCATGGCGGCGGCGCGGAGCGGACCGTGGCGCTTATGAGGTAGCCGCTTG	545
Db	996	TyrrLysTyrrTrpPro---AspAprThrGlnValTyrrIleLysPheLysValIlnThrcysVal	1014
OY	546	GACACAGTGGAGCTGGGCGGCACATACACTGTGCGGCACTTGCATCCCAAGATGGCTCC	605
Db	1015	GlnMetGluProLeuAlaGluTyrrValValAlaArgThrPheHnIleuGlnArgArgIlyr	1034
OY	606	AGTAGAAGCGTGAAGTGGCGCTCAAGTTCATGTCATGGCCCTGGCCAGACCATGAGTCTT	665
Db	1035	AsnGluIleArgGluValLysGlnPheHisPheThcIlyrProAspHisCylValPro	1054
OY	666	GAGTACCCCAATCCCAATCCCAATCCCGCTTCTCGACAGGCGTCAAGGCCGTGCACCCCTAAC	725
Db	1055	TyrrHisAlaThrGlyIleuLeuSerPheIleArgValIlysLeuSerSnProProser	1074
OY	726	GCAGGAGCCCATGGTGTGGTGCATCGACAGCGGCGGTGGCGGCACCGGTGCTTCATCTG	785
Db	1075	AlaGlyProIleValHisLysSerAlaGlyAlaGlyArgHnIlyrHnIlyrStryrIleVal	1094
OY	786	ATTGATGCCATGTTGGAGCGGATGAGACACGAGAGACGGTGGACATCTATGGCCAGTG	845
Db	1095	IleAspIleMetLeuAspMetAlaGluArgGluGlyValValAspIleTyrrAsncysVal	1114
OY	846	ACCTGCATGCATACAGAGAGAACTACATGTCAGACGCGAGGACAGACAGTACGGTTCATC	905
Db	1115	LysAlaLeuArgSerAlaArgIleAsnMetValGlnThrGluGlnIlyrIlePheIle	1134
OY	906	CATGAGGCGCTGTGAGGCTGCCACGCTGGCGGCACACAGAGGTGCTCCCGCAACCTG	965
Db	1135	HisAspAlaIleLeuGlnIlaCysLysCysGlyGluThrAlaIlePheValCysGluPhe	1154
OY	966	TATGCCCATTCACAGAAAGCTGGGCCAAGTCCCTTCACAGGGAGAGTGTACCCCATGGAG	1022
Db	1155	LysAlaIlaIlyrPheAspMetIleArgIleAspSerGlnThrAsnSerHisLysLys	1174
OY	1026	CTCGAGTTTCAGTGTGGGGCCAGC-----TCCAAAGCCCAACGTCGCCGTTCAACAGC	1072
Db	1175	AspGluPheGlnThrLeuAsnSerValThrProArgLeuGlnAlaGluAspCysSerIle	1196


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FT ACT_SITE 1394 1394 BY SIMILARITY.
FT DISULFID 215 269 POTENTIAL.
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 139 139 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 210 210 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 415 415 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 423 423 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 435 435 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 551 551 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 585 585 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 589 589 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 606 606 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 689 689 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1457 AA; 164185 MW; 19D4B99B7E0E8605 CRC64;

Alignment Scores:
Pred. No.: 3 91e-67 Length: 1457
Score: 1243.00 Matches: 261
Percent Similarity: 61.95% Conservative: 107
Best Local Similarity: 43.94% Mismatches: 206
Query Match: 19.29% Indels: 20
DB: 1 Gaps: 10

US-09-743-492-1 (1-3467) x PTPK_MOUSE (1-1457)
QY 66 TACGAGACCCGAGTATCGAGACCCACCACCATCCCATCCGAGACCTGCGGACAAAC 125
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 870 TyrglnThrGlnGlnLeu-----HisProAlaIleArgValAlaAspLeuLeuInHis 887
QY 126 ATCGAGCCCTCAAGCCAGCATGCGCTCAAGTTCTCCCGAGAGTATGATCGATCGAC 185
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 888 IleasnLeuMetLysThrSerAspSerTyrgLysGlnGlnTyrgLysSerPhePhe 907
QY 186 COTGACACGAGTTCGAGGAGAAATTCAAACCTGAGAGTGAACAGCCCAAGCAACGCC 245
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 908 GlnGlnGlnSerAlaSerThrAspAlaLysLysAspGlnAsnAspAlaLysAsnArg 927
QY 246 TATGCGAATGTCATCGCTAGCAGCAGCAGCTGAGTATCTTACCTATGATGATGCGCTC 305
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 928 TyrgLysnIleIleAlaTyrgLysPheSerArgValIleLeuGlnProValGlnAsp 947
QY 306 CCCGGAGTACTACATCAATGCCACTACATC-----GATGGCTAC 347
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 948 ProSerSerAspTyrgLysnAlaAsnLysnIleAspIleTrpLeuTyrgAspLysTyrg 967
QY 348 CGCAGACGAAATGCTTACATCGCCAGCGAGGCCCTGCGCGAGACCATGGCGCATTC 407
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 968 GlnArgProSerHisTyrgLysnIleAlaThrGlnGlnProValHisGlnIleValTyrgAspPhe 987
QY 408 TGGAGATGATGTGGGAACAGCGCAGCGCAGCTGTGATGATGACAGCGCTGGAGAG 467
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 988 TrpArgMetValTrpGlnGlnGlnSerAlaCysIleValMetValThrAsnLeuValGln 1007
QY 468 AAGTCCGGGTTAAATGTGATCATGACTGGCCAGCCCTGGCAGCCGAGACCTGTGGCTT 527
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1008 ValGlnArgValLysCysTyrgLysTyrgPro---AspAspThrGlnValTyrgLysAsp 1026
QY 528 ATTGAGGAGCCCTGTGTGACACAGTGGAGCCACATGAGTGGCGGCGGCGCATTCGA 587
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1027 PheLysValThrCysValGlnMetLeuProLeuAlaGlnTyrgValAlaThrPheThr 1046
QY 588 CTCACAGAGTGGCTCCAGTGAAGAGCGTGAAGTTCGCTCAAGTTTCATGCTGAGCGCTG 647
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1047 LeuGlnArgValGlyTyrgAsnGlnIleArgValLysGlnPheHisPheHisLeuThr 1066
QY 648 CCAAGCATGAGATTCTGAGTACCAACTCCATCTGCGCTTCTGACAGCGGCTCAAG 707
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DB 1067 ProAspHisGlyValProTyrgHisAlaThrGlyLeuLeuSerPheIleAlaArgValLys 1086
QY 708 GCGTCGACACCGCCATGAGCGGCGCATGGTGCACATGAGGCGGCGGCGGCGCGC 767
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1087 LeuSerAsnProProSerAlaGlyProIleValValHisCysSerAlaGlyAlaGlyArg 1106

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QY 768 ACCGCGCTGCTCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 827
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DB 1107 ThrGlyCysTyrgLysIleValIleLeuIleLeuIleLeuIleLeuIleLeuIleLeuIle 1126
QY 828 GACATCTATGAGCGAGTGAATGCTGATGATGATGATGATGATGATGATGATGATGATGAT 887
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1127 AspIleTyrgAsnCysValLysAlaLeuArgSerArgValIleAsnMetValIleThrGln 1146
QY 888 GACCATGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 947
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1147 GlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 1166
QY 948 GTGCTGCGCCGACCACTGTATGCCACATCCAGAACTGGGCGGCGGCGGCGGCGGCGG 1007
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1167 IleProValCysGlnPheLysAlaAlaTyrgLysPheAspMetIleArgIleAspSerGlnThr 1186
QY 1008 AGTGTGACCCCATGAGTGAAGTTCATGATGATGATGATGATGATGATGATGATGATGATGAT 1061
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1187 AsnSerSerHisLysLysAspGlnPheGlnThrLeuAsnSerValThrProArgLeuGln 1206
QY 1062 ACGTCCCGCTCATGAGCGCCCAACCTGCGCTGCAACAAAGTTCAAGACCGGCTGCGTGAAC 1121
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1207 AlaGlnAspCysSerIleAlaCysLeuProArgAsnHisAspLysAsnArgPheMetLysP 1226
QY 1122 ATCATGCGCTTACGAATTCACCCGCTGTGTCTGACAGCCCATCTGTGTGAGGAGCTCT 1181
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1227 MetLeuProProAspArgCysLeuProPheLeuIleThrIleAspGly---GlnSerSer 1245
QY 1182 GACTCATCATGATGACAGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1241
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1246 AsnTyrgLysnAlaAlaLeuMetAspSerTyrgLysGlnProAlaAlaPheIleValThr 1265
QY 1242 CAGGGGCGCTGCGCAGAGAGCAGCAGCAGCTGCGCGCATGATGAGGAGCAATTC 1301
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1266 GlnTyrgProLeuProAsnThrValLysAspPheThrPheValLeuValTyrgLys 1285
QY 1302 ACCATCATGCTCATGCTGACCAAGCTTGGGAGATGGGAGGAGAGAAATGCCACAGATAC 1361
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1286 ThrSerIleValMetLeuAsnGlnValAspLeu-----SerGlnGlyCysProGlnTyrg 1303
QY 1362 TGGCCAGCAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1415
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1304 TrpProGlnGlnGlnGlnMetLeuArgTyrgLysProIleGlnValGlnCysMetSerCysSer 1323
QY 1416 ---GAGTCAACATGATCCCGAGTATCCGCTGAGTTCAGATGATGATGATGATGATGATGAT 1472
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1324 MetAspCysAspValIleAsnArgIlePheArgIleCysAsnLeuThrArgProGlnGln 1343
QY 1473 GGGCAGTCAAGGACATCCGCGCAGTTCAGATTCACAGACTGG---CGAAGCAGGCGGTG 1529
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1344 GlyTyrg---LeuMetValGlnGlnPheGlnTyrgLysIleTrpLysSerHisArgGlnVal 1362
QY 1530 CCCAAGACAGGAGGAGGATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 1589
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1363 ProGlySerLysArgSerPheLeuLysLeuIleLeuGlnValGlnIleTrpLysGln 1382
QY 1590 TTTGAGCAG---GATGGCGCTATCACGGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 1646
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1383 CysGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 1402
QY 1647 GTTTCATCACTGATGAGATGCTCTGAGAGCGCATGAGCGCTATGAGGCGGCTGTGATGAT 1706
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1403 MetPheCysAlaIleGlyIleValValGlnMetValLysArgGlnAsnValAlaAspVal 1422
QY 1707 TTTGAGACCGTGAAGACCTGCGTACACAGCCTCTGCGCATGCTGTCACAGACAGACAG 1766
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1423 PheHisAlaValLysThrLeuArgAsnSerLysProAsnMetValGlnAlaLeuProGlnGln 1442
QY 1767 TATCATGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1808
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DB 1443 TyrgArgPheCysTyrgAspValAlaLeuGlnIleValLeuGlnSer 1456

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RESULT 13
PRTG_HUMAN STANDARD; PRT; 1445 AA.
AC P23470; Q15623;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Protein-tyrosine phosphatase gamma precursor (EC 3.1.3.48) (R-PTP-
  gamma).
GN PTPRG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RX MEDLINE=93180796; PubMed=8382771;
RA Barnea G., Silvennoinen O., Shaanan B., Honegger A.M., Canoll P.D.,
RA D'Eustachio P., Morse B., Levy J.B., Laforgia S., Huebner K.,
RA Musacchio J.M., Sap J., Schlessinger J.;
RT "Identification of a carbonic anhydrase-like domain in the
RT extracellular region of PTP gamma defines a new subfamily of
RT receptor tyrosine phosphatases."
RL Mol. Cell. Biol. 13:1497-1506(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96429999; PubMed=8833149;
RA Kastury K., Ohta M., Lasota J., Molr D., Dorman T., Laforgia S.,
RA Druck T., Huebner K.;
RT "Structure of the human receptor tyrosine phosphatase gamma gene
RT (PTPRG) and relation to the familial RCC t(3;8) chromosome
RT translocation."
RL Genomics 32:225-235(1996).
RN [3]
RP SEQUENCE OF 836-1445 FROM N.A.
RX TISSUE-Placenta;
RC MEDLINE=91006018; PubMed=2170109;
RA Krueger N.X., Streuli M., Saito H.;
RT "Structural diversity and evolution of human receptor-like protein
RT tyrosine phosphatases."
RL EMBO J. 9:3241-3252(1990).
RN [4]
RP SEQUENCE OF 874-1118 AND 1175-1409 FROM N.A.
RX TISSUE-Brain;
RC MEDLINE=90384936; PubMed=2169617;
RA Kaplan R., Morse B., Huebner K., Croce C., Howk R., Ravera M.,
RA Ricca G., Jaye M., Schlessinger J.;
RT "Cloning of three human tyrosine phosphatases reveals a multigene
RT family of receptor-linked protein-tyrosine-phosphatases expressed in
RT brain."
RL Proc. Natl. Acad. Sci. U.S.A. 87:7000-7004(1990).
CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC -1- TISSUE SPECIFICITY: FOUND IN A VARIETY OF TISSUES. IT IS
CC DEVELOPMENTALLY REGULATED IN THE BRAIN (BY SIMILARITY).
CC -1- SIMILARITY: IN THE N-TERMINAL SECTION, BELONGS TO THE EUKARYOTIC-
CC TYPE CARBONIC ANHYDRASE FAMILY.
CC -1- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L09247; AAA60224.1; -
CC EMBL; U46116; AAC50439.1; -
CC EMBL; U46089; AAC50439.1; JOINED.
CC EMBL; U46090; AAC50439.1; JOINED.

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DR EMBL; U46091; AAC50439.1; JOINED.
DR EMBL; U46092; AAC50439.1; JOINED.
DR EMBL; U46093; AAC50439.1; JOINED.
DR EMBL; U46094; AAC50439.1; JOINED.
DR EMBL; U46095; AAC50439.1; JOINED.
DR EMBL; U46096; AAC50439.1; JOINED.
DR EMBL; U46097; AAC50439.1; JOINED.
DR EMBL; U46098; AAC50439.1; JOINED.
DR EMBL; U46099; AAC50439.1; JOINED.
DR EMBL; U46100; AAC50439.1; JOINED.
DR EMBL; U46101; AAC50439.1; JOINED.
DR EMBL; U46102; AAC50439.1; JOINED.
DR EMBL; U46103; AAC50439.1; JOINED.
DR EMBL; U46104; AAC50439.1; JOINED.
DR EMBL; U46105; AAC50439.1; JOINED.
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DR EMBL; U46107; AAC50439.1; JOINED.
DR EMBL; U46108; AAC50439.1; JOINED.
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DR EMBL; U46115; AAC50439.1; JOINED.
DR EMBL; X54132; CAA38067.1; -
DR PIR; S12051; S12051.
DR HSSP; P18052; TYRO.
DR Genew; HGNC:9671; PTPRG.
DR MIM; 176886; -.
DR InterPro: IPR001148; Euk_Coanhd.
DR InterPro: IPR003961; FN_TIT.
DR InterPro: IPR000387; Tyr_phosphatase.
DR InterPro: IPR00242; Tyr_PP.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF00102; Y_phosphatase; 2.
DR Pfam; PF00194; carb_anhydrase; 1.
DR PRINTS; PR00700; PRTYPHPTASE.
DR PRODOM; PD000865; Euk_Coanhd; 1.
DR SMART; SM00060; FN3; 1.
DR SMART; SM00194; PTPG; 2.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
KW Glycoprotein; Transmembrane; Hydrolyase; Phosphorylation; Repeat;
KW signal.
FT SIGNAL 1 19
FT CHAIN 20 1445
FT DOMAIN 737 762
FT TRANSMEH 737 762
FT DOMAIN 763 1445
FT DOMAIN 347 322
FT DOMAIN 347 441
FT DOMAIN 869 1125
FT DOMAIN 1126 1445
FT ACT_SITE 1060 1060
FT SITE 1351 1351
FT CARBOHYD 109 109
FT CARBOHYD 113 113
FT CARBOHYD 156 156
FT CARBOHYD 359 359
FT CARBOHYD 444 444
FT CARBOHYD 619 619
FT CARBOHYD 631 631
FT CARBOHYD 722 722
FT CONFLICT 80 80
FT CONFLICT 92 92
FT CONFLICT 549 549
FT CONFLICT 756 756
FT CONFLICT 1407 1407
SQ SEQUENCE 1445 AA; 162058 MW; 350FB9D0C94E80BD CRC64;

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Alignment Scores:

RA	Bathnea G., Silvennoinen O., Shaanin B., Honegger A.M., Canoll P.D., D'Eustachio J.P., Morse B., Levy J.B., Latorgia S., Huebner K., Muscachio J.M., Sap J., Schlessinger J.;
RA	"Identification of a carbonic anhydrase-like domain in the extracellular region of RPPV gamma defines a new subfamily of receptor tyrosine phosphatases".
RL	Mol. Cell Biol. 13:1497-1506(1993).
CC	-1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2O) = protein tyrosine + phosphate.
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC	-1- TISSUE SPECIFICITY: DETECTED IN BRAIN, LUNG, KIDNEY, HEART, LIVER, SKELETAL MUSCLE, SPLEEN AND TESTES. IT IS DEVELOPMENTALLY REGULATED IN THE BRAIN.
CC	-1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE EUKARYOTIC- TYPE CARBONIC ANHYDRASE FAMILY.
CC	-1- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS. -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
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CC	-----
DR	EMBL: L09562; AAA40022.1; .
DR	PIR: B48148; B48148.
DR	HSPSP, P18052; 1YFO.
DR	MGD; MG1:97814; PTPrg.
DR	InterPro: IPRO01148; Euk_Coanhd.
DR	InterPro: IPRO03961; FN_III.
DR	InterPro: IPRO00387; TYR_phosphatase.
DR	InterPro: IPRO00242; Tyr_BP.
DR	Pfam: PF00041; fn3; 1.
DR	Pfam: PF00102; Y-phosphatase; 2.
DR	Pfam: PF00194; carb_anhydrazse; 1.
DR	PRINTS: PR00700; PTYPHPTPHASE.
DR	Prodom: PD000865; Euk_Coanhd; 1.
DR	SMART: SMO0060; FN3; 1.
DR	SMART: SMO0194; PTPc; 2.
DR	PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
DR	PROSITE: PS50056; TYR_PHOSPHATASE_2; 2.
DR	PROSITE: PS50055; TYR_PHOSPHATASE_PMP; 2.
KW	Glycoprotein; Transmembrane; Hydrolase; Repeat; Signal. BY SIMILARITY.
FT	SIGNAL 1..19
FT	CHAIN 20..1442
FT	DOMAIN 20..733
FT	TRANSMEM 734..759
FT	DOMAIN 760..1442
FT	DOMAIN 56..322
FT	DOMAIN 347..441
FT	DOMAIN 866..1122
FT	DOMAIN 1123..1442
FT	ACT_SITE 1057..1057
FT	SITE 1348..1348
FT	CARBOHYD 109..109
FT	CARBOHYD 113..113
FT	CARBOHYD 156..156
FT	CARBOHYD 359..359
FT	CARBOHYD 444..444
FT	CARBOHYD 719..719
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Alignment Scores:

Pred. No.:	2,79e-62	Length:	1442
Score:	1162.00	Matches:	242
Percent Similarity:	57.05%	Conservative:	98
Best Local Similarity:	40.60%	Mismatches:	228
Query Match:	18.03%	Indels:	28
Gaps:	1	Gaps:	9

JS-09-743-492-1 (1-3467) x PTPG-MOUSE (1-1442)

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DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE LAR, leukocyte common antigen-related PROTEIN-TRANSMEMBRANE receptor
DE phosphotyrosine phosphatase.
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92278755; PubMed=1317540;
RA Yu Q., Lenardo T., Weinberg R.A.;
RT "The N-terminal and C-terminal domains of a receptor tyrosine
RT phosphatase are associated by non-covalent linkage.",
LL Oncogene 7:1051-1057(1992).
DR HSSP: P18057; IYPO.
DR InterPro: IPR003962; FNIII-repeat.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003958; IY_c2.
DR InterPro: IPR003600; IY_c1like.

DR InterPro: IPR003006; IQ_MHC.
 DR InterPro: IPR001005; Myb_DNA_binding.
 DR InterPro: IPR000387; Tyr_phosphatase.
 DR InterPro: IPR000242; Tyr_PP.
 DR Pfam: PF00041; fn3; 7.
 DR Pfam: PF00047; Ig; 3.
 DR Pfam: PF00102; Y_phosphatase; 2.
 DR PRINTS: PR00014; ENTPETII.
 DR PRINTS: PR00700; PRTYPPHPTASE.
 DR SMART: SM00060; FN3; 6.
 DR SMART: SM00408; IGC2; 2.
 DR SMART: SM00410; IG_Like; 1.
 DR SMART: SM00194; PTPC; 2.
 DR PROSITE: PS00037; MYB_1; UNKNOWN_1.
 DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 2.
 DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 2.
 DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 2.
 KW Hydroxylase; Immunoglobulin domain; Repeat.
 SQ SEQUENCE 1887 AA; 210453 MW; B84B33E7E4E70281 CRC64;

Alignment Scores:
 Pred. NO.: 1.23e-242 Length: 1887
 Score: 3192.00 Matches: 599
 Percent Similarity: 99.34% Conservative: 4
 Best Local Similarity: 98.68% Mismatches: 0
 Query Match: 49.53% Indels: 0
 DB: 11 Gaps: 0

US-09-743-492-1 (1-3467) x Q9QW67 (1-1887)

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QY 66 TACGAGCCCAAGGATGAGAGACACACCCATCCCATCCATCCAGGACCTGGGAGACAC 125
 DB 1301 TyrGlnThrProGluMetArgAspHisProProIleProIleThrAspLeuAlaAspHisn 1320

QY 126 ATCGAGCCCTCAAGACCAAGCATGCGCTCAAGTTCTCCAGAGATGATGCTCATCGAC 185
 DB 1321 IleGluArgLeuLeuAlaAsnAspGlyLeuLysPheSerGlnGluTyrGluSerIleAsp 1340

QY 186 CCTGACACGACGTTACGTTGGGAGAAATTCAACTGGAGGTGACACAGGCCCAAGACGCC 245
 DB 1341 ProGlyGlnGlnPheThrTrpGluAsnSerAsnSerGluValAsnLysProLysAsnArg 1360

QY 246 TATGAGATGTCATGCGCTACAGACACATCTGAGTCATCATCTTACCTATGATGCGCTC 305
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QY 366 ATCGCCACGACGAGGCCCTGGCCGACAGCATGGGCGATTTTGGAGAAATGCTGGGAA 425
 DB 1401 IleAlaThrGlnGlyProLeuThrProGluThrMetGlyAspPheTrpArgMetValTrpGlu 1420

QY 426 CAGCCACGCGCCACTGTGTATGATGACAGCGCTGGAGAGAAATCCCGGTAATAAATG 485
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 DB 1441 AspGlnTyrTrpProAlaArgGlyThrGluThrTyrGlyLeuIleGlnValThrIleVal 1460

QY 546 GACACAGTGGAGCTGGCCACATACACTGTGGCGACCTTGGCAGTCCACAGAGTGGCTTC 605
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QY 906 CATGAGGCGCTCTGGAGGCTGCCACGTCGCGCCACACAGAGGTGCTGCGCCGAACTG 965
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QY 1626 GCTGCGTGGGCGGACCGGGGTGTTCACTGAGAGCATGCTCTGGAGCGCATGGCC 1685
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QY 1686 TATGAGGCGGTGCGACATGTTTCAGACCGGGAAGACCTTCGTAACAGAGGCTCTGCC 1745
 DB 1841 TyrGluGlyValValAspMetPheGlnThrValLysThrLeuArgThrGlnArgProAla 1860

QY 1746 ATGGTCAGACAGAGACAGATATCACTGTCACCGTCGGCCCTGGAGTACCTGCGC 1805
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Db 1861 MeVtAlGlnThrGlnuSpGlnTyrGlnLeuCySTyrArgAlaAlaLeuGlnTyrLeuGly 1880
QY 1806 ACCTTGACCACTATGCAACG 1826
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Db 1881 SerPheAspHisTyrAlaThr 1887
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ID 09E017 PRELIMINARY: PRT; 1898 AA.
AC 09E017;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Tyrosine phosphatase LAR.
GN PTPFR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RX MEDLINE=2135493; PubMed=11241288;
RA Terzowski G., Jankowski A., Hendriks W.J.A.J., Rolink A.G.,
Kistelow P.;
RT "Within the hemopoietic system, LAR phosphatase is a T cell lineage-
specific adhesion receptor-like protein whose phosphatase activity
RT appears dispensable for T cell development, repertoire selection and
RT function.";
RT Eur. J. Immunol. 31:832-840(2001).
DR EMBL: AF300943; AAG40194.1; -;
DR HSP: P18052; 1YFO.
DR InterPro: IPR003962; FNIII_repeat.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003598; Ig_C2.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003595; PTPC_motif.
DR InterPro: IPR000387; Tyr_phosphatase.
DR InterPro: IPR00242; Tyr_Pp.
DR Pfam: PR00041; fn3; 7.
DR Pfam: PR00047; Ig; 3.
DR Pfam: PR00102; Y_phosphatase; 2.
DR PRINTS: PR00014; FNTPETII.
DR PRINTS: PR00700; PRTYRPHPTASE.
DR SMART: SM00600; FN3; 6.
DR SMART: SM00409; IG; 3.
DR SMART: SM00408; IGC2; 3.
DR SMART: SM00410; Ig_Like; 2.
DR SMART: SM00194; PTPC; 2.
DR SMART: SM00404; PTPC_motif; 2.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 2.
KW Hydrolase; Immunoglobulin domain; Repeat.
SQ SEQUENCE 1898 AA; 211504 MW; EFD48DD11B352A4A CRC64;

Alignment Scores:
Pred. No.: 2,7e-241 Length: 1898
Score: 3175.00 Matches: 595
Percent Similarity: 99.01% Conservative: 6
Best Local Similarity: 98.02% Mismatches: 6
Query Match: 49.27% Indels: 0
DB: 11 Gaps: 0

US-09-743-492-1 (1-3467) x 09E017 (1-1898)

QY 6 GGACGTGAAGACACTCTGTCGGCCCACTCTGACCTGTGGAGATGGCGAGCTCAAC 65
|||||
Db 1292 GlyLeuLysAspSerLeuLeuAlaHisSerAspProValGlnLueMetArgLysLeuAsn 1311

QY 66 TACCAGACCCAGGATATGGAGACCAACCCACCATCCCATCCAGCCGTGGGAGAAC 125
|||||
Db 1312 TyrGlnThrProGlnMetArgAspHisProProlLeuThrAspLeuAlaAspHis 1331
QY 126 ATCGAGCGCTCAAGAGCAACAGATGGCCATGTCCTCCAGAGATGAGTGCATGAC 185
|||||
Db 1332 IleGlnArgLeuLysAlaAsnAspGlyLeuLysPheSerGlnGlnTyrGlnSerIleAsp 1351
QY 186 CCTGGACAGCACTTCACGTGGGAGAAATTCAACCTGGAGGTGAACAAGCCCAAGACCGC 245
|||||
Db 1352 ProGlyGlnGlnPheThrTyrGlnAsnSerAsnSerGlnValAsnLysProLysAsnArg 1371
QY 246 TATGCCAATGTCATCGGCTTCAGACCACTCCGAGTATCTCTTCACCTATGATGGGTC 305
|||||
Db 1372 TyrAlaAspValIleAlaTyrAspHisSerArgValLeuLeuThrSerIleAspGlyVal 1391
QY 306 CCCGGAGTGACTATACATCAATGCCCACTCATGATGCTACCGCAAGCAAGATGCCCTAC 365
|||||
Db 1392 ProGlySerAspTyrIleAsnAlaAsnTyrIleAspGlyTyrArgLysGlnAsnAlaTyr 1411
QY 366 ATCGCCACGCGAGGCCCCCTGCCGAGACCATGGGCGATTTCGAGAAATGTGTGGAA 425
|||||
Db 1412 IleAlaThrGlnGlnProLeuProGlnTyrMetGlyAspPheThrArgMetValITrPGlu 1431
QY 426 CACGCGACGCGCACTGTGTCATGATGACACGGCTGGAGAGAAAGTCCGGTAAATGT 485
|||||
Db 1432 GlnArgThrAlaThrValAlaMetMetThrArgLeuGlnLysSerArgValLysCys 1451
QY 486 GATCAGTACGTGGCGAGCCCTGGCAGCAGACCTGTGGCTTATTCAGTGAGCCCTGTG 545
|||||
Db 1452 AspGlnTyrTrpProValArgGlyThrGlnThrTyrGlyLeuIleGlnValITrLeuVal 1471
QY 546 GACACAGTGAGCTGGCCACATGACACTGTGCGCACTTCGACATCCACAAGATGGCTCC 605
|||||
Db 1472 AspThrValGlnLeuAlaThrTyrThrMetArgThrPheAlaLeuHisLysSerGlySer 1491
QY 606 AGTGAGAAGCGTAGCGCTGCAGTTTCAGTTCATGGCTGGCCAGAACCTGAGTTCT 665
|||||
Db 1492 SerGlnLysArgGlnLeuArgGlnPheGlnPheMetAlaTrpProAspHisGlyValPro 1511
QY 666 GAGTACCACTGCCATCCATCGGCTTCGCTCTGAGAGGGTCAAGGCGTTCACACCCCTAGAC 725
|||||
Db 1512 GlnTyrProThrProIleLeuAlaPheLeuArgArgValLysAlaCysAsnProLeuAsp 1531
QY 726 GCAGGGCCCATGCTGTGTCACCTGACGCGCGGGCTGGGCCGCAACGGCTTCATCTG 785
|||||
Db 1532 AlaGlyProMetValValHisCysSerAlaGlyValGlnTyrArgThrGlyCysPheIleVal 1551
QY 786 ATTGATGCCCATGTTGGAGCGGATGAAGACACGAGAAGACGGTGGACATCTATGGCCACGTG 845
|||||
Db 1552 IleAspAlaMetLeuGlnLysGlyMetLysHisGlnLysThrValAspIleTyrGlnHisVal 1571
QY 846 ACCTGCATGCGATCACAGAGACTACATGTCGAGCGGAGGACCGCATCGATGTCATC 905
|||||
Db 1572 ThrCysMetArgSerGlnArgAsnTyrMetValGlnThrLysAspGlnTyrValPheIle 1591
QY 906 CATGAGCGCGTGTGGAGGCTGCGACGTGCGGCGACACAGAGGTGCTGCCGCCCACTGTG 965
|||||
Db 1592 HisGlnAlaLeuLeuGlnAlaAlaMetCysGlyHisThrGlnValLeuAlaArgAsnLeu 1611
QY 966 TATGCCCACTCCAGAAAGCTGGGCAAGTGCCTTCAGAGGAGAGTGTGACCGCCATGAG 1025
|||||
Db 1612 TyrAlaHisIleGlnLysLeuGlnValArgProProGlyLysLeuValITrAlaMetGln 1631
QY 1026 CTCGAGTCAAGTGTGGCGCACCTCCAAAGCCCAACGTCGCGTTCATCAGACGGCAAC 1085
|||||
Db 1632 LeuGlnPheLysLeuLeuAlaAsnSerLysAlaHisThrSerArgPheValSerAlaAsn 1651
QY 1086 CTCGCCCTGCAACAAGTTCAGAAACCGGCTGGTGAACATCATGCTACGAATGTACCCGT 1145
|||||
Db 1652 LeuProCysAsnLysPheLysAsnArgLeuValAsnIleMetProTyrGlnLeuThrArg 1671


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QY 1146 GTGTCTCTACAGCCATCCGCTGTGAGGCTGTACTACATCATGCCAGCTCTCTG 1205
DB 1672 VALCYSLGSLNPRQLLEARGGLVALGLGLYSERASPTYRILEASNALESERPHLEU 1691
QY 1206 GATGGTTATAGACAGAGAGAGGCTCATAGCTACAGACAGGCGCTGTGCAGAGACACC 1265
DB 1692 ASPTGLTYTARGLNGLNLSALATYRILEALATHGLNGLYPROLEUALGLUSERTHR 1711
QY 1266 GAGGACTTGTGCGCATGCTATGAGAGACAAATTCACCATCATCTCATGCTGACCAAG 1325
DB 1712 GLUASPHETRPAIRMETLEUTRPGIUNHISASNSERTHILLELEVALMETLEUTHLYS 1731
QY 1326 CTTCGGAGATGGCGAGAGAGAAATCCACCATGCTGCGCAGAGAGCGCTCTGCTGCG 1385
DB 1732 LEUATRGVLUMETGLYARGGLNLYSCYSHISGLNLYTRPRCALAAGLARGSERALARG 1751
QY 1386 TACACGACTTGTGTGTGACCCGATGCTGAGTACACATGCGCCAGATATCTGCGCT 1445
DB 1752 TYRGLNLYRPHETVALVALASPRQKELALAGLUTYRASMETPRQGLNLYRILLEUARG 1771
QY 1446 GATTCAGAGTCACGATGCCCGGATGGCAGTCAGAGACATCCGCGAGTTCAGATTC 1505
DB 1772 GLUPHELYSVALTHRASPLAARGSPGLYGLNLSERARGTHRILEARGLNPHGLNPH 1791
QY 1506 AACAGATGGCCAGAGAGAGGCGCTGCCAAGACAGAGCGAGGATTCATTGACTTCATCGG 1565
DB 1792 THRASPTRPRQGLNGLNGLYVALPROLYSTHNGLYGLNGLYPHEILLEASP**ILEGLY 1811
QY 1566 CAGGTGCATTAAGACCAAGAGAGAGATTTGACAGATGGCGCTCATGCGCTGACCTGACT 1625
DB 1812 GLNVALHLSLSTHLYSLGSLNPHGLYGLNLSAPGLYPROILETHRYALHSCYSSSR 1831
QY 1626 GCTGCGCTGCGGCGGACCGGCGGTTCATCACTGTGAGCATGCTGCGGAGCGCATGCGC 1685
DB 1832 ALAAGLYVALIGLYARGTHRGLYVALPHETIETHNLEUSERILLEVALLEULARGMETARG 1851
QY 1686 TATGAGGCGGTGTGACATGTTTGCAGACCGTGAGACCCCTGCGTRACAGCGTCTGCG 1745
DB 1852 TYRGLNGLYVALVALASPMETPHEGLNTHVALYSTHLEAARGTHRIARGPROALA 1871
QY 1746 ATGGTGACAGACAGAGACCATGATGCTGTCTACCGCGGCGCTGAGTACCTCGCGC 1805
DB 1872 METVALGINTHGLNLSAPGLNLYRGLNLEUCSYTYRARGALALALEUGLNLYRLEUGLY 1891
QY 1806 AGCTTTGACACTATGCAACG 1826
DB 1892 SERPHEASPHISTYRALARATHR 1898

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RESULT 3

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ID 064604 PRELIMINARY; PRT: 1898 AA.
AC 064604; Q63294; Q63295; Q63296;
DT 01-NOV-1996 (TREMBLREL. 01. Created)
DT 01-NOV-1996 (TREMBLREL. 01. Last sequence update)
DT 01-MAR-2002 (TREMBLREL. 20. Last annotation update)
DE Protein-tyrosine phosphatase, receptor-type, F polypeptide precursor
DE (EC 3.1.3.48) (LAR protein) (Leukocyte antigen related) (Leukocyte
DE common antigen-related phosphatase) (Protein-tyrosine-phosphatase)
DE (Phosphotyrosine phosphatase) (PTPase).
GN LAR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=LIVER;
RX MEDLINE=94347119; PubMed=8068021;
RA Zhang W.R., Hashimoto N., Ahmad F., Ding W., Goldstein B.J.;
RT "Molecular cloning and expression of a unique receptor-like protein-
RT tyrosine-phosphatase in the leukocyte-common-antigen-related phosphate
RT family.";
RL Biochem. J. 302:39-47(1994).

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RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS PRLAR4.0 AND PRLAR631).
RC STRAIN=SPAGUE-DAWLEY; TISSUE=HIPPOCAMPUS;
RX MEDLINE=95146548; PubMed=7844155;
RA Zhang J.S., Longo F.M.;
RT "LAR tyrosine phosphatase receptor: alternative splicing is
RT preferential to the nervous system, coordinated with cell growth and
RT generates novel isoforms containing extensive CAG repeats.";
RL J. Cell Biol. 128:415-431(1995).
RN [3]
RP SEQUENCE OF 1035-1898 FROM N.A., AND MUTAGENESIS.
RC TISSUE=HYPOPHALAMUS;
RX MEDLINE=92011772; PubMed=1918076;
RA Pot D.A., Woodford T.A., Remboutsika E., Haun R.S., Dixon J.E.;
RT "Cloning, bacterial expression, purification, and characterization of
RT the cytoplasmic domain of rat LAR, a receptor-like protein tyrosine
RT phosphatase.";
RL J. Biol. Chem. 266:19688-19696(1991).
CC -1- FUNCTION: IT IS POSSIBLE THAT LAR IS A CELL ADHESION RECEPTOR. IT
CC POSSESSES AN INTRINSIC PROTEIN TYROSINE PHOSPHATASE ACTIVITY
CC (PTPASE). IT MODULATES SIGNALING BY THE INSULIN, EPIDERMAL GROWTH
CC FACTOR, AND HEPATOCYTE GROWTH FACTOR TYROSINE KINASE RECEPTORS.
CC MAY PLAY A ROLE IN NEURITE OUTGROWTH AND/OR CELL-CELL INTERACTIONS
CC MODULATING STRAISE FORMATION. MAY INFLUENCE CELL MOTILITY.
CC -1- FUNCTION: THE FIRST PTPASE DOMAIN HAS ENZYMACTIC ACTIVITY, WHILE
CC THE SECOND ONE SEEMS TO AFFECT THE SUBSTRATE SPECIFICITY OF THE
CC FIRST ONE (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O = PROTEIN
CC TYROSINE + PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- ALTERNATIVE PRODUCTS: AT LEAST FIVE ISOFORMS; PRLAR (SHOWN HERE),
CC PRLAR631, PRLAR4.0, PRLAR18.1 AND PRLARCB9 ; ARE PRODUCED BY
CC ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: EXPRESSED PREFERENTIALLY IN NEURAL OR
CC NEUROMUSCULAR TISSUE.
CC -1- DEVELOPMENTAL STAGE: THE ALTERNATIVE SPLICED ISOFORMS ARE
CC DEVELOPMENTALLY REGULATED.
CC -1- SIMILARITY: EXTRACELLULAR REGION TYPIC OF A CAM FAMILY (3 IG-LIKE
CC DOMAINS FOLLOWED BY 8 FIBRONECTIN TYPE III-LIKE DOMAINS), AND A
CC CYTOPLASMIC REGION COMPOSED OF TWO PTPASE DOMAINS (BY SIMILARITY).
DR EMBL: L11586; AAC37655.1; -;
DR EMBL: M60103; AAA41510.1; -;
DR EMBL: X83505; CAA58495.1; -;
DR EMBL: X83546; CAA58537.1; -;
DR HSSP: P18052; IYFO.
DR InterPro: IPR003962; FmIII_repeat.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003598; I9_c2.
DR InterPro: IPR003600; I9_c2.
DR InterPro: IPR003006; I9_MHC.
DR InterPro: IPR000387; TYR_phosphatase.
DR InterPro: IPR000242; TYR_PP.
DR Pfam: PF00041; fn3; 7.
DR Pfam: PF00047; Ig_3; 3.
DR Pfam: PF00102; Y_phosphatase; 2.
DR PRINTS: PR001014; FNTYPEIII.
DR PRINTS: PR00700; PRTPHPTASE.
DR SMART: SM00060; FN3; 6.
DR SMART: SM00408; IGC2; 2.
DR SMART: SM00410; IGC2; 2.
DR SMART: SM00194; PTPc; 2.
DR PROSITE: PS00194; TYR_PHOSPHATASE_1; FALSE_NEG.
DR PROSITE: PS00194; TYR_PHOSPHATASE_2; 2.
DR PROSITE: PS00194; TYR_PHOSPHATASE_3; 2.
DR PROSITE: PS00194; TYR_PHOSPHATASE_PTP; 2.
DR Hydrolase: Receptor; Glycoprotein; Signal; Transmembrane;
DR Cell adhesion; Immunoglobulin domain; Duplication;
DR Alternative splicing; Repeat.
FT SIGNAL 1 27
FT CHAIN 28 1898
FT DOMAIN 28 1254
FT DOMAIN 1165 1169
FT TRANSMEM 1255 1275
FT POTENTIAL.
FT PROTEIN-TYROSINE PHOSPHATASE, RECEPTOR-
FT TYPE, F POLYPEPTIDE.
FT EXTRACELLULAR (POTENTIAL).
FT POLY-ARG.
FT POTENTIAL.

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FT	DOMAIN	1276	1898	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	47	114	IG-LIKE C2-TYPE DOMAIN.
FT	DOMAIN	149	214	IG-LIKE C2-TYPE DOMAIN.
FT	DOMAIN	246	305	IG-LIKE C2-TYPE DOMAIN.
FT	DOMAIN	317	?	FIBROECTIN TYPE-III.
FT	DOMAIN	435	?	FIBROECTIN TYPE-III.
FT	DOMAIN	1361	1607	PROTEIN-TYROSINE PHOSPHATASE.
FT	DOMAIN	1650	1898	PROTEIN-TYROSINE PHOSPHATASE.
FT	ACT_SITE	1539	1539	BY SIMILARITY.
FT	ACT_SITE	1830	1830	POTENTIAL.
FT	DISULFID	54	107	POTENTIAL.
FT	DISULFID	156	207	POTENTIAL.
FT	DISULFID	253	298	POTENTIAL.
FT	CARBOHYD	117	117	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	250	250	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	295	295	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	721	721	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	941	941	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	957	957	CYTOPLASMIC (POTENTIAL).
FT	VARSPLIC	600	707	CYTOPLASMIC (POTENTIAL).
FT				Q -> QMPRESEDED (IN PRLAR631).
FT	VARSPLIC	771	771	G -> S (IN REF. 2).
FT	CONFLICT	777	777	MISSING (IN PRLAR631).
FT	VARSPLIC	812	1004	T -> S (IN REF. 2 AND 3).
FT	CONFLICT	1073	1073	G -> GSSARSPCNIS (IN PRLAR4.0, PRLAR631 AND PRLAR18.1).
FT	VARSPLIC	1316	1316	I -> T (IN REF. 2 AND 3).
FT	CONFLICT	1434	1434	G -> N (IN REF. 2 AND 3).
FT	CONFLICT	1639	1639	RA -> HT (IN REF. 2 AND 3).
FT	MUTAGEN	1539	1539	C->S: LOSS OF ACTIVITY.
FT	VARSPLIC	810	810	A -> AGE (IN PRLARCB9).
FT	VARSPLIC	811	1898	MISSING (IN PRLARCB9).
FT	VARSPLIC	1276	1276	K -> KSKOE (IN PRLAR18.1).
Q0	SEQUENCE	1898	AA: 211492	MD: DF4DIE46F5896F4B CRG64:

Alignment Scores:	
Pred. No.:	4,666-241
Score:	3172.00
Percent Similarity:	98.688
Best Local Similarity:	98.198
Query Match:	49.228
DB:	11
US-09-743-492-1 (1-3467) x Q64604 (1-1898)	

OY	6	GGACTGAAGACACTCTTTGGTGGCCCACTCTTGACCCCTGTGGAATGCGGAGGCTCAAC	65
Db	1292	GLIleuYAspSerLeuIleuAlaHisSerAspProValGIuMetArgIleuAsn	1311
OY	66	TACAGACCCCGGTATGCGAGACACCCACCATCCCATACCGACTGGCCGGACAC	125
Db	1312	TYTIdmThrProGIuMetAlaGAspHisProProIleProIleThrAspLeuAlaAspAsn	1331
OY	126	ATCGAGCGCCCTCAAGAGCCACAGATGGCGCTCAATGTTCCACGAGATGAGTCCATCAC	185
Db	1332	ILleGIuArgIleuYAspAlaAspArgIleuYAspHisSerGIuIleuTYGIuSerIleAsp	1351
OY	186	CCTGAGACAGCTTCACGTGGGAGAAATTCAAACCTTGAGGTGAGAACAGCCCAAGAACGC	245
Db	1352	ProGIuGlnGlnPheThrTrpGIuAsnSerAsnSerGIuValAsnIleProIleAsnArg	1371
OY	246	TATGCGAATGTCATCGGCTTACAGACACTCTCGAGTATATCTTAACCTTATGATGGCTC	305
Db	1372	TYRAlaAsnValIleAlaTYRAspHisSerArgValIleuLeuThrSerIleAspIleVal	1391
OY	306	CCGGGAGTGACTCATCATCATATGCCCACTCATATGATGGGTACCGCAAGAGAAATCCCTAC	365
Db	1392	ProIleSerAspTYRLeuAsnAlaAsnTYRLeuAspGIUTYRArgIleuIleAsnIleValTYR	1411
OY	366	ATTCGCACAGCAGGCCCCCTGCCCCGAGACCATGGCGGAATTTGTGAGATGGATGGCGAA	425

[illegible]

Db	1772	GLuPhelYsValThrSpAlaArgAspGlyGlnSerArgThrIleArgGlnPheGlnPhe	1791
QY	1506	ACAGACTGGCCACAGACAGGCGCGTCCCAAGACAGCGGAGGATTCAATTGACTTCAATCGGG	1565
Db	1792	ThrAspTrpProGlnGlnGlyValProLysThrGlyGlnGlyPheIleLeuSphenIleGly	1811
QY	1566	CAGTGGATTAAGACCAAGAGGCGATTGGACAGGATGGGCGTACAGGGTGACATGCGAGT	1628
Db	1812	GlnValHisLysThrLysGlnGlnPheGlyGlnAspGlyProIleThrValHisCysSer	1831
QY	1626	GCTGGCGTGGGCGGACCGCGGGGTTCATACACTCTGACATCGTCCTGGAGCGCATGGCG	1685
Db	1832	AlaGlyValGlyArgThrGlyValPheIleThrLeuSerIleValLeuGlnArgMetArg	1851
QY	1686	TATGAGGCGGTGTGCATGTTTCAGACCGTAGACCCCTGCTGACACAGCGCTCTGCC	1745
Db	1852	TyrGlnGlyValValAspMetPheGlnThrValLysThrLeuArgThrGlnArgProAla	1871
QY	1746	ATGGTGCAGACAGAGGACCGATTCAGCTGTGCTACCGGTGGCGCCCTGGAGTACTCTGGC	1805
Db	1872	MetValGlnThrGlnAspGlnTyrGlnLeuCysTyrArgAlaIleValGlnIleTyrIleGly	1891
QY	1806	AGCTTGACCACTATGGCAACG	1826
Db	1892	SerPheAspHisTyrAlaThr	1898

RESULT 4
Q9IAJ0
ID Q9IAJ0 PRELIMINARY; PRT; 1788 AA

DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Receptor protein tyrosine phosphatase LAR.
GN xPPT-LAR.
OS Xenopus laevis (African clawed frog).
OC Amphibia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP
RX MEDLINE=20193505; PubMed=10727868;
RA Johnson K.G., Holt C.E.;
RT Expression of GRYP-alpha, LAR, PTP-delta, and PTP-rho in the
RL developing xenopus visual system";
RT Mech. Dev. 92:291-294(2000).
DR EMBL; AF197945; AAF43606.1; -.
DR HSSP; P18052; 1F0.
DR InterPro: IPR003962; F011.repeat.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003598; IG_C2.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR000387; TYR_phosphatase.
DR InterPro: IPR000242; TYR_PP.
DR Pfam: PF00041; fn3; 7.
DR Pfam: PF00047; Ig_3.
DR Pfam: PF00102; Y-phosphatase; 2.
DR PRINTS; PR00014; ENTPEP11.
DR PRINTS; PR00700; PRTYPPHPTASE.
DR SMART; SM00060; FN3; 7.
DR SMART; SM00408; IGC2; 3.
DR SMART; SM00194; PTPC; 2.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
KW Hydrolase; Immunoglobulin domain; Repeat
SEQUENCE 1788 AA; 200271 MW; AB192549866D9067 CRC64;
SQ

Alignment Scores:		
Pred. No.:	3.68e-232	length: 1788
Score:	3059_00	Matches: 567
Percent Similarity:	97.53%	Conservative: 25

Best Local Similarity:	93.41%	Mismatches:	15
Query Match:	47.47%	Indels:	0
DB:	13	Gaps:	0

[illegible]

QY 1026 CTGAGATTCAAGTTGGTGGCCAGCTCCAAAGCCACAGCTCCGCTTCATCAGGCGCAAC 1085
 |||||
 Db 1522 LGGIHPheIysLeuEuAlaAsnSerLySAIhISthSerArpHeIleSeAlaAsn 1541
 QY 1086 CTGCCCCGACAAAGTTCAAGAACCGGCTGTGTAGACATCATGCGCTACAGAAATGACCCGT 1145
 |||||
 Db 1542 LGGIHPheIysLeuEuAlaAsnSerLySAIhISthSerArpHeIleSeAlaAsn 1561
 QY 1146 GTGTGTCTGAGCCCATCCGTGGTGTGGAGGGCTGTGACTACATCAATGCGACCTTCG 1205
 |||||
 Db 1562 ValSerLeuGlnProIleArGlyValGluGlySerAspLyrlleAsnAlaSerPheIle 1581
 QY 1206 GATGGTTATAGACAGAGAAGAGGCTCATATAGCTACACAGAGGGGCTGTGGAGAGACACC 1265
 |||||
 Db 1582 AspGlyTyrArGInGlnInuysGlyTyrIleAlaThrGlnGlyProLeuAlaGlnTyrThr 1601
 QY 1266 GAGAGCTTGGCGCATGCTATGGAGACAAATTCACATCATGCTCATGAGCAAG 1325
 |||||
 Db 1602 GluAspPheIrrArpGmetLeuTrpGluHISAsnSerThrIleValIleMetLeuThrLys 1621
 QY 1326 CTTCGGAGATGGGACAGGAGAAATGCCACCACTACTGGCCAGACAGCGCTGTGCTGCG 1385
 |||||
 Db 1622 LeuArGInuMetGlyArGInuysGlySHISGlnTyrTrpProAlaGlnArGSerAlaArG 1641
 QY 1386 TACCACTACTTGTGTGTGACCCGATGGCTGAGTACACATGCGCCAGTATACCTGCGT 1445
 |||||
 Db 1642 TGTGInTyrPheValIAlaSPrometAlaGlnTyrAsnmetProGlnTyrIleLeuArG 1661
 QY 1446 GAGTTCAAGGTACAGGATGCCCGGATGGGACAGTCAAGCAATCCGGAGCTTCAGTTTC 1505
 |||||
 Db 1662 GluPheIysValIthrAspAlaArGAspGlyGlnSerArGThrIleArGInPheGlnPhe 1681
 QY 1506 ACAGACTGGCCAGACAGAGCGCTGCCCAAGACAGCGAGGAGATTCATGACTTCATCGGG 1565
 |||||
 Db 1682 ThrAspTrpProGlnInuGlyValProLysThrGlyGluGlyPheIleAspPheIleGly 1701
 QY 1566 CAGGTGCATAAGACCAAGAGGAGGATTTGGACAGATGGGCTTCACCGGGGCACTGCAGT 1625
 |||||
 Db 1702 GluValHISLysThrLysGlnInuPheGlyGlnAspGlyProIleThrValHISCySer 1721
 QY 1626 GCTGGCGTGGCGGACACCGGGGTGTTTCATCATCTGATGAGTCCGCTGTGGAGCGCAAC 1685
 |||||
 Db 1722 AlaGlyValGlyArGInuGlyValPheIleThrLeuSerIleValLeuGlnArGmetArG 1741
 QY 1686 TATGAGGGCGTGTGCATGTTTCAGACCGGTAAAGACCCCTGGCTACACAGCGTCTGCC 1745
 |||||
 Db 1742 TYRGLuGlyValIAlaSPmetPheGlnThrValLysThrLeuArGThrGlnArGProAla 1761
 QY 1746 ATGGTGCACAGACAGAGACCAAGTATCAGCTGTGTACCGTCCGCGGCTGTGGAGTACCTGCG 1805
 |||||
 Db 1762 MetValGlnThrGlnuysGlnTyrGlnLeuCySerTyrArGAlaIleLeuGlnTyrLeuGly 1781
 QY 1806 AGCTTGGACCATATGCAACG 1826
 |||||
 Db 1782 SerPheAspHISLysTyrAlaThr 1788
 RESULT 5
 064696
 ID 064696 PRELIMINARY; PRT; 582 AA.
 AC 064696;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Protein-tyrosine phosphatase, receptor-type, F polypeptide
 DE (EC 3.1.3.48) (LAR protein) (Leukocyte antigen related) (Fragment).
 GN PTPRF OR LAR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCBI_TaxID=10090;
 RX [1]
 RN
 RP SEQUENCE FROM N.A.

RC STRAIN-BALB/C; TISSUE-BRAIN;
 RX MEDLINE=95394448; PubMed=7665159;
 RA Schaapveld R.Q.J., Van den Maadenberg A.M.J.M., Schepens J.T.G.,
 RA Weghuis D.O., van Kessel A.G., Wieringa B., Hendriks W.J.A.J.;
 RT "The mouse gene Ptpfr encoding the leukocyte common antigen-related
 RT molecule LAR: cloning, characterization, and chromosomal
 RT localization.";
 RL Genomics 27:124-130(1995).
 RN [2]
 RN SEQUENCE OF 116-221 AND 405-512 FROM N.A.
 RC STRAIN-BALB/C; TISSUE-BRAIN;
 RX MEDLINE=93086603; PubMed=1454056;
 RA Schepens J., Zeeuwen P., Wieringa B., Hendriks W.;
 RT "Identification and typing of members of the protein-tyrosine
 RT phosphatase gene family expressed in mouse brain.";
 RL Mol. Biol. Rep. 16:241-248(1992).
 RN [3]
 RN SEQUENCE OF 116-221 FROM N.A.
 RC STRAIN-BALB/C; TISSUE-BRAIN;
 RX MEDLINE=95134232; PubMed=7832766;
 RA Hendriks W., Schepens J., Brugman C., Zeeuwen P., Wieringa B.;
 RT "A novel receptor-type protein tyrosine phosphatase with a single
 RT catalytic domain is specifically expressed in mouse brain.";
 RL Biochem. J. 305:499-504(1995).
 CC -1- FUNCTION: IT IS POSSIBLE THAT LAR IS A CELL ADHESION RECEPTOR. IT
 CC POSSESSES AN INTRINSIC PROTEIN TYROSINE PHOSPHATASE ACTIVITY
 CC (PTPASE) (BY SIMILARITY).
 CC -1- FUNCTION: THE FIRST PTPASE DOMAIN HAS ENZYMATIC ACTIVITY, WHILE
 CC THE SECOND ONE SEEMS TO AFFECT THE SUBSTRATE SPECIFICITY OF THE
 CC THE FIRST ONE (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O = PROTEIN
 CC TYROSINE + PHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: EXTRACELLULAR REGION TYPE OF A CAM FAMILY (3 IG-LIKE
 CC DOMAINS FOLLOWED BY 8 FIBRONECTIN TYPE III-LIKE DOMAINS), AND A
 CC CYTOPLASMIC REGION COMPOSED OF TWO PTPASE DOMAINS.
 CC -1- SIMILARITY: NO DPTP AND TO LAR.
 DR EMBL: Z37988; CAA86070.1; -;
 DR EMBL: Z23061; CAA80596.1; -;
 DR EMBL: Z23049; CAA80584.1; -;
 DR HSSP: P18052; IYFO.
 DR MGD: MGI:102695; Ptpfr.
 DR InterPro: IPR000387; TYR_phosphatase.
 DR InterPro: IPR000242; Tyr_PP.
 DR Pfam: PF00102; Y-phosphatase; 2.
 DR PRINTS: PR00700; PRTYPHPTASE.
 DR SMART: SM00194; PTPC; 2.
 DR PROSITE: PS00383; TYR_PHOSPHATASE_1; FALSE_NEG.
 DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 2.
 DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 2.
 KW Hydrolase; Receptor; Glycoprotein; Transmembrane; Cell adhesion;
 KW Immunoglobulin domain.
 FT NON_TER 1
 FT DOMAIN <1 582
 FT DOMAIN 45 291
 FT DOMAIN 334 582
 FT ACT_SITE 223
 FT ACT_SITE 514
 FT ACT_SITE 514
 SQ SEQUENCE 582 AA; 66965 MW; 93303C08536342FE CRC64;
 Alignment Scores:
 pred. No.: 3.57e-232 Length: 582
 Score: 3057.00 Matches: 572
 Percent Similarity: 99.14% Conservative: 5
 Best Local Similarity: 98.28% Mismatches: 5
 Query Match: 47.44% Indels: 0
 DB: 11 Gaps: 0
 US-09-743-492-1 (1-3467) x 064696 (1-582)
 QY 81 ATGCGAGACCCACCCATCCCATCAGGCTGCGGAGCAACATGAGCGCTCAAA 140
 |||||
 Db 1 MetArGAspHIStrProIleThrPheIleThrAspLeuAlaAsnIleGlnArGLeuLys 20

OY 141 GCCAAGCATGGCCTCAAGTTCTCCACGAGATGTAAGTCCATGCAACCCCTGGACGACGATTC 200
 |||||
 Db 21 AIAAaNSpGlyLeuLysPheSerGlnGluTyrGluSerIleAspProGlyGlnGlnPhe 40
 OY 201 ACGTGGGGAATTCAACCTGGAGGTGAGCAAGCCCAACAGCCGCTATCCGAAATGTCATC 260
 |||||
 Db 41 ThrTrpGluAsnSerAsnSerGlnValAsnLysProLysAsnArgTyrIleAsnValIle 60
 OY 261 GCGTACGACCACTCGAGTCACTCCCTTACCTATATGATGGGCTCCCGAGAGTACTAC 320
 |||||
 Db 61 AlaTyrAspHisSerArgValLeuLeuThrSerIleAspGlyValProLysSerAspTyr 80
 OY 321 ATCAATGCCAACTACATGATGGTACCGCAAGCAGAAATGCCATACATGCCACGACGGC 380
 |||||
 Db 81 IleAsnAlaAsnTyrIleAspGlyTyrArgLysGlnAsnAlaTyrIleAlaThrGlnGly 100
 OY 381 CCCCGCCCGAGACATGGGCGCATTTCTGGAGAAATGGTGTGGGAAACGCGGACGCGCACT 440
 |||||
 Db 101 ProLeuProGluThrMetLysPheTrpArgMetValTyrGluGlnArgThrAlaThr 120
 OY 441 GTGTCTCATGATGACACGGCTGGAGAGAAATCCCGGTAAATGTGATCAGTACGACCA 500
 |||||
 Db 121 ValValMetMetThrArgLeuGlnGluLysSerArgValLysCysAspGlnTyrTrpPro 140
 OY 501 GCCCGTGGCACCAGACCTGTGGCCTTATTCAGGTGACCCCTGTGGACACATGGAGCTG 560
 |||||
 Db 141 ValArgGlyThrGluThrGlyLeuIleGlnValThrLeuValAspThrValGluLeu 160
 OY 561 GCCAATACACCTGTGGACCTTCGACATCCCAAGAGTGGCTCCAGTGAAGAGCTGAG 620
 |||||
 Db 161 AlaTrpTyrThrMetLysArgThrPheAlaLeuHisLysSerGlySerSerLysLysArgGlu 180
 OY 621 CTGCGTCAAGTTTCATGTTATGGCTGGCCAGACATGGATGGATCTGAGTACCACTGCC 680
 |||||
 Db 181 LeuArgGlnPheGlnPheMetAlaTrpProAspHisGlyValProGluTyrProThrPro 200
 OY 681 ATCTGGCCTTCCTACGACGGGTCAAGGCGTCAACCCCTGACAGCGGCGCCATGCTG 740
 |||||
 Db 201 IleLeuAlaPheLeuArgArgValLysAlaCysAsnProLeuAspAlaGlyProMetVal 220
 OY 741 GTGCACTGCAGCGCGGCTGGGCGGCAACCGGCTGCTTCACTGATGATGATGATGCTG 800
 |||||
 Db 221 ValHisCysSerAlaGlyValGlyLysThrGlyCysPheIleValIleAspAlaMetLeu 240
 OY 801 GAGCGAGTGAAGCAGAGACGAGTGGACATCTATGGCCAGCTGATCCGATCGCATCA 860
 |||||
 Db 241 GluArgMetLysHisGlyLysThrValAspIleTyrGlnHisValThrCysMetArgSer 260
 OY 861 CAGAGGAACCTACATGCTGCAGACGAGGAGCAGTACGTGTTGATCCATGAGCGCTGCTG 920
 |||||
 Db 261 GlnArgAsnTyrMetValGlnThrGluAspGlnTyrValPheIleHisGlnAlaLeuLeu 280
 OY 921 GAGGCTGCACAGTGGGCGGCGACACAGAGTGGCTGCCCGGCAACCTGTATGGCCATCCAG 980
 |||||
 Db 281 GlnAlaAlaIleMetCysGlyHisThrGlnValLeuAlaArgAsnLeuTyrAlaHisIleGln 300
 OY 981 AAGCTGGCGCAAGTGCCTCCAGGAGAGTGTGACCGCATGAGCGCATGAGTCAAGTTG 1040
 |||||
 Db 301 LysLeuGlnGlnValProProGluLysIleSerValThrAlaMetGlnLeuGlnPheLysLeu 320
 OY 1041 CTGGCCAGCTCCCAAGGCCACACAGTCCCGCTTCATCAGAGGCCCAACCTGCCCTGCAACAG 1100
 |||||
 Db 321 LeuAlaAsnSerLysAlaHisThrSerArgPheValSerAlaAsnLeuProCysAsnLys 340
 OY 1101 TTCAGAAACCGGCTGTGTAACATCATGCCCTTACGAATTGACCCGCTGTGTCTGACGCC 1160
 |||||
 Db 341 PheLysAsnArgLeuValAsnIleMetProTyrGlnLeuThrArgValCysLeuGlnPro 360
 OY 1161 ATCCGTGTGTGGAGGCTGTGACTACATCAATGCACAGTTCAGAGTTCGATGATGACAG 1220
 |||||
 Db 361 IleArgGlyValGlnGlySerAspTyrIleAsnAlaSerPheLeuAspGlyTyrArgGln 380

OY 1221 CAGAAAGCCTACATAGCTACACAGGGGCGCTGTGGCAGAGACGAGGACTTCTGGCGC 1280
 |||||
 Db 381 GlnLysAlaTyrIleAlaThrGlnGlnProLeuAlaGluSerThrClnAspPheTrpArg 400
 OY 1281 ATGCTATGGGACACAAATCCCAACATCATGCTCATGCTTACCAAGCTTGGGAGATGGCC 1340
 |||||
 Db 401 MetLeuTrpGlnHisAsnSerThrIleIleValMetLeuThrLysLeuArgGlnMetGly 420
 OY 1341 ACGGAGAAATGCCACCACTAGTGGCCAGACAGCGCGCTGCTGCTGCTACAGTACTTGT 1400
 |||||
 Db 421 ArgGlnLysCysHisGlnTyrTrpProAlaGlnArgSerAlaArgTyrGlnPheVal 440
 OY 1401 GTTGACCCGATGGCTGAGTACAAACATGCCCAAGTATATCTCGTGGATTCAGAGTCA 1460
 |||||
 Db 441 ValAspProMetAlaGlnTyrAsnMetProGlnTyrIleLeuArgGlnPheLysValThr 460
 OY 1461 GATGCCCGGAGTGGCAGTCAAGCAAGCAATCCGGCAGTTCCACTTCCAGACAGTCCG 1520
 |||||
 Db 461 AspAlaArgAspGlyGlnSerArgThrIleArgGlnPheGlnPheThrAspTrpProGlu 480
 OY 1521 CAGGCGTCCCAAGACAGGAGGATTCATTCATGACTTTCATGCGGAGGATGATAGACC 1580
 |||||
 Db 481 GlnGlyValProLysThrGlnGlnGlyPheIleAspPheIleGlyValHisLysThr 500
 OY 1581 AAGGACCACTTGGACAGAGATGGCCCTATCACGGTGCACATGCACTGCACTGGCGCCG 1640
 |||||
 Db 501 LysGlnGlnPheGlyGlnAspGlyProIleThrValHisCysSerAlaGlyValGlyArg 520
 OY 1641 ACCGGGCTTATCATCTGTGAGCATCGTCTGGAGCGGATCGCTATGAGGGCTGGTC 1700
 |||||
 Db 521 ThrGlyValPheIleThrLeuSerIleValIleGlnArgMetArgTyrGlnValVal 540
 OY 1701 GACATGTTTCAGACCGTGAAGACCTGCTGACACAGCGTCCGATGGGTGGCAGACAG 1760
 |||||
 Db 541 AspMetPheGlnThrValLysThrLeuArgThrGlnArgProAlaMetValGlnThrGln 560
 OY 1761 GACCAATACATGCTGTGCTACCGCTCGCGCTGGAGTACCTTGGCAGCTTATGACCACTAT 1820
 |||||
 Db 561 AspGlnTyrGlnLeuCysTyrArgAlaIleLeuGlnTyrLysSerPheAspHisTyr 580
 OY 1821 GCAAGC 1826
 |||||
 Db 581 AlaThr 582

RESULT 6
 OBR169 PRELIMINARY: PRT: 749 AA.
 ID OBR169
 AC OBR169
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Hypothetical 86.1 kDa protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=KIDNEY;
 RA Strausberg R.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC025145; AAH25145.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 749 AA; 86082 MW; 421FCGB9B50C959E CRC64;

Alignment Scores:
 Pred. No.: 9.36e-223 Length: 749
 Score: 2938.00 Matches: 540
 Percent Similarity: 96.16% Conservative: 36
 Best Local Similarity: 90.15% Mismatches: 23
 Query Match: 45.59% Indels: 0
 DB: 11 Gaps: 0

US-09-743-492-1 (1-3467) x Q8R169 (1-749)

QY	30	CAC	TCCTCTACACCTGTGGAGATGGCGAGGCTTA	CTACCTACCAACCCCAAGTATGGCAGAC	89
			
Db	151	H	isProthrisp	roValGluLeuAtrgLeuAsnPhelInthProGlyMet	170
QY	90	CAC	CCACCCATCCCATCCACCCAGCTGGCGGACA	CAATGATGACGGCTCAAAACCAACAT	149
Db	171	H	isProtroller	ProIleuGluLeuAlaAspHisIleGluAtrgLeuLysAlaAsn	190
QY	150	G	GCCTCAAGTTCTCCACAGATAGATGATCCATG	ACCCCTGGACACAGCTTCACGTGGAG	209
			
Db	191	A	smLeuLysPhe	serGlnGluTrgIuSerIleAspProGlyGlnGlnPhe	TrpIu 210
QY	210	AAT	TCAAACCTGGAGGAGAACAGCCCAAGAACCCG	TATGGAGATGTCATGGCCCTACAGAC	269
Db	211	H	isSerAsnLeuGlu	ValAsnLysProLysAsnAtrgTrAlaAsnValIleAla	TruYasp 230
QY	270	CAC	TCCTGAGTCATCCCTTACCTCTATGATGGCGT	CCCCGGGAGAGTACATCATCTACCTCC	329
			
Db	231	H	isSerAtrgValLeu	LeuSerAlaIleGlnGluIleProGlySerAspTrgTrAla	AsnAla 250
QY	330	AAC	TACATGCATGGCTACCGCAAGCAAGATGCT	ACATGTCGACAGAGGCCCTCTGCC	389
			
Db	251	A	snTrgIleAsp	TrgIuTrgIysGlnAsnAlaTrgIleAlaThnGlnLys	LeuPro 270
QY	390	GAG	CAATGGGCGATTTCTGAGATGATGGTGGAGAC	AGCGAGCCCACTGGTCTCATG	449
Db	271	G	luThrPheLys	AspPheTrpAtrgMetIleTrpGlnGlnAtrgSerAlaTh	ValAlaMet 290
QY	450	ATG	ACAGCGGTGAGAGAGATCCCGGGTAAAA	TGTGATGATCTACTGGCCACCCGTGGC	509
			
Db	291	M	ethTrgIysLeu	GlnGluAtrgSerAtrgValLysCysAspGlnTrgTr	ProSerAtrgIly 310
QY	510	ACC	GAGACCTGTGGCCTTATTCAGAGTGGACCC	CTGTGGACACATGGTGGACCTGGCCACATAC	569
			
Db	311	T	hrGluThrHis	ngLysLeuValGlnValThrLeuLysPheThnValGln	LeuAlaThnTrg 330
QY	570	ACT	TGGCGCACTTTCGGCACATCCCAAGAGTGG	CTCCAGTGAACACGTCGAGCTGGTACG	629
			
Db	331	C	ysValAtrgPhe	AtrgPheAlaLeuTrgIysAsnGlySerSerGluLys	ArgGlnValAtrgGln 350
QY	630	T	TTCAGTTCATGGCGCTGGCCCAAGACATG	AGATTCCTGATACCCAACTCCATCTGGCC	689
			
Db	351	P	heInthethr	AlaTrpProAspHisGlyAtrgGlnLysProGlnLys	ProthnProPheLeuAla 370
QY	690	T	TTCCTACGAGCGGTCAAGGCTCAACCCCT	TAGACGACAGGCGCCATGGTGGTGCATGC	749
			
Db	371	P	heLeuAtrgAtrg	ValLysThnTrgCysAsnProTrpAlaGlyPro	MetValAlaHisCys 390
QY	750	AGC	GGGGGCGTGGGCGCACCGGCTCTTCATG	CTGTGATGATCCATGTTGGAGCGGATG	809
			
Db	391	S	erIleAtrgValG	lyAtrgThnGlyCysPheIleValIleAspAla	MetLeuGlnAtrgIle 410
QY	810	AAG	CACAGAGAAAGCGGTGACATCTATGGGCA	CTGATCCGATCGAACAGGAGAC	869
			
Db	411	L	ysHisGluLys	ThnValAspIleTrgGlyHisValThnLeu	MetAtrgAlaGlnTrgAsn 430
QY	870	TAC	ATGTGTGACAGACGAGACACAGTACG	TTTATCTATCATGAGAGCGCTGTGGAGCTCC	929
			
Db	431	T	rgMetValGln	ThnTrgIuAspGlnTrgIlePheThnIle	AspAlaLeuLeuGlnAlaVal 450
QY	930	ACG	TGGGGCCACACAGAGTGGCTGGCCGCA	CTGATGATGCCCAATCAGAACTGGGC	989
			
Db	451	T	hrGlySerLys	AsnThnTrgIuValProAlaAtrgAsnLeu	TrgAlaTrgIleGlnLysLeuThr 470
QY	990	CAA	TGGCTCCAGAGGAGTGTGACCGGCATG	AGCTGAGCTGGAAGTGTGGCCAGC	1049
			
Db	471	G	lnIleGluThr	TrgIleLysAsnValThnTrgIleMetGlnLeuGlu	ThnLysAtrgGluAlaSer 490
QY	1050	T	CCAGGCGCCACACGCTCCGCTTCATGAC	GGCCCAACTGCTCCGTCGAACAAGTTCA	GAAGC 1109
			
Db	491	S	erLysAlaHis	TrgSerAtrgPheIleSerAlaAsnLeuPro	CysAsnLysPheLysAsn 510

QY	1110	CGGTCGGTGAACATCATATGCCCCCTACGAATTGACCCCGTGTGTCTGTACGCCATCCGTGT	1169
Db	511	ArgLeuValAsnIleMetProTyrGluSerThrArgValCysLeuGlnProIleArgGly	530
QY	1170	GTGGAGGGCTCTGACTCATCAATGCGAGGCTTCTGGATGGTATATAGACAGAGAACCC	1229
Db	531	ValGluGlySerAspTyrIleAsnAlaSerPheLeuAspGlyTyrArgGlnGlnAspAla	550
QY	1230	TACATAGCTACACAGGGGGCCTGTGGACAGAGACCGAGACCTTCTGGCCATCGTATCG	1289
Db	551	TyrIleAlaThrGlnGlyProLeuAlaGluThrThrGluAspPheTrpArgMetLeuTrp	570
QY	1290	GAGCACATTTCCACCATCATCTGCATCTGCTGACCACAGCTTGGGGAATGGCAGGAGAA	1349
Db	571	GluHisAsnSerThrIleValIleMetLeuThrLysLeuArgGluMetCylArgGluLys	590
QY	1350	TGCCACACAGTCTGGCCAGACAGACCGCTGGCTGGCTACCACTTGTGTGTGACCG	1409
Db	591	CysHisGlnTyrTrpProAlaGluArgSerAlaArgTyrGlnTyrPheValIValAspPro	610
QY	1410	ATGGCTAGTACAAACATGCCCCCAGTATATCTGCTGCTGAGTTCAAGTCAAGTACCGCCG	1469
Db	611	MetaIaGluTyrAsnMetProGlnTyrIleLeuArgGluPheLysValIValAspAlaArg	630
QY	1470	GATGGCAGCTCAAGAGAAATCCGGCAGTTCAGTTACAGACTGGCCACAGACGGCGTG	1529
Db	631	AspGlyGlnSerArgThrValIArgGlnPheGlnPheThrAspTrpProGluGlnGlyVal	650
QY	1530	CCCAAGACAGCGCGAGGATTCATGATTCATGCTCATCGGGCAGTGCATTAAGACCAAGAGCAG	1589
Db	651	ProLysSerGlyGluGlyPheIleAspPheIleGlyGlnValHisLysThrLysGluGln	670
QY	1590	TTTGACAGAGATGGGCGCTATCACAGGTGCATCGTCAGTGCATGGCGTGGCGCAGCCGGGTG	1649
Db	671	PheGlyGlnAspGlyProIleSerValHisCysSerAlaGlyValGlyIArgThrGlyVal	690
QY	1650	TTTCATCACTCTGACATCATCTGCTGAGACCGCATGCGCTATAGAGGGCGTGTGCATATGTT	1709
Db	691	PheIleThrLeuSerIleValIleGluIValArgMetArgTyrGlnGlyIValIValAspIlePhe	710
QY	1710	CAGACCGTGAAGACCTGCTCATACACAGCGTCTGCCATGTGTCACACAGAGACCATGAT	1769
Db	711	GlnThrValLysMetLeuArgThrGlnIArgProAlaMetValGlnThrGluAspGlnTyr	730
QY	1770	CAGCTGCTACCTGCGCGCCCTGGAGTACCTGGCAGCTTTGACCACTATGCAACG	1826
Db	731	GlnPheCysTyrArgAlaIleAlaLeuGluTyrLeuGlySerPheAspHisTyrAlaThr	749
RESULT 7			
Q8BV0			
ID	Q8BV0	PRELIMINARY;	PRT; 1254 AA.
AC Q8BV0;			
DT	01-MAR-2002 (TReMBLrel. 20, Created)		
RC	01-MAR-2002 (TReMBLrel. 20, Last sequence update)		
DT	01-JUN-2002 (TReMBLrel. 21, Last annotation update)		
DE	Protein tyrosine phosphatase, receptor type, delta A.		
GN	PTPRD.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Euteheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
NC	NCBI_TaxId=10090;		
RM	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=DBA/2J, AND C57BL/6J; TISSUE=BRAIN;		
RA	Fehr C., Belknap J.K., Crabbe J.C., Buck K.J.;		
RT	"High resolution mapping of a quantitative trait locus for acute		
RT	ethanol withdrawal on mouse chromosome 4 and characterization of		
RT	potential candidate genes."		
RL	Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF326559; AL37406.1; -		
DR	EMBL; AF326559; AL37405.1; -		
DR	MGI; 97812; Ptprd.		


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QY 1710 CAGACCGTGAAGACCCCTGCTACAGACGCTCCCTGCTGACAGACAGAGGACAGTAT 1769
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Db 1216 GlnThrValLysMetLeuArgThrGlnArgProAlaMetValGlnThrGlnAspLysr 1235
QY 1770 CAGCTGTGCTACCGCTGGCGCCCTGGAGTACCTGGCAGCTTTGACCACTATGCAACG 1826
|||||
Db 1236 GlnPheCysTyrArgAlaAlaLeuGlnLysrPheAspHisTyrAlaThr 1254

RESULT 8
Q9IAJ1 PRELIMINARY; PRT; 1896 AA.
ID Q9IAJ1
AC Q9IAJ1;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Receptor protein tyrosine phosphatase delta.
GN Xprr-D.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20193505; PubMed=10727868;
RA Johnson K.G., Holt C.E.;
RT "Expression of Crp-alpha, LAR, ppp-delta, and ppp-rho in the
RT developing xenopus visual system.";
RL Mech. Dev. 92:291-294(2000).
DR EMBL: AF197944; AAF43605.1; -.
DR HSSP: P18052; IYFO.
DR InterPro: IPR003962; F0111_repeat.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003598; I9_C2.
DR InterPro: IPR003006; I9_MHC.
DR InterPro: IPR000387; Tyr_phosphatase.
DR InterPro: IPR000242; Tyr_PP.
DR Pfam: PF00041; fn3; 8.
DR Pfam: PF00047; ig; 3.
DR Pfam: PF00102; Y-phosphatase; 2.
DR PRINTS: PR00014; FNTYPEIII.
DR PRINTS: PR00700; PRTYPPHPTASE.
DR SMART: SM00060; FN3; 8.
DR SMART: SM00408; IGC2; 3.
DR SMART: SM00194; PTPc; 2.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 2.
KW Hydrolase; Immunoglobulin domain; Repeat.
SQ SEQUENCE 1896 AA; 213067 MW; 08AC9003034199A4 CRC64;

Alignment Scores:
Pred. No.: 2,37e-221 Length: 1896
Score: 2922.00 Matches: 535
Percent Similarity: 96.31% Conservative: 40
Best Local Similarity: 89.61% Mismatches: 22
Query Match: 45.34% Indels: 0
DB: 13 Gaps: 0

US-09-743-492-1 (1-3467) x Q9IAJ1 (1-1896)
QY 36 TCTGACCTGTGGAGATGGAGGCTCAACTACGACCCGAGTATGCGAGACCACCA 95
:::|||||
Db 1300 ThrAspProValGlnLeuArgArgLeuAsnPheGlnThrProGlyMetAlaAsnHisPro 1319
QY 96 CCGATCCCATACCGACCTGGCGGACAAATCGAGCGCTCAAGCCAGCATGAGCTC 155
|||||
Db 1320 ProlleProIleLeuGlnLeuGlnAspHisIleGlnArgLeuLysAlaAsnAspAsnLeu 1339
QY 156 AAGTTCTCCAGAGAGTATGACTCCATGACCCCTGGACAGCAGTTTACGTGGAGCAATTCA 215
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Db 1340 LysPheSerGlnGlnLysrGlnSerIleAspProGlyGlnGlnPheThrTrpGlnHisSer 1359
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QY 216 AACCTGGAGGTGACACAGCCCAAGAACCGCTATGGCAATGTCAATGCGCTACGACCACTCT 275
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QY 276 CGAGTCATCCTTACCTTATCGATGAGCGTCCCGGAGAGTACATATCAATGCAACTAC 335
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QY 336 ATCGATGGCTACCGCAGACAGAAATGCTATCGCATCGCCAGCGAGGCCCTGCGCAGACC 395
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QY 396 ATGGCGCAATTCCTGGAGATGGTGGAGAACCGCCAGCCACCTGCTGCTATGATGCA 455
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QY 456 CGGCTGGAGAGAACTCCCGGTAATAATGTGATCATGACTGGCCGCCCGCTGGACCCAG 515
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Db 1440 LysMetGlnGlnArgSerArgIleLysCysAspGlnTyrTrpProSerArgGlyThrGlu 1459
QY 516 ACCTGTGCTTATTCAGGTGACCTGTGGACACATGGAGCTGGCCATATCACTGTG 575
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Db 1460 ThrTyrGlyLeuIleGlnValThrLeuLeuAspThrValGlnLeuAlaThrTyrThrVal 1479
QY 576 CGCACCCTCGCACCTCCACAAGAGTGCGTCAGTGAAGCGGACCTGCGTCACTTTCAG 635
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QY 636 TTCATGGCTGGCCGACACCATGAGTCTCTGAGTACCCCAACATCCCATGCTGGCTTCTCA 695
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Db 1520 ArgArgValLysThrCysAsnProProAspAlaGlyPrometValValHisCysSerAla 1539
QY 756 GGGCGGGGCGGACCGGCTGCTCATGAGTGAATGGCATTTGGCATTTGGACGGAAGAAC 815
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QY 816 GAGAACGCTGGAGACATATGACCATGACCTGCATCGCATGACAGAGCAATCAATCATG 875
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QY 876 GTGCAGACGAGACGACGATGCTTCATTCATGAGGCGCTGCTGGAGGCTCCACGTGC 935
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QY 1116 GTGAACATCATGCGCTTAGCAATTCAGCCGCTGTGTCGACGCCCATCGGTGTGGAG 1175
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Db 1660 ValAsnIleMetProTyrGlnSerThrArgValCysLeuGlnProIleArgGlyValAlu 1679
QY 1176 GGGCTGACTCATCAATGACGAGCTTCTGTGATGGTTATGACAGCAAGAGCCATACATA 1235
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Db 1680 GlySerAspTyrIleAsnAlaSerPheIleAspGlyTyrArgGlnGlnLysAlaTyrIle 1699
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ID Q9UM81;
AC Q9UM81;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE PTPSIGMA-(brain) precursor.
GN PTPSIGMA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Endo N., Rutledge S.J., Opas E.E., Vogel R., Rodan G.A., Schmidt A.;
RT "Human protein tyrosine phosphatase-sigma: Alternative splicing and
RT inhibition by biophosphates.";
RL J. Bone Miner. Res. 0:0-0(1995).
DR EMBL: U41725; AAD09360.1; -.
DR HSSP: P18052; 1FFO.
DR InterPro: IPR003962; FNIII_repeat.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003598; Ig_C2.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR000387; TYR_MHC.
DR InterPro: IPR000242; TYR_PP.
DR Pfam: PF00041; fn3; 4.
DR Pfam: PF00047; fn3; 4.
DR Pfam: PF00102; Y_phosphatase; 2.
DR PRINTS: PR00700; EPTYHPHASE.
DR PRINTS: PR00014; EPTYHPHASE.
DR SMART: SM00060; FN3; 4.
DR SMART: SM00408; IGC2; 2.
DR SMART: SM00410; IG_Like; 1.
DR SMART: SM00194; PTPC; 2.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 2.
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DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE: PS50055; TYR_PHOSPHATASE_PP; 2.
KW HydroLase; Immunoglobulin domain; Repeat; Signal.
FT SIGNAL 1 28 POTENTIAL.
SQ SEQUENCE 1502 AA; 16878 MW; AD6705AFEB0F3CFD CRC64;

Alignment Scores:
Pred. No.: 4,46e-218 Length: 1502
Score: 2880.00 Matches: 530
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Best Local Similarity: 88.48% Mismatches: 34
Query Match: 44.69% Indels: 0
DB: 4 Gaps: 0

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QY 90 CACCCACCATCCCATCACCGACCTGGCGGACCAACATCGAGCGCTCAAGCCAGAT 149
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Db 924 HisProIleProIleAlaAspMetAlaGlnHisThrGluArgLeuLysAlaAsnAsp 943
QY 150 GGCCTCAAGTTCCTCCAGAGATATGATCCATGACCCCTGGACAGAGTTCAGTGGAG 209
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Db 944 SerLeuLysLeuSerGlnGluTyrGlnSerIleAspProGlnGlnPheThrTrpGlu 963
QY 210 AATTCAAACCTGGAGGTGACCAACCCCAAGAACCGCTATGCGAATGTCATCGCTACGAC 269
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QY 270 CACTCTGAGTCACTCTTACCTATGATGCGCTGCCCGGAGTGAATCATGATGCC 329
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Db 984 HisSerArgValIleLeuGlnProIleGluIleMetGlySerAspTyrIleAsnAla 1003
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Db 1144 SerIleGlyValGlyArgThrGlyCysPheIleValIleAspAlaMetLeuGluArgIle 1163
QY 810 AAGCAGCAAGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 869
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QY 1770 CAGCTGTGCTACGCTGGCGCTGAGTACCTGGCAGCTTGACCACTATGCAAG 1826
Db 1484 GlnPheCyslyrgrlnalalaleuGlntyrleugllyserPheasphtlstryalathr 1502

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OC Amphibia: Batrachia: Anura: Mesobatrachia: Pipoidae: Pipidae;
OC Xenopodidae: Xenopus.
OX NCBI_TaxID=8355;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=20193505; PubMed=10727868;
RA Johnson K.G., Holt C.E.;
RT "Expression of CRYP-alpha, LAR, PTP-delta, and PTP-rho in the
RT developing xenopus visual system.";
RL Mech. Dev. 92:291-294 (2000).
DR EMBL: AF198450; AAF43607.1; -.
DR HSSP: P18052; IYFO.
DR Interpro: IPR000387; TYR_phosphatase.
DR Interpro: IPR000242; tyr_PP.
DR Pfam: PF00102; Y-phosphatase; 2.
DR PRINTS: PR00700; PTPPHPTASE.
DR SMART: SM00194; PTPC; 2.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE: PS50055; TYR_PHOSPHATASE_2; 2.
DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 2.
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Best Local Similarity: 88.15% Mismatches: 35
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QY 270 CACTCTGAGTCACTCTTACCTATGCGATGGCGTCCCGGAGTGCATCATGATGCC 329
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QY 330 AACTACATCGATGGCTACCGCAGACAGATGCCATCATGCCAGCAGGAGGCCCTGCC 389
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Db 457 CysHisGlnTyrTrpProAlaGlnArgSerAlaArgTyrGlnTrpPheValIleAspPro 476
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Db 477 MetAlaGlnTyrLysMetProGlnTyrIleLeuArgGlnPheLysValIleTrpAspAlaArg 496
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Db 537 PheGlyGlnAspLysProIleSerValIleHisCysSerAlaGlyValIleArgTrpThrGlyVal 556
QY 1650 TTTCATACGTCGATCGCTGCTGAGCGGCGATGCGCTATAGGGCGGTGCGCATGTTT
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 557 PheIleThrLeuSerIleValIleGluArgMetArgTyrGlnIleValIleAspIlePhe 576

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QY 1710 CAGACCGTGAAGACCCCTGCTTACACACAGCTGCTCCATGTGTGACAGACAGACAGTAT 1769
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 577 GlnThrValLysMetLeuArgThrGlnArgProAlaMetValGlnThrGluAspGluTyr 596
QY 1770 CAGCTGTGCTACCGGTGGGGCCCTGGAGTACTCTGGCAGCTTTGACCACTATGCAAGC 1826
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 597 GlnPheCysTyrGlnAlaAlaLeuGlnTyrLeuGlySerPheAspHisTyrAlaThr 615

RESULT 11
Q90815 PRELIMINARY; PRT; 1499 AA.
ID Q90815
AC Q90815;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Protein-tyrosine phosphatase.
GN CRYPALPHAL.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE=95001563; PubMed=7918104;
RA Stoker A.W.;
RT "Isoforms of a novel cell adhesion molecule-like protein tyrosine
    phosphatase are implicated in neural development.";
RL Mech. Dev. 46:201-217(1994).
DR EMBL; L32780; AA64460.1; -.
DR HSSP; P18052; 1YFO.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003598; IG_C2.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR00242; TYR_PP.
DR Pfam; PF00041; fn3; 4.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PR00700; PRYDHPRTASE.
DR SMART; SM00060; FN3; 4.
DR SMART; SM00408; IGc2; 3.
DR SMART; SM00194; PRPC; 2.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
KW Hydroxylase; Immunoglobulin domain.
SQ SEQUENCE 1499 AA; 168570 MW; A1FBD6E3C2453F62 CRC64;

Alignment Scores:
Pred. No.: 4, 31e-217 Length: 1499
Score: 2667.50 Matches: 527
Percent Similarity: 94.328 Conservative: 38
Best Local Similarity: 87.988 Mismatches: 33
Query Match: 44,508 Indels: 1
DB: 13 Gaps: 1

US-09-743-492-1 (1-3467) x Q90815 (1-1499)
QY 30 CACTCTCTGACCCCTGTGAGATGCGAGGCTCACTACAGACCCCGATATGCGAGAC 89
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 902 HisProLysAspProValGlnMetArgArgIleAsnPheGlnThrProGlnMetLeuSer 921
QY 90 CACCCACCCATCCCATCAGCAGCTGGCGGACAACTCAAGCGCCCTCAAGCAAGCAAGAT 149
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 922 HisProIleProValSerGlnLeuAlaGlnHisThrGlnHisLeuLysAlaAsnAsp 941
QY 150 GGCCTCAAGTTCTCCCGAGGATATGATCATGCACTGACCCCTGAGACAGAGTTCACGTGAG 209
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 942 AsnLeuLysLeuSerGlnGlnTyrGlnSerIleAspProGlnGlnGlnPheThrTrpGlu 961
QY 210 AATTCAAACTTGAGAGTGAACAAGCCCAAGACCCGCTATGCGAATGTCATGCGCTACGAC 269

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DB: 13 Gaps: 0

US-09-743-492-1 (1-3467) x O90YJ4 (1-857)

QY 30 CACTCTCTGACCTGTGGAGATGGGAGGCTCACTACAGCCAGCTATGGAGAC 89
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DB 259 HISPPTHTASPRVALGLIMELARGYLLEASNPHGLTHTPROLYMETELASN 278
 ||| |||

QY 90 CACCACCCATCCCATCCAGCTGCGGAGCAACATCGAGCGCTCAACCAAGAT 149
 ||| |||

DB 279 HISPPTHTASPRVALGLIMELARGYLLEASNPHGLTHTPROLYMETELASN 298
 ||| |||

QY 150 GCGCTCAAGTCTCCAGAGATGATGATCCATCGACCTGGACAGCATTTACAGTGGAG 209
 ||| |||

DB 299 ASNLTYLLEASPRGLINTYRGLUSERLLEASPRGLYGLNGLNPHETTRPGU 318
 ||| |||

QY 210 AATTCAAACCTGGAGTGAGCAAGCCCAAGACCGCTATGCGAATGCTATGCGCTCGAC 269
 ||| |||

DB 319 HISSERASNLGLUVALASNLSPROLYSASNARGTYLLEASNVALLEALATYRASP 338
 ||| |||

QY 270 CACTCTCGATCATCTCTACCTTATCGATGGCGTCCCGGAGAGTGCATCATGACC 329
 ||| |||

DB 339 HISSERATGVALLEUENALAPROLYGLNGLYLETHTGLYSERASPTYRILLEASN 358
 ||| |||

QY 330 AACTACATGATGCTTACCCGACAGAAATGCTTACATCGCACAGGCGCCCTGCC 389
 ||| |||

DB 359 ASNTYRILLEASPRGLYTYRARGYSGINASNALATYRILLEALATHRCINGLYPROLEUPRO 378
 ||| |||

QY 390 GAGACCATGGGCGATTTCTGGAGATGGTGGGAACAGCGGACCGCCACTGGTCATG 449
 ||| |||

DB 379 GLUTHTPHEGLYASPHETTRARGMETVALTTPGGLNARGALALATHRVALALMET 398
 ||| |||

QY 450 ATGACACGGCTGGAGAGAAATCCCGGTAATGATGATCACTAGTCCACCGCTGCG 509
 ||| |||

DB 399 METHNARGLEUGLNUYSERARGILELYSCYASPRGLINTYRTPROSERARGLY 418
 ||| |||

QY 510 ACCGAGACCTGGGCTTATTCAGGTGACCTGTTGGACACAGTGGAGCTGGCCATAC 569
 ||| |||

DB 419 THRGUTHTYGLMETLEGLNVALTHRLEUENASPTHTLEGLUENALATHRPH 438
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QY 570 ACTGGGCGACTTGGACCTGCACAAGAGTGGCTCCAGAGCAAGCGTACGCTGAC 629
 ||| |||

DB 439 CYSVALATGHTPHESERLEUHLIYSSASNGLYSERSEGLNUYSRGLNUVALARGIN 458
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QY 630 TTTCAGTTCATGCTGGGCGACACCATGAGTTCCTGATACCCCACTCCATCTGCGC 689
 ||| |||

DB 459 PHEGLNPHETHTALATTPROASPHISGLYVALPROGLINTYRTPROTHRPHOHEU 478
 ||| |||

QY 650 TTCTTACGACGGGTCAAGGCTGCAACCCCTTACAGCGAGGCGCATGGTGTGCACTGC 749
 ||| |||

DB 479 PHELEUATGARGVALIYSTRHCYASNPPTROASPRALAGLYPROLLETLEALANIS 498
 ||| |||

QY 750 AGCGGGGCGTGGGCGGACCGGCTGCTCATGCTGATGATGATGATGATGATGATG 809
 ||| |||

DB 499 SERDALAGLYVALGLYARGHTGLYCSRPHLEVALLEASPRALAMETLEUGLNUAGILE 518
 ||| |||

QY 810 AAGCAGAGAAAGCAGTGCATATGAGCGACATGACCTGATGATGATGATGATGATG 869
 ||| |||

DB 519 LYSHTSGLNUYSTRHVALASPRILETYRGLYHTSVALTHRLEUMETARGSERGLNARG 538
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QY 870 TACATGCTGACAGAGGAGCAAGTACGTTTCATGATGAGGCGCTGCTGAGGCTGCC 929
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DB 539 TYRMETVALGINTHTGLIUSAPRGLINTYRSERPHEILENHSAPRALDEUENGLNUALVAL 558
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QY 930 ACGTGGGCGACACAGAGTGGCTGCCCGGACCTGATGAGCCACATCCAGAAAGTGGCG 989
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DB 559 ALACYSGIYASHTHGLUVALALALAAARGSERLEUPHESERTYRILLEGLNUYSLEUALA 578
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QY 990 PAAAGTCTCCAGGAGAGATGATGACCCGACATGATGATGATGATGATGATGATG 1049
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DB 579 GLNUVALGLNUALAGLYGLNUHTSVALSERGLYMETGLULEGLNUPHELYSRGLNUALASN 598
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QY 1050 TCCAAAGGCCACACAGTCCCGCTTCATCAGCGCCAACTGCGCTGCAACAAGTTCAAGAAC 1109
 ||| |||

DB 599 SERLYSALAHISTHRSERARPHLELSEERALASNLUPROCYSASNLYSPHELYASN 618
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QY 1110 CGGCTGTGACATCATGCTGCTTACGAATGACCCGCTGTGCTGACGCCATCCCTGCT 1169
 ||| |||

DB 619 ARGLEUVALASNLLEMETPTOTYRGLINTHTHARGVALCYLSEUGLINPROLLETARG 638
 ||| |||

QY 1170 GTGGAGGCTGTGACTTACATCAATGCCACCTCTCGATGATGATGATGATGATG 1229
 ||| |||

DB 639 LEUGLNUYLSERASPTYRILLEASNSESRPHEILEASPRGLYTYRARGINNUYSALA 658
 ||| |||

QY 1230 TACATGCTTACACAGGCGCTCTGGCAGAGACCGAGAGACTTCTGGCGCATGCTATG 1289
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DB 659 TYRILLEALATHRCINGLYPROLEUALAGINTHTHGLIUSAPHETTRARGMETLEUP 678
 ||| |||

QY 1290 GAGCAATTCACACATCATGCTGATGACCAAGCTTCGGAGATGGGAGGAGAA 1349
 ||| |||

DB 679 GLUASNASNSETHRTTLEVALVALMETLEUTHLYSLEUARGLEUMETLYARGILUYS 698
 ||| |||

QY 1350 TGCACACATGCTGGCCACAGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1409
 ||| |||

DB 699 CYSHTSGLINTYRTPROALAGIUNATGSEERALARGTYRGLINTYRPHVALIASPRO 718
 ||| |||

QY 1410 ATGGCTGATACAACTGCGCCAGTATATCTGCTGATGATGATGATGATGATGATG 1469
 ||| |||

DB 719 METALAGINTYRASNMETPTROGLINTYRILEUARGLUPHELYVALTHRASPALATG 738
 ||| |||

QY 1470 GATGGCGACTGCAAGCAATCCGCGGCTGCCAGTTCCAGTACAGACGCGCAGAGCGGCGT 1529
 ||| |||

DB 739 ASPGLYGINSETRARGHTHVALAGINPHEGLNPHETHTASPTHTPROGLINGLYVAL 758
 ||| |||

QY 1530 CCCAAGACAGGCGAGGATTCATGACTTCATCGGGCAGGTGCATGAAGCAAGAGACG 1589
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DB 759 PROLYSERGLYGLNUYTHELLEASPRHEILEGLNVALHISLYSTRHLYSGIUN 778
 ||| |||

QY 1590 TTTCGACAGATGGGCTTATTCAGGTGACCTGACAGTGTGCGTGGCGCCGACGGGGTG 1649
 ||| |||

DB 779 PHEGLYGLNAPOLYPROLLESERVALHISCYSERALAGLYVALGLYARGHTHGLYVAL 798
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QY 1650 TTTCATCATCTGACATGCTGCTGCGGAGCGCATGCGTATGAGGCGCTGGTCCGATGTT 1709
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DB 799 PHELEHTHLEUSERLLEVALLEUGIUNATGARGMETARGTYRGLIYVALIASPRILEPHE 818
 ||| |||

QY 1710 CAGACCGTGAAGACCTGCTGCTACACAGCGTCTGCTGCTGCTGCTGCTGCTGCTG 1769
 ||| |||

DB 819 GLNTHRVALIYMETLEUARGHTHARGPROALAMETVALGLNTHRGIUSAPRGLINTYR 838
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QY 1770 CAGCTGCTTACCGTGGCGCTGGAGTACCTGCGGAGCTTTGACCATGATGCAAGC 1826
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DB 839 GLNPHCYSTYRGLNALALALALEUGINTYRLEUGLYSERPHEASPHISTYRATHTHR 857
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RESULT 13

Q13332 PRELIMINARY: PRT: 1948 AA.

ID Q13332 Q15718: Q16341: 01, Created)

AC Q13332: Q15718: Q16341: 01, last sequence update)

DT 01-NOV-1996 (TREMBLrel. 01, last annotation update)

DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)

DE Protein-tyrosine phosphatase, receptor-type, S precursor (EC 3.1.3.48)

DE (Protein-tyrosine phosphatase sigma) (R-PTP-sigma) (PTPRS).

GN PTPRS.

OS Homo sapiens (Human).

OC Eukaryota; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

NCBI_TaxID:9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=FETAL BRAIN;

MD MEDLINE=96102179; PubMed=8524829;

RA Pulido R., Serra-Pages C., Tang M., Streuli M.;

RT "The LAR/prp delta/prp sigma subfamily of transmembrane protein-tyrosine-phosphatases: multiple human LAR, PTP delta, and PTP sigma isoforms are expressed in a tissue-specific manner and associated with

Db 1434 lIeUeGlnPrroIleGluclylIeMetGlySerAspTyrIlleAsnAlaSerTyrValAsp 1453
 QY 342 GGCTACCGCAGCAGATGCTCTACATCGCCACGAGGCCCCCTGCCCGCAGCATGAGC 401
 Db 1454 GtYtYArGArGlnAsnAlaTyrIlleAlaThrGlnGlyProIleuPrroGlnTThrPheGly 1473
 QY 402 GATTTCGAGAAATGGTGTGGAGACGCGCAGCGCCACTGTGGTCATGATGACAGGGCTG 461
 Db 1474 AspPheTrpArgMetValTrrpGlnArgSerAlaThrIlleValMetMetTrpArgLeu 1493
 QY 462 GAGGAGAAATCGCCGGTAAATGATGATGCTACTGGCCAGCCCGCCGACCGGAGCCTGT 521
 Db 1494 GlnGlnLysSerTrgIlleLysCysAspGlnTyrTrpProAsnTrpGlnTThrGlnTyr 1513
 QY 522 GGCTATTTCAGGTGACCTGTGTGGACAGAGTGAGAGCTGGCCACATACATCTGGCCACC 581
 Db 1514 GlyPheIlleGlnValThrIleuLeuAspThrIlleGlnLeuAlaThrPheCysValAlaGlyThr 1533
 QY 582 TTGCGACTCCACAGAGTGGCTCCAGTGAAGCGTGAAGCTGGCTGACATTTCAGTTTCATG 641
 Db 1534 PheSerLeuHisLysAsnGlySerSerGlnLysArgGlnValAlaArgGlnPheGlnPheThr 1553
 QY 642 GGCTGGCCAGACATGAGATTCCTGAGTACCCCACTCCATCCTGGCCTTCCTACAGACGG 701
 Db 1554 AlaTrpProAspHisGlnValProGlnTyrProThrProPheLeuAlaPheLeuAlaArg 1573
 QY 702 GTCAAGGCTGTCAACCCCTAGACAGAGGCGCCATGGTGTCAGTCAGACGGCGGCGTG 761
 Db 1574 ValLysThrCysAsnProProAspAlaGlyProIlleValHisCysSerAlaGlyVal 1593
 QY 762 GGCGCGACCGGCTGTTCATGTCATGTCATGCCATGTGGAGCGGATGAACAGCAGAAC 821
 Db 1594 GtYArGThrGlyCysPheIlleValIlleAspAlaMetLeuGlnArgIlleLysProGlnLys 1613
 QY 822 AGCGTGACATCATGATGGCCACGTCGATCGATCGCATACAGAGCACTACATGATGTCAG 881
 Db 1614 ThrValAspValTyrGlnHisValThrLeuMetArgSerGlnTrgAsnTyrMetValGln 1633
 QY 882 ACAGAGACCATGACTGTTTCATGTCATGAGGCGCTGTGGAGGCTGCCAGTGGCGGCAC 941
 Db 1634 ThrGlnAspGlnTyrSerPheIlleHisGlnAlaLeuLeuGlnValAlaGlyCysGlyAsn 1653
 QY 942 ACAGAGGTCCTGTCCCGCACAACCTGTATGCCCATCCACAAGCTGGCGCCAGCTGCCCA 1001
 Db 1654 ThrGlnValProAlaTrgSerLeuTyrAlaTyrIlleGlnLysLeuAlaGlnValGlnPro 1673
 QY 1002 GGGAGAGTGTGACCGCCCTGAGCTCGAGTTCAAGTTGGCTGGCCAGTCCAGAGGCCAC 1061
 Db 1674 GtYglnHisValThrGlyMetGlnLeuGlnPheLysArgLeuAlaAsnSerLysAlaHis 1693
 QY 1062 ACATCCCGCTTCATCAGCGCACAACCTGCCCTGCACACAAGTTCAAGAAGCGGTGTGAC 1121
 Db 1694 ThrSerArgPheIlleSerAlaAsnLeuProCysAsnLysPheLysAlaGlnValAsn 1713
 QY 1122 ATCATGCTTAGAATGACCGCTGTGTGTCTGTGACAGCCATCGGTGTGTGGAGGGCTCT 1181
 Db 1714 IlleMetProTyrGlnSerThrArgValCysLeuGlnProIlleArgLysValGlnGlySer 1733
 QY 1182 GACTACATCAATGCGCAGTCTCGATGGTGTATAGACAGAGAAAGGCTACATAGCTACA 1241
 Db 1734 AspTyrIlleAsnAlaSerPheIlleAspGlyTyrArgGlnGlnLysAlaTyrIlleAlaThr 1753
 QY 1242 CAGGGGCTCTGTGACAGAGACACGAGCATCTGTGGCGCATGTATAGGAGCACAATTC 1301
 Db 1754 GlnGlyProLeuAlaGlnThrThrGlnAspPheTrpArgMetLeuTrpGlnAsnAsnSer 1773
 QY 1302 ACCATCATGCTCATGCTGACCAAGCTTCGGAGATGGCAGGAGAAATGCCACCACTAG 1361
 Db 1774, ThrIlleValAlaMetLeuThrLysLeuArgGlnMetCtYArgGlnLysCysHisGlnTyr 1793
 QY 1362 TGGCAGCAGAGCGCTCTGCTGCTACCACTCTTGTGTGTGACCGCATGGCTGAGTAC 1421
 Db 1794 TrpProAlaGlnArgSerAlaArgTyrGlnTyrPheValValAspProMetAlaGlnTyr 1813

QY 1422 AACATGCCCCAGTATATACCTGCTGAGTTCAAGTCACGAGTCCCGGAGTGGCAGTCA 1481
 Db 1814 AsnMetProGlnTyrIlleLeuArgGlnPheLysValThrAspAlaArgAspGlyGlnSer 1833
 QY 1482 AGCACAATCCGGCAGTTCACATTCCACAGACTGCCACAGACGCGCTGCCAAGACAGCC 1541
 Db 1834 ArgThrValArgGlnPheGlnPheThrAspTrpProGlnGlnGlyValProLysSerGly 1853
 QY 1542 GAGGAGTTCATTCATTCATCGGCGAGTGCATTAAGCCAAAGGACGATGTGGACAGCAT 1601
 Db 1854 GlnGlyPheIlleAspPheIlleGlnValHisLysThrLysGlnGlnPheGlyGlnAsp 1873
 QY 1602 GGCCCTATCAGCGTGCACATGCTGCTGGCGTGGCGGCGCAGCGGGGTTCATCACTGTG 1661
 Db 1874 GlyProIlleSerValHisCysSerAlaGlyValGlyArgThrGlyValPheIlleThrLeu 1893
 QY 1662 AGCATGCTCTGGAGCGCATGCCCTATGAGGGCGTGGTGCACATGTTTCAGACCGTGAG 1721
 Db 1894 SerIlleValLeuGlnArgMetArgTyrGlnGlyValAlaAspIllePheGlnThrValLys 1913
 QY 1722 ACCCTGGTACAGCGGTCTCTGTCATGTCAGACAGAGGACGATACAGCTGTGCTAC 1781
 Db 1914 MetLeuArgThrGlnArgProAlaMetValGlnThrGlnAspGlnTyrGlnPheCysTyr 1933
 QY 1782 CGTGGCGCCCTGGAGTACCTCGGCGACCTTGGACCACTATGCAACG 1826
 Db 1934 GlnAlaAlaLeuGlnTyrLeuGlnGlySerPheAspHisTyrAlaThr 1948
 RESULT 14
 Q90M00
 ID Q90M00 PRELIMINARY: PRT: 1501 AA.
 AC Q90M00:
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Receptor protein tyrosine phosphatase-sigma, Rptp-sigma.
 OS Rattus sp.
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NC NCBL_TaxID=10118;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94043351; PubMed=8227050;
 RA Yan H., Grossman A., Wang H., D'Eustachio P., Mossie K.,
 RA Musacchio J.M., Silvennoinen O., Schlesinger J.;
 RT "A novel receptor tyrosine phosphatase-sigma that is highly expressed
 RT in the nervous system".
 RL J. Biol. Chem. 268:24880-24886(1993).
 DR HSP; P18052; IYFO.
 DR InterPro: IPRO03962; Enfil_repeat.
 DR InterPro: IPRO03961; FN_III.
 DR InterPro: IPRO03598; IG_C2.
 DR InterPro: IPRO03006; Ig_MHC.
 DR InterPro: IPRO00387; Tyr_MHC.
 DR InterPro: IPRO00242; Tyr_PP.
 DR Pfam: PF00041; fn3; 4.
 DR Pfam: PF00047; Ig; 3.
 DR Pfam: PF00102; Y_phosphatase; 2.
 DR PRINTS; PRO0014; ENTPEPITI.
 DR PRINTS; PRO0700; PRTYPHPTASE.
 DR SMART; SM00060; FN3; 4.
 DR SMART; SM00408; IGc2; 3.
 DR SMART; SM00194; PTPC; 2.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
 DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 2.
 DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 2.
 KW Hydroxylase; Immunoglobulin domain; Repeat.
 SQ SEQUENCE 1501 AA; 168336 MW; C3E089B4BEF430D CRC64;

Alignment Scores: 1,03e-215 Length: 1501
 Pred. No.: 2850.00 Matches: 523

Percent Similarity: 93.99% Conservative: 40
 Best Local Similarity: 87.31% Mismatches: 36
 Query Match: 44.23% Indels: 0
 DB: 11 Gaps: 0

US-09-743-492-1 (1-3467) x Q90M00 (1-1501)

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OY 30 CACTCTGACCCCTGGAGATGGAGGAGGCTCACTACACAGCCCGAGGTATGCGAGAC 89
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DB 903 HISProlYAspProValGIuMeLArGIuLeAsnPhelInThrProGIuMeLLeuSer 922
OY 90 CACCCACCCATCCCATCAGCCAGCTGGCGGACACATGAGCGCCCTCAAGCCAAAGC 149
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 923 HISProlLeuProIleThrAspMetAlaGIuHisMeGIuArgLeuYSAlaAsnAsp 942
OY 150 GGCCTAACTTCTCCAGAGATAGAGTCCATGACCTGGAGACAGATTCACCTGGAG 209
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 943 SerLeuLYLeuSerGIuInGIuSerIleAspProGIuInGIuPhelThrProGIu 962
OY 210 AATTCAACTGGAGGTGAACAAGCCCAAGAACCGCTATGCGAATGCTAGCTGGTGCAG 269
    :|||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 963 HISSerArgLeuGIuAlaAsnLYsProLYsAsnArgTYrAlaAsnValIleAlaTYrAsp 982
OY 270 CACTCTGAGATCACTCTTACTCTATGATGGCTCCCGGAGAGTACTACATCAATGCG 329
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 983 HISSerArgValIleLeuGIuInProLeuGIuInGIuIleMeGIuSerAspTYrIleAsnAla 1002
OY 330 AACTCATGATGAGTACCGCAAGCAAGATGCTTACATGCGACGACGAGGGCCCTGGCCC 389
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1003 AsnTYrValAspLYrTYrArgArgInAsnAlaTYrIleAlaThrGIuInGIuProLeuPro 1022
OY 390 GAGACATGGCGGATTTGAGAAATGATGTGGGAACAGCGGACGCGGCACTGTGGTCAAG 449
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1023 GIuThrPhelLYsAspPhelThrArgMeValTYrGIuInArgSerAlaThrValIleMeL 1042
OY 450 ATGACACGGCTGGAGAGAGATCCCGGTAATAATGTATGATCACTAGTCCGCGCCCTGGCC 509
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1043 MeLThrArgLeuGIuInGIuLYsSerArgValLYsCysAspGLTYrTrpProAsnArgGIu 1062
OY 510 ACCGAGACCTGTGGCTTATTCAGGTGACCCCTGTGGACACAGTGGAGCTGGCCACATAC 569
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1063 ThrGIuThrTYrGLYrPhelIleGIuValIThrLeuLeuAspThrMeLGIuLeuAlaThrPhel 1082
OY 570 ACTGGCGGACCTGGCATCCACAGAGAGGGCTCAGAGAGAGGCTAGAGCTGGCTCGAC 629
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1083 CysValArgTYrPhelSerLeuHisLYsAsnGLYrSerGIuLYsArgGIuValAlaArgHis 1102
OY 630 TTTCAGTTATGAGCTTGGCCGAGACATGAGATTCCTGAGTACCAACTCCATCCTGGCC 689
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1103 PhelGIuPhelThrAlaTrpProAspHisGLYrAlaProGIuTYrProThrProPhelLeuAla 1122
OY 690 TTTCATGACAGGGGTCAAGGCTTCGAACCCCTAGACGACAGGGCCCATGGTGTGACCTGC 749
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1123 PhelLeuArgArgValLYsTYrCysAsnProProAspAlaGLYrProValValAlaHisCys 1142
OY 750 AGCGGGGGGTGGCGCGCCGCTTCATGCTGATGATGATGCCATGTGGAGCGGATG 809
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1143 SerAlaGLYrValLeuArgTYrThrGLYsPhelIleValIleAspAlaMeLLeuGIuArgIle 1162
OY 810 AAGCAGCAAGAGAGCGGTGACATCTATGCGCAGCTGACCTGCATGCGATCAGACAGAGAAC 869
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1163 ArgTYrGIuLYsThrValAspValTYrGLYHisValIThrLeuMeLArgSerGIuArgAsn 1182
OY 870 TACATGCTGACAGAGGAGACAGATAGCTGATTCATCCATGAGAGGCGCTGTGAGGCTGCC 929
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1183 TYrMeLValAlaThrThrGIuAspGIuTYrSerPhelIleHisGIuAlaLeuLeuGIuAlaVal 1202
OY 930 AGTGGCGGACACAGAGGTGCTGCCGCAACCTGATGCCACATCCAGAAAGCTGGGCG 989
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1203 GLYCysGLYAsnThrGIuValProAlaArgSerLeuTYrThrTYrIleGIuInLYsLeuAla 1222
OY 990 CAAGTCTCTCCAGGGAGAGTGTGACCGCATGAGCTGAGTTCAAAGTTCGCGGCACG 1049
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DB 1223 GIuValGIuProGIuInGIuHisValIThrGLYMeLGIuLeuGIuPhelYsArgLeuAlaSer 1242
OY 1050 TCCAAAGGCCACACGTRCCGCTTCATCAGCGGCCACACCTGCGCAACAAGTCAAGAAC 1109
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1243 SerLYsAlaHisThrSerArgPhelIleThrAlaSerLeuProCysAsnLYsPhelYsAsn 1262
OY 1110 CGGCTGGTGAACATATGCCCTTCAGAAATGACCCGGTGTGTGTGGACGCCATCCGGCT 1169
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1263 ArgLeuValAsnIleLeuProTYrGIuSerSerArgValAlCysLeuGIuProIleArgGIu 1282
OY 1170 GTGAGAGGCTGTACTATCATCATATGCCAGGCTCTGTGATGGTATAGACAGCAAGAGCC 1229
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1283 ValGIuInGIuSerAspTYrIleAsnAlaSerPhelIleAspLYrArgGIuInGIuYSAla 1302
OY 1230 TACATGCTTACACAGGGGCTGTGGCAGAGACAGCAAGGACTTGTGGCGCATGTATGG 1289
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1303 TYrIleAlaThrGIuInGIuProLeuAlaGIuThrThrGIuAspPhelThrArgAlaLeuTrp 1322
OY 1290 GACCCAAATTCSCACATCATGCTGATGCTGACCAAGCTTGCGGAGATGGCGCAGGAGAA 1349
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1323 GIuAsnAsnSerThrIleValAlaMeLLeuThrLYsLeuArgGIuMeLGIuArgGIuLYs 1342
OY 1350 TGCACACAGTACTGGCCAGCAGAGCGCTGTCTGCTACCACTATTGTGTGTGAACCG 1409
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1343 CysHisGIuInTYrTrpProAlaGIuArgSerAlaArgTYrGIuInTYrPhelValAlaAspPro 1362
OY 1410 ATGGCTGAGTACACATGCCCCAGATATCTCTGCGTGAAGTTCAGAGTACAGATGCCCGG 1469
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1363 MeLAlaGLYrTYrAsnMeLProGIuInTYrIleLeuArgGIuPhelYsValIThrAspAlaArg 1382
OY 1470 GATGGGACGTCAAGGACAAATCGCGAGTTCACATTCACACAGCGGACGAGCGGGCGTG 1529
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1383 AspGIuInSerArgThrValArgInAlaArgInPhelInPhelThrAspTrpProGIuInGIuAla 1402
OY 1530 CCCAAGACAGCGGAGGATTCATTGACTTTCATGCGGAGGCTGCATTAAGACCAAGAGCAG 1589
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1403 ProLYsSerGLYGIuInGIuPhelIleAspPhelIleGLYInValHisLYsThrLYsGIuIn 1422
OY 1590 TTTCGACAGAGATGGCCCTATCAGCGTGCACGTGACAGTGTGGCTGGCGCCGACCGGGGTG 1649
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1423 PhelGIuInAspGLYrProIleSerValHisCysSerAlaGLYrAlaGIuArgThrGIuVal 1442
OY 1650 TTTCATCTGTGAGCATTCGTCGCGAGCGCATGCGCTATGAGGCGCGTGCACATGTT 1709
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1443 PhelIleThrLeuSerIleValLeuGIuArgMeLArgTYrGIuValAlaAspIlePhe 1462
OY 1710 CAGACCGGTGAAGACCTGTGCATCAGACAGCGTCTGCATGTTGTCAGACAGACAGATAT 1769
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1463 GIuThrValLYsValLeuArgThrGIuArgProAlaMeLValGIuInThrGIuAspGIuTYr 1482
OY 1770 CAGCTGTGCTACCGTGGCGGCTGTGAGATACCTTCGCGACGTTTGACCACTATGCAAGC 1826
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1483 GIuPhelCysPhelInAlaIleLeuGIuTYrLeuGLYSerPhelAspHisTYrAlaThr 1501

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RESULT 15

064605 PRELIMINARY; PRT; 1863 AA.

AC 064605: 064675; 007808; 064621;

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

DE Leukocyte common antigen-related phosphatase ptp2 precursor

DE (EC 3.1.3.48) (Protein-tyrosine phosphatase LAR-PTP2) (Phosphotyrosine

DE phosphatase LAR-PTP2) (PTPase LAR-PTP2) (PTP-PI) (CPTP1)

DE (PTP-sigma).

DE LAR-PTP2.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORMS LAR-PTP2 AND LAR-PTP2B).

RC STRAIN=SPRAGUE-DAWLEY; TISSUE=LIVER, AND BRAIN;


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Db 1325 HisSerAsnLeuGluAlaAsnLysProLysAsnArgTyrAlaAsnValIleAlaTyrAsp 1344
QY 270 CACTCTCGAGTATCTCTTACCTCTATCGATGGCGTCCCGGAGAGTACATCAATGCC 329
Db 1345 HisSerArgValIleLeuEnlProLeuGluGlyIleMetGlySerAspTyrIleAsnAla 1364
QY 330 AACTCATCATGATGGTACCGCAAGCAAGATGCTCATCGCCACGAGGCGCCCGGCC 389
Db 1365 AsnTyrValAspGlyTyrArgArgGlnAsnAlaTyrIleAlaThrGlnLysProLeuPro 1384
QY 390 GAGACCATGGGCGGATTTCTGAGAAATGTGTGGAAACACGCGACGCGCCACTGTGTCATG 449
Db 1385 GlnThrPheGlyAspPheThrParGmetValTrpGlnGlnArgSerAlaThrValValMet 1404
QY 450 ATGACACGCGCTGGAGAGAGAGTCCGGGTAATAATGTGATCACTAGTCCGACCGCTGGC 509
Db 1405 MetThrArgLeuGluGlnLysSerArgValLysCysAspGlnTyrTrpProAsnArgGly 1424
QY 510 ACCGAGACCTGTGGCTTATTCAGGTGACCTGTGGACACAGTGGAGCTGGCCACATAC 569
Db 1425 ThrGlnThrTyrGlyPheIleGlnValThrLeuLeuAspThrMetGlnLeuAlaThrPhe 1444
QY 570 ACTGTGCGACCTTGGCACTCCACAAGATGGCTCCAGTGAAGACGTCGAGCTGCGTCAG 629
Db 1445 CysValArgTyrPheSerLeuHisLysAsnGlySerSerGlnLysArgGlnValArgHis 1464
QY 630 TTTCACTCATGCGCTTGGCCAGACCATGAGTGTCTGAGTACCAATCCATCCTGGCC 689
Db 1465 PheGlnPheThrAlaTrpProAspHisGlyValProGlnTyrProThrProPheLeuAla 1484
QY 690 TTCCTACGAGCGGTCAAGCGCTGCAACCCCTAGACGCGGCGCCATGGTGGTGCATC 749
Db 1485 PheLeuAspArgValLysThrCysAsnProProAspAlaGlyProValValHisCys 1504
QY 750 AGCGGCGCGTGGCGCGCACCGGCTGCTCATCGTATGATGATGATGATGATGATGATGATG 809
Db 1505 SerAlaGlyValGlyArgThrGlyCysPheIleValIleAspAlaMetLeuGlnArgIle 1524
QY 810 AAGCAGAGAGAGCGGTGACATCTATGGCAGCTGACCTGCATCGCATCAGAGAGAAC 869
Db 1525 ArgThrGlnLysThrValAlaSerValTyrGlyHisValThrLeuMetArgSerGlnArgAsn 1544
QY 870 TACATGGTGCACAGGAGGAGGACGATACGTCATCCATGAGGCGCTGCGAGGCTGCC 929
Db 1545 TyrMetValGlnThrGluAspGlnTyrSerPheIleHisGlnAlaLeuLeuGlnAlaVal 1564
QY 930 ACGTGGCGCCACAGAGAGGTGCTGCCGACACCTGTATGCCACATCCAGAGCTGGCG 989
Db 1565 GlyCysGlyAsnThrGlnValProAlaArgSerLeuTyrThrTyrIleGlnLysLeuAla 1584
QY 990 CAAGTGCTCCAGGGGAGAGTGAACCGCATGAGCTCGAGTCAAGTTGCTGGCCAGC 1049
Db 1585 GlnValGlnProGlyGlnHisValThrGlyMetGlnLeuGlnPheLysArgLeuAlaSer 1604
QY 1050 TCCAGAGCCCAACAGCTCCCGCTTCATACGCGCCACACCTCCCTGCAACAAGTTCAAGAAC 1109
Db 1605 SerLysAlaHisThrSerArgPheIleThrAlaSerLeuProCysAsnLysPheLysAsn 1624
QY 1110 CGGCTGGTGAACATATGCCCTACCAATGACCTGATGCTGTCGACGCGCATCCGCTGGT 1169
Db 1625 ArgLeuValAsnIleLeuProTyrGlnLysSerArgValCysLeuGlnProIleArgGly 1644
QY 1170 GTGAGGCGCTGATACATCAATGCCAGCTTCGTGATGTTATAGACAGAGAGGCC 1229
Db 1645 ValGlnGlySerAspTyrIleAsnAlaSerPheIleAspGlyTyrArgGlnGlnLysAla 1664
QY 1230 TACATAGCTACACAGGCGCTTGGCAGAGAGACACCGAGAGACTTCTGGCGCATGCTATGG 1289
Db 1665 TyrIleAlaThrGlnGlyProLeuAlaGlnThrThrGlnAspPheThrArgAlaLeuTrp 1684
QY 1290 GAGCACATTCACCATCATGCTCATGTCAGCAAGCTTCGAGATGGGAGGAGAAA 1349

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Db 1685 GluAsnAsnSerThrIleValValMetLeuThrLysLeuArgGlnMetGlyArgGlnLys 1704
QY 1350 TGGCACCATACTGGCGCACAGAGCGCTCTGCTCGCTACCACTATTGTGTGACCGG 1409
Db 1705 CysHisGlnTyrTrpProAlaGlnArgSerAlaArgTyrGlnTyrPheValValAspPro 1724
QY 1410 ATGGCTGATACAAACATGGCCCGCATATTCCTGCGGAGTTCAGAGTTCAGGATGCCCGG 1469
Db 1725 MetAlaGlnTyrAsnMetProGlnTyrIleLeuArgGlnPheLysValThrAspAlaArg 1744
QY 1470 GATGGCAGTCAAGACAAATCCGGCAGTTCCAGTTCCACAGACTGGCCAGAGAGCGCTG 1529
Db 1745 AspGlyGlnSerArgThrValArgGlnPheGlnPheThrAspThrProGlnGlnGlyAla 1764
QY 1530 CCCAGACAGCGGAGGATTCATTCATTCATTCGCGCAGCTGATTAAGACAGAGAGCAG 1589
Db 1765 ProLysSerGlyGlnGlyPheIleAspPheIleGlyGlnValHisLysThrLysGlnGln 1784
QY 1590 TTTGGACAGATGGGCTTATTCAGCGGTGACCTGCACTGAGTGGGCTGGGCGCACCGGGGTG 1649
Db 1785 PheGlyGlnAspGlyProIleSerValHisCysSerAlaGlyValGlyArgThrGlyVal 1804
QY 1650 TTCATCATCTGAGCATCCGCTGGAGCGCATGCGCTATGAGGCGCTGGTCGACATGTT 1709
Db 1805 PheIleThrLeuSerIleValLeuGlnArgMetArgTyrGlnGlyValValAspIlePhe 1824
QY 1710 CAGACCGTGAAGACCTCGCTACACAGCGTCTGCTGATGCTGCGACAGAGAGCAGTAT 1769
Db 1825 GlnThrValLysValLeuArgThrGlnArgProAlaMetValGlnThrGlnAspGlnTyr 1844
QY 1770 CAGCTGTGTACCGTGGGCGCTGAGAGTACCTCGGACGCTTGACACATGCAAG 1826
Db 1845 GlnPheCysPheGlnAlaAlaLeuGlnTyrLeuGlySerPheAspHisTyrAlaThr 1863

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Search completed: January 17, 2003, 10:12:15
Job time : 288.5 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES					
Result No.	Score	Query Match	Length	DB	ID
1	3236	50.2	607	21	AAV81783
2	3236	50.2	607	21	AAV56098
3	3236	50.2	647	22	AAV27746
4	3236	50.2	647	22	AAU14379
5	3236	50.2	1897	21	AAV19712
6	3236	50.2	1897	21	AAV81785
7	3236	50.2	1897	21	AAV56100
8	3236	50.2	1907	22	AAU14143
9	2880	44.7	1911	16	AAV71726
10	2880	44.7	1911	16	AAV71725
11	2880	44.7	1911	20	AAV94027
12	2880	44.7	1911	22	AAU01459
13	2874.5	44.6	1291	16	AAV75201
14	2850	44.2	1501	16	AAV87588
15	2823.5	43.8	1504	23	AAV57100
16	2753.5	42.7	1495	23	AAV57128
17	2503	38.8	2037	22	AAV71928
18	2347	36.4	442	21	AAV56372
19	1552	24.1	793	13	AAV20743
20	1552	24.1	793	17	AAV02282
21	1552	24.1	793	20	AAV04695
22	1551	24.1	802	17	AAV02283
23	1551	24.1	802	20	AAV04694
24	1551	24.1	807	23	AAV42006
25	1544	24.0	802	13	AAV20744
26	1429	22.2	700	22	AAV3827
27	1429	22.2	700	22	AAV3831
28	1429	22.2	717	22	AAV04617
29	1423	22.1	699	18	AAV27226
30	1423	22.1	699	20	AAV94028
31	1423	22.1	699	22	AAU01460
32	1421	22.1	699	23	AAV57081
33	1358	21.7	870	22	AAU30244
34	1335	20.7	306	22	AAV78268
35	1327	20.6	250	22	AAV59370
36	1297	20.1	623	22	AAV56755
37	1297	20.1	1452	22	AAV79159
38	1297	20.1	1455	22	AAV80147
39	1295	20.1	294	22	AAV78287
40	1288	20.0	245	22	AAV53389
41	1255	19.5	1439	15	AAV66332
42	1255	19.5	1440	20	AAV2591
43	1244.5	19.3	1462	23	AAV97521
44	1243	19.3	1457	23	AAV57308
45	1240	19.2	1407	15	AAV66331

ALIGNMENTS

RESULT 1	AAV81783	standard; Protein; 607 AA.
AC	AAV81783:	
XX	AAV81783:	
DT	07-JUN-2000	(first entry)
DE		
XX		
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DB 521 GlnValHisLysThrLysGlnInPheGlyGlnAspGlyProIleThrValHisCysSer 540
QY 1626 GCTGGCGTGGCCGACCGGGGTTCATCACTCTGACATCGTCTCGAGCCCATGCC 1685
DB 541 AlaGlyValGlyArgThrGlyValPheIleThrLeuSerIleValLeuGlnArgMetArg 560
QY 1686 TATGAGGGGGTGGTCGACATGTTTCAGACCGGTGAAGCCCTGGCTACACAGCGTCCCGC 1745
DB 561 TTTGTTTTTValValAlaAspMetPheGlnThrValLysThrLeuArgThrGlnArgProAla 580
QY 1746 ATGGTCAGACAGAGACAGATATCACTGCTGCTACCGTGGCGCCCTGGAGTACCTCGGC 1805
DB 581 MetValGlnThrGlnAspGlnThrValGlnLeuGlnCysArgArgAlaIleLeuGlnIleuGly 600
QY 1806 AGCTTGACCACTATGCAACG 1826
DB 601 SerPheAspHisThrAlaThr 607
RESULT 2
AAV56098
ID AAV56098 standard; Protein; 607 AA.
AC AAV56098;
XX 17-APR-2000 (first entry)
DT XX
DE LAR tyrosine phosphatase intracellular domain.
XX Intracellular domain; P-subunit; human; leucocyte antigen related; LAR;
KW tyrosine phosphatase; antibody; thyroid cancer.
XX
OS Homo sapiens.
XX
PN WO964591-A1.
XX
PD 16-DEC-1999.
XX
PF 07-JUN-1999; 99WO-JP03054.
XX
PR 08-JUN-1998; 98WO-JP02542.
XX
PA (FUSO) FUSO PHARM IND LTD.
XX
PI Yamamoto H, Tsujikawa K, Uchino Y, Konishi N;
XX
DR WPI: 2000-097539/08.
XX
DR N-PSDB; AA259132.
XX
PT Antibody recognizing the intracellular domain of the human tyrosine
PT phosphatase LAR -
XX
PS Claim 4; Page 73-78; 104pp; Japanese.
XX
XX This sequence represents the intracellular domain (P-subunit) of the
CC human leucocyte antigen related (LAR) tyrosine phosphatase (complete
CC sequence in AAV56098). The invention relates to the generation of an
CC antibody recognizing the intracellular domain of the human LAR tyrosine
CC phosphatase. The antibody is used for the diagnosis and treatment of
CC thyroid cancer.
XX
SO Sequence 607 AA.

Alignment Scores:
Pred. No.: 3,38e-257 Length: 607
Score: 3236.00 Matches: 607
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.22% Indels: 0
DB: 21 Gaps: 0

US-09-743-492-1 (1-3467) x AAV56098 (1-607)

QY 6 GGACTAAGAGACTCTTGGTGGCCACACTCTCTGACCCCTGTGGAGATCGGAGGCTCAAC 65

DB 1 GlnLeuLysAspSerLeuLeuAlaHisSerSerAspProValGlnMetAlaArgLeuAsn 20
QY 66 TACCAGACCCAGAGTATGAGACACACCCATCCCATCAACGACCTGGGAGACAC 125
DB 21 TyrGlnThrProGlnMetArgAspHisProProIleThrValPheIleAspAsn 40
QY 126 ATGAGCGGCTCAAGCCAAAGCATGGCCCTCAAGTCTCCAGAGATATGATCCATGAC 185
DB 41 IleGlnArgLeuLysAlaAsnAspGlyLeuLysPheSerGlnGlnSerIleAsp 60
QY 186 CCGGACAGAGATTCACGTGGGAGAAATTCAACTGAGGTGAACAAGCCCAAGAACCGC 245
DB 61 ProGlnGlnGlnPheThrProGlnAspSerAsnLeuGlnValAsnLysProLysAsnArg 80
QY 246 TATCCGAATGTCAATCGCTACGACACACTCTGAGTCAATCCCTTACATTCATGAGCGTC 305
DB 81 TyrAlaAsnValIleAlaTyrAspHisSerArgValIleLeuThrSerIleAspGlyVal 100
QY 306 CCCGGAGTACTATCAATCAATGCCACTACATGAGTGTACCGCAAGCAAGATCCCTAC 365
DB 101 ProGlnSerAspTyrIleAsnAlaAsnTyrIleAspGlyTyrArgGlnAsnAlaTyr 120
QY 366 ATGCGCCAGGAGGCGCCCGCCGAGACCATGCGCATTTTCGGAATGCGTGGGAA 425
DB 121 IleAlaThrGlnGlnProLeuProGlnThrMetGlyAspPheThrArgMetValTyrGln 140
QY 426 CACCGCAGGCGCATGTGTCATGATGACACGCGCTGAGGAGAAAGTCCCGGTAATGT 485
DB 141 GlnArgThrLarThrValAlaMetMetThrArgLeuGlnGlnLysSerArgValLysCys 160
QY 486 GATCAGTACTGGCCAGCCCTGGCACCGAGACCTGTGCGCTTATTCAGGTGACCTGTG 545
DB 161 AspGlnTyrTrpProAlaArgGlyThrGlnThrCysGlyLeuIleGlnValThrLeuLeu 180
QY 546 GACACAGTGGAGCGTGGCCACATACACCTGCGCACCTTCGCACATCCACAGAGTGGCTC 605
DB 181 AspThrValGlnLeuAlaThrTyrThrValArgThrPheAlaLeuHisLysSerGlySer 200
QY 606 AGTGAGAACCGTGAAGCTGCTCAGTTTCAGTTATGAGCTGCGCAGACATGAGTTCCT 665
DB 201 SerGlnLysArgGlnLeuAlaGlnPheGlnPheMetLarTrpAlaAspHisGlyValPro 220
QY 666 GAGTACCAACTCCCATCTGCGCTTCTTACGACGCGGTCAAGCGCTGCAACCCCTAGAC 725
DB 221 GlnTyrProThrProIleLeuAlaPheLeuArgArgValLysAlaCysAsnProLeuAsp 240
QY 726 GCAAGCGCCATGTGTGGCATCTGACGCGCGGGCGTGGCCGACCGGCTCTTATGTCG 785
DB 241 AlaGlyProMetValValHisCysSerAlaGlyValGlyArgThrGlyCysPheIleVal 260
QY 786 ATTAGTGCATGTGTGAGCGGATGAAGCAGAGAAAGCGGTGACATCTTGGCCACGTG 845
DB 261 IleAspAlaMetLeuGlnArgMetLysGlnLysThrValAspIleTyrGlnHisVal 280
QY 846 ACCTGCATGCGATACAGAGAACTACATGTGTGACAGCAGAGACAGTACGTTCATC 905
DB 281 ThrCysMetArgSerGlnArgAsnTyrMetValGlnThrGlnAspGlnTyrValPheIle 300
QY 906 CATGAGGCGCTGCTGGAGGCTGCGACGTGGCGACACAGAGTGGCTGGCCCAACCTG 965
DB 301 HisGlnAlaLeuLeuGlnAlaAlaThrCysGlyHisThrIleValProAlaAlaArgAsnLeu 320
QY 966 TATGCCACATCCAGAAGTGGGCGCAAGTCCCTCAGAGAGAGATGAGCCGATGAG 1025
DB 321 TyrAlaHisIleGlnLysLeuGlnValProProGlyLysSerValThrAlaMetGln 340
QY 1026 CTCGAGTTCAAGTTGCTGGCCAGCTCCAAAGGCCACAGCTCCGCTTCATCACGCCAAC 1085
DB 341 LeuGlnPheLysLeuLeuAlaSerSerLysAlaHisThrSerArgPheIleSerAlaAsn 360
QY 1086 CTGCGCTGCAACAAGTTCAAGAAACGGGCTGTGAACATCATGCCCTTACGAATGACCCGT 1145

Db 361 LeuProCysAsnLysPheLysAsnArgLeuValAsnIleMetProTyrGluLeuThrArg 380
 QY 1146 GTGTCTGTGCACCCATCCGTGGTGTGGAGGCTGTGACTACATCAATGCCAGCTTCGTG 1205
 Db 381 ValCysLeuGlnProIleArgIleValGluLysSerAspTyrIleAsnIleSerPheLeu 400
 QY 1206 GATGCTTTATGACACAGAGAGCCCTACATAGCTTACACAGAGGCGCTGTGGCAGAGACACC 1265
 Db 401 AspGlyTyrArgGlnGlnIleLysAlaTyrIleAlaIleThrGlnGlyProLeuAlaGluSerThr 420
 QY 1266 GAGGACTTGTGGCGATGTATGGGAGGACCAATCCACATCATGCTGTCGTGACCAAG 1325
 Db 421 GluAspPheThrPargMetLeuThrPoliLysAsnSerThrIleValMetLeuThrLys 440
 QY 1326 CTTCGGAGATGGCAGGAGAGAAATGCCACCACTAGTGGCCAGAGAGCGCTGTGCTGCC 1385
 Db 441 LeuArgGluMetGlyArgGluLysCysGlnTyrTrpProAlaGluArgSerAlaArg 460
 QY 1386 TACCACTACTTTGTTGTGTGACCCGATGGCTGAGTACACATCCCGCAGTATATCTGGCT 1445
 Db 461 TyrGlnTyrPheValValAspProMetAlaGluTyrAsnMetProGlnTyrIleLeuArg 480
 QY 1446 GAGTCAAGGTCACGAGGAGCCGGGATGGGAGGAGCAATCCGCGAGTTCAGCTTC 1505
 Db 481 GluPheLysValThrAspAlaArgAspGlyGlnSerArgThrIleArgGlnPheGlnPhe 500
 QY 1506 ACAGACTGGCCAGAGCAGGCGCTGCCCAAGACAGCAGGAGATTCATTCATTCAGCTTC 1565
 Db 501 ThrAspTrpProGlnGlnIleValProLysThrGlyGluGlyPheIleAspPheIleGly 520
 QY 1566 CAGTGGCATTAAGACCAAGAGAGCATTTGGACAGATGGCGCTATACAGCTGCACTGCACT 1625
 Db 521 GlnValHisLysThrLysGlnGlnIlePheGlyGlnAspGlyProIleThrValHisCysSer 540
 QY 1626 GCTGCGGAGGCGGCGGAGGCGGTTCATCACTGAGATGCTGAGATGCTGAGGAGGCGGCG 1685
 Db 541 AlaGlyValGlyArgThrGlyValPheIleThrLeuSerIleValLeuGlnArgMetArg 560
 QY 1686 TATGAGGCGCTGGTGGATGTTTCAGACCCGTGAAGACCCCTGCTACACAGCGTCTGCGC 1745
 Db 561 TyrGlnGlyValValAspMetPheGlnThrValLysThrLeuArgThrGlnArgProAla 580
 QY 1746 ATGGTGCAGACAGAGAGAGCATGATGCTGCTACCGTGGCGCCCTGGAGTACCTCGGC 1805
 Db 581 MetValGlnThrGluAspGlnTyrGlnLeuGlyTyrArgAlaAlaLeuGlnTyrLeuGly 600
 QY 1806 AGCTTTGACCACTATGCAACG 1826
 Db 601 SerPheAspHisTyrAlaThr 607
 RESULT 3
 ID AAM23746
 ID AAM23746 standard; Protein: 647 AA.
 AC AAM23746:
 DT 12-OCT-2001 (first entry)
 DE Human EST encoded protein SEQ ID NO: 1271.
 XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
 KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
 KW diagnostics; forensic test; gene mapping; genetic disorder;
 KW biodiversity; gene therapy; nutrition.
 OS Homo sapiens.
 XX MO200154477-A2.
 PN 02-AUG-2001.
 PD 25-JAN-2001; 2001WO-US02687.
 FE
 XX

PR 25-JAN-2000; 2000US-0491404.
 PR 17-JUL-2000; 2000US-0617746.
 PR 03-AUG-2000; 2000US-0631451.
 PR 15-SEP-2000; 2000US-0663870.
 XX
 PA (HSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
 PI Cao Y, Drmanac RA, Zhang J, Werhman T;
 XX
 DR WPI: 2001-476164/51.
 DR N-PSDB: AAH98405.
 XX
 PT Isolated polypeptide for treatment of diseases, diagnostics, raising
 PT antibodies and research use -
 PS Claim 20; Page 916-917; 1275pp; English.
 CC The present invention provides the protein and coding sequences of novel
 CC proteins from a variety of organisms, including human, dog, cat, horse,
 CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
 CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
 CC from the organism of interest. They can be used in diagnostics,
 CC forensics, gene mapping, identification of mutations, to assess
 CC biodiversity and for nutritional purposes. The present sequence is a
 CC protein of the invention.
 XX
 SQ Sequence 647 AA:
 Alignment Scores:
 Pred. No.: 3,496-257 Length: 647
 Score: 3236.00 Matches: 607
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 50.22% Indels: 0
 Db: 22 Gaps: 0
 US-09-743-492-1 (1-3467) x AAM23746 (1-647)
 QY 6 GGAGTGAAGAGCATCCCTGGTGGCCCACTGCTGACCCCTGGAGAGTGGGAGGCTCAAC 65
 Db 41 GlnLeuLysAspSerLeuLeuAlaHisSerSerAspProValGluMetArgIleuAsn 60
 QY 66 TACAGAGCCCGCATGATGGAGAGACCAACCACCATCCCATCAGCAGCTGGCGGACAC 125
 Db 61 TyrGlnThrProGlyMetArgAspHisProIleProIleThrAspLeuAlaAspAsn 80
 QY 126 ATCGAGCGCTAAAGCCACAGATGGCTCAAGTTCTCCAGAGATGATGCTATCGAC 185
 Db 81 IleGluArgLeuLysAlaAsnAspGlyLeuLysPheSerGlnGluTyrGluSerIleAsp 100
 QY 186 CCTGGACAGCATTCACCGGGAGGAATCAACCTGGAGAGTGAACAGCCCAAGAACCCG 245
 Db 101 ProGlyGlnGlnPheThrTrpIleuAsnSerAsnLeuValAsnLysProLysAsnArg 120
 QY 246 TATGCAATGTCATCGCTACGACCACTCTGAGTCACTTACCTTATCGATGGCGCTC 305
 Db 121 TyrAlaAsnValIleAlaIleTyrAspHisSerArgValIleLeuThrSerIleAspGlyVal 140
 QY 306 CCCGGAGTGTACTACATCAATGCCAACTACATGATGCTTACCGCAGACAGAAATGCTTAC 365
 Db 141 ProGlySerAspTyrIleAsnAlaAsnTyrIleAspGlyTyrArgGlnAsnAlaTyr 160
 QY 366 ATCGCCAGCAGAGGCGCCCTGCGCCAGACCAATGGCGGATTTCTGGAGAAATGCTGGGAA 425
 Db 161 IleAlaThrGlnGlyProLeuProGlnThrMetGlyAspPheThrPargMetValTrpGlu 180
 QY 426 CAGCCAGAGGCGCATGTGTGATGATGACAGCGCTGGAGAGAGCCCGGTAATAATGT 485
 Db 181 GlnArgThrAlaThrValValMetMetThrArgLeuGlnLysSerArgValLysCys 200
 QY 486 GATCAGTACTGGCCAGCCCGTGGACCGAGACCTGTGGCTTATTCAGGTGACCTGTTG 545

```

Db      201 AspgIntYrPrroalaarglyThrGluThrCysglyLeuIleGlnValThrLeuLeu 220
QY      546 GACACAGTGGAGTGGCCACATPACACTGTGGCAGCTTGGCACTCCACAGAGTGGCTCC 605
      |||
Db      221 AspThrValGluLeuIleThrYrThrValArgThrPheAlaLeuHisLysSerGlySer 240
QY      606 AGTGGAGAACGTCGAGTGGGTGAGTTCAGTTTCATGGCTGGCCGACACAGTGAAGTTCCT 665
      |||
Db      241 SerGluLysArgGluLeuArgGlnPheGlnPheMetAlaTrpProAspHisGlyValPro 260
QY      666 GAGTACCACTCCATCCCTGGCTTCTACAGACGGGTCAAGGCTCAAGCCCTCAAGAC 725
      |||
Db      261 GluTyPrThrProIleLeuAlaPheLeuArgArgValIlysalAcysAsnProLeuAsp 280
QY      726 GCAGGGCCCATGGTGGTGCACATGCAGCGGGCGTGGCCGACCGGCTTCATCGTG 785
      |||
Db      281 AlaGlyProMetValValHisCysSerAlaGlyValGlyArgThrGlyCysPheIleVal 300
QY      786 ATTGATGCCATGTTGGAGGGGATGAAGCAGAGACGGTGGACATTCATGGCCACGTCG 845
      |||
Db      301 IleAspAlaMetLeuGluIleArgMetLysHisGluLysThrValAspIleTyrglyHisVal 320
QY      846 ACCTGCATCGCATCAGACAGAGAACTACATGTCGACAGCAGAGACCATACGTGTTCATC 905
      |||
Db      321 ThrCysMetArgSerGlnArgAsnTyrgMetValGlnThrGluAspGlnTyrgValPheIle 340
QY      906 CATGAGGCGCTGTGGAGGCTGCACGTGGCGGCGACACAGAGGTGCTGCCGCCAACCTG 965
      |||
Db      341 HisGluAlaLeuLeuGluIleAlaIleThrCysGlyHisThrGluValProAlaArgAsnLeu 360
QY      966 TATGCCCAATCCAGAAAGTGGGGCCCAAGTCCCTCCAGGGGAGAGTGTGACCCGATCGAG 1025
      |||
Db      361 TyraIleHisIleLeuLysLeuGlyGlnValProProGlyGlySerValThrAlaMetGlu 380
QY      1026 CTCGAGTTCAAGTCTGCGCCAGCTCCAGAGCCACACGCTCCGCTTCATCAGCGCCAC 1085
      |||
Db      381 LeuGluPheLysLeuLeuAlaSerSerLysAlaHisThrSerArgPheIleSerAlaAsn 400
QY      1086 CTGCCCTGCAGACAGTTTCAGAAACCGGCTGGTGAACATCATGCGCTACGAATTGACCCGT 1145
      |||
Db      401 LeuProCysAsnLysPheLysAsnArgLeuValAsnIleMetProTyrGluLeuThrArg 420
QY      1146 GTGTGCTGCAGCCCATCCGTGGTGTGGAGGGCTGTGCATCACTCAATGCCACCTTCCTG 1205
      |||
Db      421 ValCysLeuGlnProIleArgGlyValGluGlySerAspTyrIleAsnIleSerPheLeu 440
QY      1206 GATGGTTATAGACAGCAGAGGCTCTACATAGCTACACAGGGGCTGTGGCAGAGCACC 1265
      |||
Db      441 AspgIlyTyrArgGlnGlnIlysalATyrIleAlaThrGlnGlyProLeuAlaGlnSerThr 460
QY      1266 GAGGACTTCTGGGCGCATGCTATGGAGACACAATTCACCATCATGCTCATGCTGACCAAG 1325
      |||
Db      461 GluAspPheTrpArgMetLeuTrpGlnHisAsnSerThrIleIleValMetLeuThrLys 480
QY      1326 CTTTCGGGAATGGCGCAGGAGAAATCCACACAGTACTGGCCAGCAGAGCGCTGTGCTCGC 1385
      |||
Db      481 LeuArgGluMetGlyArgGluLysCysHisGlnTyrTrpProAlaGluArgSerAlaArg 500
QY      1386 TACCACTACTTGTGTTTACCCGATGGCTGAGTACACATGGCCCAAGTATATCCGCGG 1445
      |||
Db      501 TyrgIlyTrpPheValValAspProMetAlaGluTyrgAsnMetProGlnTyrIleLeuArg 520
QY      1446 GAGTTCAAGGTCAAGGATCCCGGATGGGAGTCAGAGACAAATCCGCGAGTTCCAGTTTC 1505
      |||
Db      521 GluPheLysValIleThrAspAlaArgAspGlyGlnSerArgThrIleArgGlnPheGlnPhe 540
QY      1506 ACAGACTGGCCAGAGCAGGCGCTGCCAAGACAGCGGAGGAGATTCAATTCATTCAGCGG 1565
      |||
Db      541 ThrAspTrpProGluGlnGlyValProLysThrGlyGluGlyPheIleAspPheIleGly 560
QY      1566 CAGGTGCATATAGACCAAGAGCAGTTTGACAGAGATGGCGCTTCACGGTGCACCTGCAGG 1625
      |||
Db      561 GluValHisLysThrLysGlnPheGlyGlnAspGlyProIleThrValHisCysSer 580

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QY      1626 GCTGGCGTGGGCCGACCGGGGTTCATCATCTGACATCGTCTTGGAGCCATGCGC 1685
      |||
Db      581 AlaGlyValGlyArgThrGlyValPheIleThrLeuSerIleValLeuGluArgMetArg 600
QY      1686 TATGAGGGGTGGTGCACATGTTTCAGACCGGTGAAGCCCTGGCTCACAGGCTCCCTGCC 1745
      |||
Db      601 TyrgIleGlyValValAspMetPheGlnThrValLysThrLeuArgThrGlnArgProAla 620
QY      1746 ATGGTCAGACAGAGAGACCATGATCAGCTGTGCTACCGTGGCGCCCTGGAGTACCTCGGC 1805
      |||
Db      621 MetValGlnThrGluAspGlnTyrgIleuLysCysTyrgAlaIleLeuGluTyrgLeuGly 640
QY      1806 AGCTTGACCATCATGACACG 1826
      |||
Db      641 SerPheAspHisTyraIleThr 647

RESULT 4
AAU14379
ID      AAU14379 standard; Protein; 647 AA.
XX
XX      AAU14379;
AC
XX      24-OCT-2001 (first entry)
DT
XX
DE      Human novel protein #250.
XX
KW      Human; novel protein; Antianaemic; osteopathic; antiinflammatory;
KW      immunomodulatory; cytoskeletal; neuroprotective; vulnerrary; nootropic;
KW      anticonvulsant; antirheumatic; cerebroprotective; antifungal; antiviral;
KW      antibacterial; antiallergic; dermatological; haemostatic; antiasclmatic;
KW      thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
KW      Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
KW      tissue regeneration; immune disorder.
XX
OS      Homo sapiens.
XX
PN      WO200155437-A2.
XX
XX      02-AUG-2001.
PD
XX
PF      25-JAN-2001; 2001WO-US02623.
XX
PR      25-JAN-2000; 2000US-0491404.
XX
PA      (HYSE-) HYSEQ INC.
XX
PI      Tang YT, Liu C, Drmanac RT;
XX
DR      WPI; 2001-451939/48.
XX
DR      N-PSDB; AAS22684.
XX
PT      Isolated polypeptides useful for treating anti-inflammatory diseases,
XX      nervous system disorders, and for regenerating bone and cartilage -
XX
XX      Example 4; Page 792-793; 894pp; English.
XX
CC      The invention relates to polynucleotides encoding novel human
CC      proteins or their active domains. The polypeptides, polynucleotides and
CC      antibodies raised against the polypeptides are used in a method of
CC      treatment of a mammal and prevention of disorders caused by the aberrant
CC      protein expression or activity. The polypeptides can be used as
CC      molecular weight markers, food supplements, and in antibody production.
CC      The polypeptides are used to identify compounds which bind to the
CC      polypeptides. Polynucleotides of the invention are used as probes and
CC      primers, for sequencing, for chromosome or gene mapping, in the
CC      production of recombinant proteins, and in generating anti-sense DNA or
CC      RNA and in gene therapy. Polypeptides of the invention can be used to
CC      target drugs to a tumour, in assays to determine biological activity, to
CC      raise antibodies/elicite an immune response, to determine quantitative
CC      protein levels, as tissue markers, and to isolate receptors or ligands.
CC      Polypeptides of the invention may also be useful in treating platelet
CC      disorders, stem cell disorders, regenerating bone, cartilage, tendon,

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CC ligament and/or nerve tissue, wound healing, treating burns, promoting
CC the proliferation, differentiation and survival of stem cells, as a
CC contraceptive, treating osteoporosis and osteoarthritis, anemia,
CC Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral
CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
CC fungal infection or from autoimmunity, cancer, allergy, asthma,
CC graft-versus-host disease, eczema, hemophilia, thrombosis,
CC anti-inflammatory diseases, nervous system disorders, and infection.
CC The present sequence represents a protein of the invention.

xx Sequence 647 AA;

Alignment Scores:

Pred. No.:	3,49e-257	Length:	647
Score:	3236.00	Matches:	607
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	50.22%	Indels:	0
DB:	22	Gaps:	0

US-09-743-492-1 (1-3467) x AAU14379 (1-647)

QY 6 GGACTGAAGGAGCTCTTGTGGCCACCTGCTGACCTGAGAGATGGGAGGCTCAAC 65
DB 41 GlyLeuLysAspSerLeuLeuAlaHisSerSerAspProValGluMetArgArgLeuAsn 60
QY 66 TACGAGACCCGAGGTATCGAGACCCACCACCCATCCCATCCAGCCAGCTGGGAGAAC 125
DB 61 TyrGlnThrProGlyMetArgAspHisProProIleProIleThrAspLeuAlaAspAsn 80
QY 126 ATCGAGCCCTCAAGCCACAGCATGGCTCAAGTTCTCCAGAGATATAGTCCATCGAC 185
DB 81 IleGluArgLeuLysAlaAsnAspLysLeuLysPheSerGlnGluTyrGluSerIleAsp 100
QY 186 COTGACAGCAGATTACGCGGAGATCAAAACCTGGAGGAGAACAGCCCAAGACCGC 245
DB 101 ProGlyGlnGlnPheThrTTPeLunSerAsnLeuGluValAsnLysProLysAsnArg 120
QY 246 TATGCGAATGTCATCGCTAGACCACTCTCGATCATCTTACCTATCGATGCGCTC 305
DB 121 TyrAlaAsnValIleAlaTyrAspHisSerArgValIleLeuThrSerIleAspGlyVal 140
QY 306 CCCGGAGTGAATCATATATATGSCCACTACATCGATGCTGACCGGAGACAGATCCCTAC 365
DB 141 ProGlySerAspTyrIleAsnAlaAsnTyrIleAspGlyTyrArgLysGlnAsnAlaTyr 160
QY 366 ATCGCAGCAGGGGCGCCCTGGCCGAGACCAATGGGCGATTTCTGGAGATGGTGGGAA 425
DB 161 IleAlaThrGlnGlyProLeuProGluThrMetGlyAspPheTyrArgMetValITrGlu 180
QY 426 CAGGCGACGGCCACTGTGTGTCATGATGACACGGCTGGAGAGAACTCCCGGTAAATGT 485
DB 181 GlnArgThrAlaThrValIleMetMetThrArgLeuGluGluLysSerArgValLysCys 200
QY 486 GATCAGTACTGGCCAGCCCGTGGGACCGAGACCTGTGGCTTATTCAGATGACCTGTGG 545
DB 201 AspGlnTyrTyrProAlaArgGlyThrGluThrCysGlyLeuIleGlnValIThrLeuLeu 220
QY 546 GACGACAGGAGGAGTGGCCACATACACCTGGGCACTTCGACATCCACAAGAGTGGCTCC 605
DB 221 AspThrValGluLeuAlaThrTyrThrValArgThrPheAlaLeuHisLysSerIlySer 240
QY 606 AGTGAAGAGCGTGAAGCTGCTCAGTTCAGTTTCATGAGCTGGCCGACCATGAGATTTCT 665
DB 241 SerGluLysArgGluLeuArgGlnPheGlnPheMetAlaITrProAspHisGlyAlaITrPro 260
QY 666 GAGTACCCCACTCCCATCTGGCTCTCTACGAGCGGTCAAGGCGCTGCAACCCCTAGAC 725
DB 261 GluTyrProThrProIleLeuAlaPheLeuArgArgValLysAlaCysAsnProLeuAsp 280
QY 726 GCAGGGCCCATGAGTGGTCACTGACCGCGGCGGTGGGCGCCACCGGCTGCTCATCTGTG 785
DB 281 AlaGlyProMetValValHisCysSerAlaGlyAlaGlyArgThrGlyCysPheIleVal 300

QY 786 ATTGATGCCATGTTGGAGCGGATGAAGCAGAGACGCGTGAGACATCTATGCGCACGTG 845
DB 301 IleAspAlaMetLeuGluLysArgMetLysHisGlyLysThrValAspIleTyrGlnHisVal 320
QY 846 ACCCTGATGCCGATCACAGAGAACTACATAGTGTGCACAGCAGGACGACGATGCTTCAAC 905
DB 321 ThrCysMetArgSerGlnArgAsnTyrMetValGlnThrGluAspGlnTyrValPheIle 340
QY 906 CATGAGGCGCTGCTGAGGCTGCGACGTGCGGCCACACAGAGAGTGGTCCCGCAACTG 965
DB 341 HisGluAlaLeuLeuGluAlaAlaThrCysGlnHisThrGluValITrAlaITrAsnLeu 360
QY 966 TATGCCCATCCAGAAAGCTGGGCGCAAGTCCCTCCAGGGGAGAGTGTGACCCGATGAG 1025
DB 361 TyrAlaHisIleGlnLysLeuGlyGlnValITrProGlyGlnSerValIThrIleMetGlu 380
QY 1026 CTCGAGTTCAGATTGCTGTGGCCAGCTCCAAAGGCCACACGCTCCCGCTTCAACGCCCAAC 1085
DB 381 LeuGluPheLysLeuLeuAlaSerSerLysAlaHisThrSerArgPheIleSerAlaAsn 400
QY 1086 CTGCCCTGCAACAGTTCAAGAACCGGCTGTGAACATCATGCTCCATGGAATTGACCGGT 1145
DB 401 LeuProCysAsnLysPheLysAsnArgLeuValAsnIleMetProTyrGluLeuThrArg 420
QY 1146 GTGTGCTGCAACCCCATCCGTGCTGTGGAGGCTCTGACTACATCAATGCGCAGTTCTGT 1205
DB 421 ValCysLeuGlnProIleArgGlyValGluGlySerAspTyrIleAsnAlaSerPheLeu 440
QY 1206 GATGGTATACAGCAGAGAGGCTTACATAGCTACACAGAGGCGCTGTGGCAGAGACACC 1265
DB 441 AspGlyTyrArgGlnGlnLysAlaTyrIleAlaThrGlnGlyProLeuAlaGluSerThr 460
QY 1266 GAGGACTTGTGGCGCATGGTATGGAGGACCAATTCACCATCATGTCATGCTGACCAAG 1325
DB 461 GluAspPheITrPArgMetLeuITrPLeuHisAsnSerThrIleIleValMetLeuThrLys 480
QY 1326 CTTGCGGAGATGGGAGGAGAAATGCCACCACTAGTGGCCAGCAGACGCTGCTGCTGC 1385
DB 481 LeuArgGluMetGlyArgGluLysCysHisGlnTyrITrProAlaGluArgSerAlaArg 500
QY 1386 TACCACTACTTGTGTGTGACCCGATGGCTGAGTACAAACATGCCCCATATCTGCGGT 1445
DB 501 TyrGlnTyrPheValValAspProMetAlaGluTyrAsnMetProGlnTyrIleLeuArg 520
QY 1446 GAGTCAAGGTCACGAGATGCCGGGATGGGCGAGTCAAGACAAATCCGCGAGTCCAGTTC 1505
DB 521 GluPheLysValIThrAspAlaArgAspGlyGlnSerArgThrIleArgGlnPheGlnPhe 540
QY 1506 ACAGACTGGCCAGACAGCGCGCTGCCCAAGACAGGCGAGGATTCATGACTTTCATCGGG 1565
DB 541 ThrAspITrProGluGlnGlyAlaITrProLysThrGlyGlnGlyPheIleAspPheIleGly 560
QY 1566 CAGGTGCATTAAGACCAAGAGACGATTTGGACAGAGATGGGCGCTATGACGCTGACGACT 1625
DB 561 GlnValHisLysThrLysGluGlnPheGlyGlnAspGlyProIleThrValHisCysSer 580
QY 1626 GCTGGCGTGGGCGGACCGGGGTGTCAPCACTCGACATGCTCGGAGCGGCGATGGGC 1685
DB 581 AlaGlyValGlyArgThrGlyValPheIleThrLeuSerIleValLeuGluArgMetArg 600
QY 1686 TATGAGGCGCTGTGTCAGATGTTTCAGACCGGTGAAGACCTTCGCTACAGCGTCTGCC 1745
DB 601 TyrGluGlyValValIThrAspMetPheGlnIThrValLysIThrLeuArgIThrGlnArgProAla 620
QY 1746 ATGGTGCAGACAGAGGACGATGATGCTGTGCTACCGCTGGCGGCGCTGGAGTACCTCGGC 1805
DB 621 MetValGlnIThrGluAspGlnTyrGlnLeuCysTyrArgAlaAlaLeuGlnTyrITrLeuGly 640
QY 1806 AGCTTGAACCACTATGCAAGC 1826
DB 641 SerPheAspHisTyrAlaIThr 647

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RESULT 5
AAB19712
ID AAB19712 standard; Protein; 1897 AA.
XX
AC AAB19712;
XX
DT 19-FEB-2001 (first entry)
XX
DE Human protein tyrosine phosphatase PTP LAR.
XX
KW PTP LAR; protein tyrosine phosphatase; leukocyte antigen related;
KW human; epithelial cell; cell migration; cell proliferation; cancer;
KW antitumour; metastasis; antimetastatic; wound healing; vulnery;
KW diagnosis; therapy.
XX
OS Homo sapiens.
XX
XX
FH Key
FH Peptide
FT 1..16
FT /label= Signal_peptide
FT 17..1897
FT /label= Mature_protein
FT 37..99
FT /label= Immunoglobulin_domain
FT 139..199
FT /label= Immunoglobulin_domain
FT 236..290
FT /label= Immunoglobulin_domain
FT 309..391
FT /label= Fibronectin-type-III_domain
FT 403..490
FT /label= Fibronectin-type-III_domain
FT 502..584
FT /label= Fibronectin-type-III_domain
FT 596..686
FT /label= Fibronectin-type-III_domain
FT 698..799
FT /label= Fibronectin-type-III_domain
FT 811..894
FT /label= Fibronectin-type-III_domain
FT 905..990
FT /label= Fibronectin-type-III_domain
FT 1365..1596
FT /label= Protein-tyrosine_phosphatase
XX
FN WO200061180-A2.
XX
PD 19-OCT-2000.
XX
PE 06-APR-2000; 2000WO-US09274.
XX
PR 09-APR-1999; 9905-0128673.
XX
PA (PLAC ) MAX PLANCK INST.
XX
PI Ullrich A, Muller T;
XX
DR WPI: 2000-647399/62.
DR N-PSDB: AAA88739.
XX
PT Treating a disease or a disorder characterized by epithelial cell
PT migration comprises administering a pharmaceutically acceptable
PT composition comprising PTP LAR -
XX
PS Disclosure; Fig 9; 107pp; English.
XX
XX
CC The present sequence is that of human protein tyrosine phosphatase
CC PTP LAR (leukocyte antigen related), a negative regulator of
CC epithelial cell migration and tumor formation, for which
CC beta-catenin is a substrate. A dysfunction of PTP LAR may lead to
CC tumor invasion and metastasis. The invention provides methods for
CC diagnosing, preventing, or treating a disease or disorder
CC characterized by epithelial cell migration, increased tyrosine

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CC phosphorylation of beta-catenin, and/or increased levels of
CC the pool of free beta-catenin, especially cancer, metastasis and
CC aberrant wound healing (claimed). The methods may also be used to
CC treat diseases and disorders with abnormal cell proliferative
CC conditions, including fibrotic and mesangial disorders, abnormal
CC angiogenesis and vasculogenesis, psoriasis, diabetes mellitus and
CC inflammation. Methods are provided for identifying compounds that
CC modulate PTP LAR activity for use in treatment.
XX
SQ Sequence 1897 AA:
XX
Alignment Scores:
Pred. No.: 6 16e-257 Length: 1897
Score: 3236.00 Matches: 607
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.22% Indels: 0
DB: Gaps: 21
US-09-743-492-1 (1-3467) x AAB19712 (1-1897)
QY 6 GCACGTGAGGACCTCTTGCCTGCGCCACATCTCTGACCTGTGAGATGCGAGCTCAAC 65
DB 1291 GILYLEULYASPSERILEUENALAHISSESRASPRVVALGLUETARGTGLEUASN 1310
QY 66 TACCAGACCCAGTAGTATGCGAGACCAACCCATCCCATCCAGACCTGGCGGCAAC 125
DB 1311 TYRGLNTHRPROGLYMETARGSPHISPROPOLLEPHRASPHEUALAASPASN 1330
QY 126 ATCGAGCGGCTCAAGCAACGATGGCCCAATTTCTCCAGAGATGATGTCATCGAC 185
DB 1331 ILEGLIARLEULYSALASNASPGLYLEULYSPHSEGLNLIUITYRGLUSERRILEASP 1350
QY 186 CCTGACACAGCTTCACGCTGGGAGAAATTCAACTGGAGGTGAACAAGCCCAACACCG 245
DB 1351 PROGLYGLNGLNHERHTRPRGLUASNSERASLIEUGLIVALSINLYSPROLYSASNAY 1370
QY 246 TATGCAATGTCAATGCGCTTACGACCACTCTCGAGTATCTTACCTATGATGGCGTC 305
DB 1371 TYRATAASVALILLEALATYRASPHISSEARVALILLEUHRSERILLEASPIYVAL 1390
QY 306 CCCGGAGTAGTACATGCAATGCGCACTACATGATGAGTACCGGCAAGAAATGCTTAC 365
DB 1391 PROGLYSERASPIYRILLESNALASNTYRILEASPIYTYRARGYSGINSNALATYR 1410
QY 366 ATGCCACCGACGAGGCCCTGCGCCGAGACCATGGCGATTTCGAGAAATGGTGGGAA 425
DB 1411 ILEALATHRGLNGLYPROLEUPROGLIUTHRMETGLYASPHETRRPARMETVALITRPGIU 1430
QY 426 CAGCGCAGCGCCACTGTGTCATGATGACAGCGCTGGAGAGAGATCCCGGTTAAATGT 485
DB 1431 GINARGTHRALATHRALVALMETWETTRARGLEUGLIULYSERARVALYSCYS 1450
QY 486 GATCAGTACTGGCCACCGCTGGACCGAGACCTGTGGCTTATTCAGTGACCCGTG 545
DB 1451 ASPGLNTRYTRPRVALARGGLYTRNGIUTHRCYSGILEULIEGLNVALITRLEULAU 1470
QY 546 GACACAGTGAGCTGGCCACATATACACTGTGCGACCTTGCACTCCAAAGATGGCTCC 605
DB 1471 ASPTHRVALGLUENALATHRYTRHRVALARGTHRPHALALEUHSISYSSERGLYSER 1490
QY 606 AGTGAGACCGTGAGCTGCGTCAATTTCAGTTTCAGTTCGGCTGGCCAGACCATGAGTTCT 665
DB 1491 SERGLIYSARGLIUENARGLINPHEGLINPHEMETALATRPPOASPHISGLYALPRO 1510
QY 666 GAGTACCAGACCTCCCTGCGCTTCCAGACAGGCGTCAAGCCGCAACCCCTAGAC 725
DB 1511 GLUTYRPROTHRPROLLEULNALPHELEUARGVALYLSALYASNSNPROLEUASNP 1530
QY 726 GCAGGCGCCATGATGTGCTGCACTGACGCGGCGGTGGCGGACCGGCTTCATCTGTG 785
DB 1531 ATAGLYPROMETVALVALHSYSSERIALAGLYVALGLYARGTHRGLIYSPHEHLEVAL 1550

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QY 786 ATGTGATCCATGTTGGAGCGCATGAGACAGAGAGCGGTGACATCTATGCGCCACGTG 845
 Db 1551 ILeaspAlaMetLeuGluaRgMetLysHsIgLuYstHnValaSpIleTylGlyHsVal 1570
 QY 846 AACTGCAATGCGGTCACAGAGGAACTACATGGTGCAGAGGAGGAGACAGTGTGCATC 905
 Db 1571 ThrCysMetArgSerGlnhArgsnntYrMetValGlnThnGluaspGlnTyrValPheIle 1590
 QY 906 CATGAGGCGCTGCTGAGAGCTGCGACGTCGCGCCACAGAGAGTCCCTGCCCAACCTG 965
 Db 1591 HsIgLuAlaLeuLeuGluaIalaIaIaThrCysGlyHsThnGluValProAlaRgsnLeu 1610
 QY 966 TATGCCACATTCAGAGAGCTGGGCCAAGTGCCTCCAGGGAGAGTGTGACCGCATGGAG 1025
 Db 1611 TyrAlaHsIleGlnLysLengLysLengLysValProProGlyGlnSerValThraIaMetGln 1630
 QY 1026 CTCGAGTTCAGTGTGCGGCGCTCCCAAGGCCACAGCTCCCGTTCATCCGCGCCAAC 1085
 Db 1631 LeuGlnPheLysLeuLeuAlaSerLysAlaHsThnSerArgPheIleSerAlaasn 1650
 QY 1086 CTGCGCTGCACAAAGTTCAGAAACCGGCTGTGATCATCATCTACGATTCAGCCGT 1145
 Db 1651 LeuProCysasnLysPheLysasnArgLeuValasnIleMetProTyrGlnLeuThraArg 1670
 QY 1146 GTGTGTCTGACAGCCCATCCGTGTGTGAGAGGCTCTGACTATCATGATGCCAGCTTCG 1205
 Db 1671 ValCysLengLysProIleArgGlyValaGlnLysSerAspTyrIleasnAlaSerPheLeu 1690
 QY 1206 GATGCTTATAGACACAGAAAGGCTTACATAGCTACACAGAGGCGCTCTGGCAAGAGCAC 1265
 Db 1691 AspGlyTyrArgGlnGlnLysAlaTyrIleAlaThnGlnGlyProLeuAlaLysSerThr 1710
 QY 1266 GAGAGCTTCTGCGCATGCTTATGAGAGACAAATTCACCATCATGCTGATGAGCAAG 1325
 Db 1711 GluaspPheTrpArgMetLeuTrpLuhHsasnSerThrIleIleValMetLeuThraLys 1730
 QY 1326 CTTCGGGAGATGCGGAGAGCAAAATGCCAGTACTGCGCGAGAGCGCTCTGCTGCC 1385
 Db 1731 LeuArgGlnMetGlyArgGlnLysCysHsIgLnTyrTrpProAlaGlnArgSerAlaArg 1750
 QY 1386 TACCACTCTTGTGTGTGATCCCGATGGCTGATACAAACATGCCAGATATCTCTGCT 1445
 Db 1751 TyrGlnTyrPheValaValaSprometLagLutYrAsnMetProGlnTyrIleLeuArg 1770
 QY 1446 GAGTTCAGAGTTCAGGATGCCCGGAGATGGGAGTCAAGAGACAATCCGCGAGTTCAGTTC 1505
 Db 1771 GluPheLysValaThraSpAlaArgspGlyGlnSerArgThrIleArgGlnPheGlnPhe 1790
 QY 1506 ACAGACTGGCCAGAGAGGCGCTGCCAAGACAGCGGAGGATTCATGACTTCATCGGG 1565
 Db 1791 ThrAspTrpProGlnGlnGlyValaProLysThnGlyGlnGlyPheIleaspPheIleGly 1810
 QY 1566 CAGGTGCATTAAGACCAAGAGAGAGTGTGACAGAGTGGGCTATACGCTGACGTGCACT 1625
 Db 1811 GlnValHsLysLysThnLysGlnGlnPheGlyGlnaspGlyProIleThnValHsCysSer 1830
 QY 1626 GCTGCGTGGGCGGCGGCGGCTGTCATCACTGAGCATGCGTCTGAGAGCGCATGGCG 1685
 Db 1831 AlaGlyValaGlyArgThnGlyValaPheIleThnLeuSerIleValaLengLuhRgMetArg 1850
 QY 1686 TATGAGGCGTGTGTCAGATGTTTCAGACCGTGAAGACCTGCTGATACAGAGCGTCTGCG 1745
 Db 1851 TyrGlnGlyValaValaSpmetPheGlnThnValaLysThnLeuArgThrGlnaRgProAla 1870
 QY 1746 ATGTGCGACAGAGAGGAGCAGTATGCTGTGCTACCGTGGCGGCTGGAGTACTCTCGCG 1805
 Db 1871 MetValGlnThnGlnaspGlnTyrGlnLeuCysTyrArgAlaIalaLeuGlnTyrLengLys 1890
 QY 1806 AGCTTTCAGCACTATGCAAGC 1826
 Db 1891 SerPheaspHsIlyrAlaThr 1897

AAy81785
 ID AAY81785 standard: Protein: 1897 AA.
 AC AAY81785;
 XX
 DT 07-JUN-2000 (first entry)
 XX
 DE Human protein tyrosine phosphatase, LAR, protein sequence.
 XX
 KW Human: protein tyrosine phosphatase; antibody: intracellular domain; LAR;
 KW CD45; PTP; diagnosis; insulin resistance related disease; syndrome X;
 KW non-insulin dependent diabetes mellitus; arteriosclerosis; therapy;
 KW heart disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200002922-AI.
 XX
 PD 20-JAN-2000.
 XX
 PF 06-JUL-1999; 99WO-JP03656.
 XX
 PR 10-JUL-1998; 98WO-JP03120.
 XX
 PA (FUSO) FUSO PHARM IND LTD.
 XX
 PI Yamamoto H, Tsujikawa K, Uchino Y;
 XX
 DR WPT: 2000-182215/16.
 DR N-PSDB: AAZ91908.
 XX
 PT Antibody for diagnosis and treatment of insulin resistance disorders
 PT and syndrome X recognises the intracellular domains of tyrosine
 PT phosphatase -
 XX
 PS Example 1; Page 61-77; 83pp; Japanese.
 XX
 CC This sequence is the protein tyrosine phosphatase LAR. The invention
 CC relates to an antibody specifically recognising the intracellular domains
 CC of two or more protein tyrosine phosphatases (PTPs). The antibody is
 CC useful for the detection and assay of PTP including novel phosphatases
 CC generated by cloning; and diagnosis, treatment and prevention of insulin
 CC resistance related diseases and non-insulin dependent diabetes mellitus,
 CC syndrome X and arteriosclerosis and heart disorders.
 XX
 SQ Sequence 1897 AA;
 Alignment Scores:
 Pred. No.: 6.16e-257 Length: 1897
 Score: 3236.00 Matches: 607
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 50.22% Indels: 0
 DB: 21 Gaps: 0
 US-09-743-492-1 (1-3467) x AAY81785 (1-1897)
 QY 6 GCAGTGAAGAGATCTCTGCTGGCCCACTCTGTGACCTGTGAGATGCGAGGCTCAAC 65
 Db 1291 GlyLeuLysAspSerLeuLeuAlaHsSerSerAspProValGlnMetArgArgLeuasn 1310
 QY 66 TACGAGCCCGCAGTATGAGACACACACCCATCCCATCAGCCGACCTGCGGAGCAAC 125
 Db 1311 TyrGlnThnProGlyMetLuhRgAspHsProProlleProlleThraSpLeuAlaSpasn 1330
 QY 126 ATGAGCGCGCTCAAGCAACAGATGCGCTCAAGTTCCTCCAGAGTATGATCATCGAC 185
 Db 1331 IleGluArgLeuLysAlaAsnaspGlyLeuLysPheSerGlnGlnLutYrGlnSerIleasp 1350
 QY 186 CTGAGACAGCACTTACGCTGGAGAAATTCAAACCTGAGAGTGAACAAGCCCAAGACCGC 245
 Db 1351 ProGlyGlnGlnPheThnTrpGluasnSerAsnLeuGlnValaSnLysProLysasnArg 1370

QY 246 TATGCAATGTCATCGGCTAGACACATCTGAGTCATCTTACCTGATCATGAGCGTC 305
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 Db 1371 TyAlaAsnValIleAlaIleTyAspHisSerArgValIleLeuThrSerIleAspGlyVal 1330
 QY 306 CCGGGAGTACTACATCAATGCCAACTACATGCGTACCGCAAGCAAGATCGCTAC 365
 |||||
 Db 1391 ProGlySerAspTyrIleAsnAlaAsnTyrIleAspGlyTyrArgGlyGlnAsnAlaTyr 1410
 QY 366 ATGGCCAGCGAGGGCCCCCGGAGACACATGGGCGCATTTCTGGAATAATGGTGGAA 425
 |||||
 Db 1411 IleAlaThrGlnGlyProLeuProGlyIleThrMetGlyAspPheTyrPargMetValTyrGlu 1430
 QY 426 CACGCGACGGGCACTGTGTCAATGATGACACGGCTGGAGGAAGTCCCGGGTAAATGT 485
 |||||
 Db 1431 GlnArgThrIleThrValIleMetMetThrArgLeuGlnGlySerArgValIleGlyCys 1450
 QY 486 GATCACTACTGGCCACGCCGTGGACACGACCTGTGGCTTATTCAGTGCACCTGTG 545
 |||||
 Db 1451 AspGlnTyrTyrProAlaArgGlyThrGlnThrCysGlyLeuIleGlnValIleThrLeu 1470
 QY 546 GACACAGTGGAGCTGGCCACATACACTGTGGCACCTTGGCACTCCACAAAGTGGCTCC 605
 |||||
 Db 1471 AspThrValGlyLeuAlaThrTyrThrValArgThrPheAlaLeuHisLysSerGlySer 1490
 QY 606 AGTGAGAGCGTAGCTGCTGCTCACTTCACTGCTGCGCCAGACCATGGAGTTCCT 665
 |||||
 Db 1491 SerGlnLysArgGlnLeuAlaGlnGlnPheGlnPheMetAlaThrProAspHisGlyValPro 1510
 QY 666 GAGTACCCAACTCCACTCTGGGCTTCTTACGACGGGTCAAGGCTGGCAACCCCTAGAC 725
 |||||
 Db 1511 GlnTyrProThrProIleLeuAlaPheLeuArgArgValLysAlaCysAsnProLeuAsp 1530
 QY 726 GCAGGGCCCATGGTGGTGCATCGACGGCGGCGTGGCCCGCCAGCTGCTCATGTG 785
 |||||
 Db 1531 AlaGlyProMetValIleHisCysSerAlaGlyValGlyArgThrGlyCysPheIleVal 1550
 QY 786 ATTGATGCGCATGTGGAGCGGATGAACACAGAGAGAGCGGTGACATCTATGGCCAGCTG 845
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 Db 1551 IleAspAlaMetLeuGlnAlaGlnMetLysHisGlnLysThrValAspIleTyrGlnHisVal 1570
 QY 846 ACCTGCATGCGATACACAGAGAACTACATGCTGCAGAGGAGGACAGCATGTTTCATC 905
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 Db 1571 ThrCysMetArgSerGlnArgAsnTyrMetValGlnThrGlnAspGlnTyrValPheIle 1590
 QY 906 CATGAGGCGGTGTGGAGGCTGCCACCTGGCGGCACACAAAGTGCCTGCCCGCCAGCTG 965
 |||||
 Db 1591 HisGlnAlaLeuLeuGlnAlaAlaThrCysGlyHisThrGlnValProAlaArgAsnLeu 1610
 QY 966 TATGCCCATCTCGAAGCTGGGCGCAAGTGCCTGCAGGAGAGTGTGACCGCATGAG 1025
 |||||
 Db 1611 TyrAlaHisIleGlnLysLeuGlnValProProGlyLysSerValIleThrAlaMetGln 1630
 QY 1026 CTGCACTTCAAGTGTGGCCAGCTCCAAAGGCCACACAGTCCCGCTTCATCAGCGCCAC 1085
 |||||
 Db 1631 LeuGlnPheLysLeuLeuAlaSerSerLysAlaHisThrSerArgPheIleSerAlaAsn 1650
 QY 1086 CTGCGCTGCACAAAGTTCAGAGAACCGGCTGTGAACATCATGCTGCATGCAATGACCCCT 1145
 |||||
 Db 1651 LeuProCysAsnLysPheLysAsnArgLeuValAlaHisIleMetProTyrGlnLeuThrArg 1670
 QY 1146 GTGTGCTGTGAGCCCATCCCTGTGTGGAGGCGTGTGACATCAATGACATGCGCATGCTG 1205
 |||||
 Db 1671 ValCysLeuGlnProIleArgGlyValGlnGlySerThrAspTyrIleAsnAlaSerPheLeu 1690
 QY 1206 GATGCTTATAGACAGAGAAAGCTTACATGCTACACAGGCGGCTGTGGCAGAGAGACCC 1265
 |||||
 Db 1691 AspGlyTyrArgGlnGlnLysAlaTyrIleAlaThrGlnGlnProLeuAlaGlnSerThr 1710
 QY 1266 GAGGACTTCTGGGGCATGCTATGAGGAGACAAATTCACACATCTGCTCATGCTGACCAAG 1325
 |||||
 Db 1711 GlnAspPheThrPargMetLeuTyrGlnHisAsnSerThrIleIleValMetLeuThrLys 1730
 QY 1326 CTTCGGGAGATGGGCGAGGAGAAATGCGCACCACTAGTGGCCAGAGCGCTGTGGTGGC 1385

Db 1731 LeuArgGlnMetGlyArgGlnLysCysHisGlnIleTyrThrProAlaGlnArgSerAlaArg 1750
 QY 1386 TACCAGTACTTGTGTGTGACCCGATGGCTGAGTACAAATGCCAGTATATCTTCGCT 1445
 |||||
 Db 1751 TyrGlnIleThrPheValIleAspProMetAlaGlnIleTyrAsnMetProGlnTyrIleLeuArg 1770
 QY 1446 GAGTTCAAAGTCCACGGATGCCCGGATGGGCAGTCAAGAGCAATCCGGCAGTTCCAGTTC 1505
 |||||
 Db 1771 GlnPheLysValIleThrAspAlaArgAspGlyGlnSerArgThrIleArgGlnPheGlnPhe 1790
 QY 1506 ACAGACTGGCCAGAGCGAGGGCGTCCCAAGACAGCGAGGGATTCATTGATTCATGGGG 1565
 |||||
 Db 1791 ThrAspThrProGlnGlnGlnValAlaProLysThrGlnGlnGlyPheIleAspPheIleGly 1810
 QY 1566 CAGGTGCATTAAGACCAAGAGACAGTTCGACAGAGATGGGCTTACAGGTGCATCGCACT 1625
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 Db 1811 GlnValHisLysThrLysGlnGlnPheGlyGlnAspGlyProIleThrValHisCysSer 1830
 QY 1626 GCTGGCGTGGCGCCGACCGGGGTGTTCATCACTGTAGCATCGTCTGGAGCGCATGGC 1685
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 Db 1831 AlaGlyValGlyArgThrGlyValPheIleThrLeuSerIleValIleuGlnArgMetArg 1850
 QY 1686 TATGAGCGCGTGGTGCACATGTTTCAGACCGGTGAAGACCGTGGCTACACAGCGCTGGCC 1745
 |||||
 Db 1851 TyrGlnGlyValValAspMetPheGlnThrValLysThrLeuArgThrGlnAlaGlyProAla 1870
 QY 1746 ATGGTCGACAGAGAGACAGATACAGTGTGCTACCGGTGCGGCGCTGAGTACCTGGC 1805
 |||||
 Db 1871 MetValGlnThrGlnAspGlnTyrGlnLeuCysTyrArgAlaIleLeuGlnTyrLeuGly 1890
 QY 1806 AGCTTGACCATATGCAAGC 1826
 |||||
 Db 1891 SerPheAspHisTyrAlaThr 1897.
 RESULT 7
 AAY56100
 ID AAY56100 standard; Protein; 1897 AA.
 AC AAY56100;
 XX
 DT 17-APR-2000 (first entry)
 XX
 DE LAR tyrosine phosphatase.
 XX
 KW Intracellular domain; P-subunit; human; leucocyte antigen related; LAR;
 KW tyrosine phosphatase; antibody; thyroid cancer.
 XX
 OS Homo sapiens.
 XX
 PN W09964591-A1.
 XX
 PD 16-DEC-1999.
 XX
 PF 07-JUN-1999; 99MO-JP03054.
 XX
 PR 08-JUN-1998; 98MO-JP02542.
 XX
 PA (FUSO) FUSO PHARM IND LTD.
 XX
 PI Yamamoto H, Tsujikawa K, Uchino Y, Konishi N;
 XX
 DR WPI; 2000-097539/08.
 DR N-PSDB; AA259133.
 XX
 PT Antibody recognizing the intracellular domain of the human tyrosine
 PT phosphatase LAR -
 XX
 PS disclosure; Page 81-97; 104pp; Japanese.
 XX
 CC This sequence represents the complete human leucocyte antigen related
 CC (LAR) tyrosine phosphatase. The invention relates to the generation of
 CC an antibody recognizing the intracellular domain of the human LAR

CC tyrosine phosphatase (AAV56098). The antibody is used for the diagnosis
 CC and treatment of thyroid cancer.

XX Sequence 1897 AA;

Alignment Scores:

Pred. No.:	6,16e-257	Length:	1897
Score:	3236.00	Matches:	607
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	50.22%	Indels:	0
	21	Gaps:	0

US-09-743-492-1 (1-3467) x AAV56100 (1-1897)

```

QY 6 GGAAGTGAAGAGCTCTTGGTGGCCCACTCTGACCTGTGGAGATGGCGAGCTCAAC 65
    |||
Db 1291 GYleuLysAspSerleuLeuAlaHisSerSerAspProValGluMetArgValLeuAsn 1310
QY 66 TACCAAGACCCAGATATGCGAGACACCCACCATTCCCATCAGCAGCTGGCGAGCAAC 125
    |||
Db 1311 TYrGlnThrProGlyMetArgAspHisProIleProIleThrAspLeuAlaAspAsn 1330
QY 126 ATCGAGCGGCTCAAAAGCCACGATGGCTCAAGTTCTCCGAGAGATATGATCATCGAC 185
    |||
Db 1331 TleGluArgLeuLysAlaAsnAspGlyLeuLysPheSerGlnGlnIleuSerIleAsp 1350
QY 186 CCTGGACAGACAGTTCACGTGGGAGAAATTCAAACCTGAGAGTGAACAGCCCAAGAACCGC 245
    |||
Db 1351 ProGlyGlnGlnPheThrTrpGluAsnSerAsnLeuGluValAsnLysProLysAsnArg 1370
QY 246 TATGGGAATGTCATGCGCTACGACCACTCTGACATCCATTACCTATATCGATGGCGTC 305
    |||
Db 1371 TYrAlaAsnValIleAlaIleThrAspHisSerArgValIleLeuThrSerIleAspGlyVal 1390
QY 306 CCCGGAGTGTACTATCATCATGCTCAACTACATGATGGCTACCGCAGACAGAAATGCTTAC 365
    |||
Db 1391 ProGlySerAspTYrIleAsnAlaAsnTYrIleAspGlyTYrArgLysGlnAsnAlaTYr 1410
QY 366 ATCGCAGACAGGCGCCCTGGCCCGGACCAATGGCGGATTTGGGAAATGGTGGGAA 425
    |||
Db 1411 TleAlaThrGlnGlyProLeuProGluThrMetGlyAspPheTrpArgMetValTrpGlu 1430
QY 426 CAGCCACAGCGCCACTGTGTGATGATGACAGCGCTGGAGAGAAAGTCCCGGTAAATGT 485
    |||
Db 1431 GlnArgThrAlaThrValValMetMetThrArgLeuGlnGluLysSerArgValLysCys 1450
QY 486 GATCAGTACTGGCCAGCCCGGCGACCGAGACCTGTGGCTTATTTAGGTGACCTGTGG 545
    |||
Db 1451 AspGlnTYrTrpProAlaArgGlnTYrThrGlnTYrCysGlyLeuIleGlnValThrLeuLeu 1470
QY 546 GACACAGTGGAGCTGGCCACATACACTGTGGCAGCTTGGCAGCTCCACAAAGATGGCTCC 605
    |||
Db 1471 AspThrValGluLeuAlaThrTYrThrValArgThrPheAlaLeuHisLysSerGlySer 1490
QY 606 AGTGAAGACGTGAGCTGGCTGAGTTTCAGTTTCATGCGCTGGCCAGACCATGGAGTTCT 665
    |||
Db 1491 SerGlnLysArgGluLeuArgGlnPheGlnPheMetAlaTrpProAspHisGlyValPro 1510
QY 666 GAGTACCCCACTCCATCTGGCTTCCCTACGAGCGGTAAAGGCTTCGAACCCCTTAGAC 725
    |||
Db 1511 GlnTYrProThrProIleLeuAlaPheLeuArgValLysAlaCysAsnProLeuAsp 1530
QY 726 GCAGGCGCCATGGTGTGACTGACGCGCGGGGCTGGCGGACCGGCTTCATCGTG 785
    |||
Db 1531 AlaGlyProMetValValHisCysSerAlaGlyValGlyArgThrLeuLysPheIleVal 1550
QY 786 ATTGATGCCATGTTGGAGCGGATGAAGCAGAGAAGACCGGTGACATTCATGCGCACGTG 845
    |||
Db 1551 TleAspAlaMetLeuGlnArgMetLysHisGlnLysThrValAspIleTYrGlnHisVal 1570
QY 846 ACCTGCATGCGATCACAGAGAACTACATGTGCGAGACGAGACCATGATCGTTTCATC 905
    |||
  
```

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Db 1571 ThrCysMetArgSerGlnArgAsnTYrMetValGlnThrGlnAspGlnTYrValPheIle 1590
QY 906 CATGAGGCGCTGCTGGAGCGTCCGACCTGGCGGCCACACAGAGTGGCTGGCCCAACTG 965
    |||
Db 1591 HisGluAlaLeuLeuGlnAlaIleThrProGlyHisIleThrGluValProAlaArgAsnLeu 1610
QY 966 TATGCCACATCCAGAAAGCTGGGCGCAAGTGGCTTCCAGGGGAGAGTGTGACCGCATGAG 1025
    |||
Db 1611 TYrAlaHisIleGlnLysLeuGlnValProProGlyGlnSerValThrAlaMetGlu 1630
QY 1026 CTCGAGTTCAGATTGGCTGGCCACTCCCAAGGGCCACACGTCGGCTTCATCAGCGCCAAC 1085
    |||
Db 1631 LeuGlnPheLysLeuLeuAlaSerSerLysAlaHisIleThrArgPheIleSerAlaAsn 1650
QY 1086 CTCGCCCTGCACAAGTTTCAAGAACCGGCTGGTGAACATCATGCGCTTACGAAATGACCGCT 1145
    |||
Db 1651 LeuProCysAsnLysPheLysAsnArgLeuValAsnIleMetProTYrGlnLeuThrArg 1670
QY 1146 GTGTGTCTGCAGGCCATCCGTGGTGTGACAGCGCTGTACTACATCCAAATCCACCTTCTG 1205
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Db 1671 ValCysLeuGlnProIleArgGlyValGlnGlySerAspTYrIleAsnAlaSerPheLeu 1690
QY 1206 GATGCTTATAGACAGCAGAAAGGCTTACATAGCTACACAGAGGCGCTTGGCAGAGACACC 1265
    |||
Db 1691 AspGlyTYrArgGlnGlnLysAlaTYrIleAlaThrGlnLysProLeuAlaGlnSerThr 1710
QY 1266 GAGCACTTCTGGCGCATGCTATGGAGAGACAAATTCACCACTCAATCCGTCATGTGACCAAG 1325
    |||
Db 1711 GlnAspPheTrpArgMetLeuTrpGlnHisAsnSerThrIleIleValMetLeuThrLys 1730
QY 1326 CTTCGGGAGATGGCGAGGAGAAATGCCACACAGTACTGGCGCAGAGCGCTGCTGCTCG 1385
    |||
Db 1731 LeuArgGluMetGlyArgGlnLysCysHisGlnTYrTrpProAlaGlnArgSerAlaArg 1750
QY 1386 TACCACTACTTGTGTGTACCCGATGGCTGAGTACAAACATGCCCAAGTATATCTGCGGT 1445
    |||
Db 1751 TYrGlnTYrPheValValAspProMetAlaGlnTYrAsnMetProGlnTYrIleLeuArg 1770
QY 1446 GAGTTCAGAGTTCAGGATGCGCGGATGGGAGCTCAAGGACATCCGGCGAGTTCCAGTTCC 1505
    |||
Db 1771 GlnPheLysValThrAspAlaArgAspGlyGlnSerArgThrIleArgGlnPheGlnPhe 1790
QY 1506 ACAGACTGGCCACAGCAGGCGCTGCCCAAGACAGCGGAGGAGATTGATGACTTCATCGGG 1565
    |||
Db 1791 ThrAspTrpProGlnGlnGlyValProLysThrGlyGlnGlyPheIleAspPheIleGly 1810
QY 1566 CAGGTGCATAAAGCCAAAGAGCAGTTTGGACAGAGATGGGCTTACAGGTGCACTGACGT 1625
    |||
Db 1811 GlnValHisLysThrLysGlnGlnPheGlnPheGlnAspGlyProIleThrValHisCysSer 1830
QY 1626 GCTGGCGTGGCGCCAGCGGCGGTTCATCACCTGTGAGCATGCTGCGAGCGCATGGCG 1685
    |||
Db 1831 AlaGlyValGlyArgThrGlyValPheIleThrLeuSerIleValLeuGluArgMetArg 1850
QY 1686 TATGAGCGCGTGGTGCATGTTTCAGACCGTGAAGACCTGGCTGACACAGCGTCTGCGC 1745
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Db 1851 TYrGlnGlyValValAspMetPheGlnThrValLysThrLeuArgThrGlnArgProAla 1870
QY 1746 ATGCTGCAACAGAGACCATGATCAGCTGTGTGTACCGTGGCGGCTTGGAGTACTCTGGC 1805
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Db 1871 MetValGlnThrGlnAspGlnTYrGlnLeuCysTYrArgAlaAlaLeuGlnLysTYrLeuGly 1890
QY 1806 AGCTTGCACCATATGACAGC 1826
    |||
Db 1891 SerPheAspHisIleTYrAlaThr 1897
  
```

RESULT 8

AAU14143

ID AAU14143 standard; Protein; 1907 AA.

XX

AC AAU14143;

XX

DT 24-OCT-2001 (first entry)


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QY 1146 GGTGTCTGACACCCATCCGTGTGTGAGGGCTCTGACTACATCAATGCCAGCTTCCGTG 1205
DB 1681 ValCysLeuGlnProIleArgIleValGlnGlySerAspTyrIleAsnIleSerPheLeu 1700
QY 1206 GATGGTTATAGACAGCAAGAGCCCTACATAGCTACACAGGGCCTTGGCAGACAGCACC 1265
DB 1701 AspGlyTyrArgGlnGlnGlnIleValIleAlaThrGlnGlyProLeuAlaGlnSerThr 1720
QY 1266 GAGGACTTGGCGGATGCTATGGGAGCAATTCACCATCATGCTCATGGTGAGCAAG 1325
DB 1721 GluAspPheThrParGmetLeuThrPgluHisSerThrIleIleValIleLeuThrLys 1740
QY 1326 CTTGGGGAGATGGGAGGAGGAATGCCACAGTACTGGCCAGCAGAGCGCTCTGCTGCC 1385
DB 1741 LeuArgGlnMetGlyArgGlnLysCysHisGlnTyrTrpProAlaGlnArgSerAlaArg 1760
QY 1386 TACCACTACTTTGTTGTTACCCGATGCTGAGTACACATGCCCGCATATATCTGCGCT 1445
DB 1761 TyrGlnTyrPheValIleValAspPheMetAlaGlnTyrAsnMetProGlnTyrIleLeuArg 1780
QY 1446 GAGTTCACAGTCACGAGATCCCGGATGGGAGTCACAGCAATCCGAGTTCACATGC 1505
DB 1781 GluPheLysValThrAspAlaArgAspGlyGlnSerArgThrIleArgGlnPheGlnPhe 1800
QY 1506 ACAGACTGGCCAGACAGGCGCTGCCCAAGACAGCGGAGGATTCATTGACTTCATCGGG 1565
DB 1801 ThrAspTrpProGlnGlnGlnIleValProLysThrGlnGlyPheIleAspPheIleGly 1820
QY 1566 CAGGTGCATAAACACCAAGAGCAATTTGGACAGAGATGGCCCTATCAGGTGCACCTGCAC 1625
DB 1821 GlnValHisLysThrLysGlnGlnPheGlyGlnAspGlyProIleThrValHisCysSer 1840
QY 1626 GCTGGGCTGGCGGACCGGGGTTGTCATCACTGAGATGCTCGTGAGGCGCATGGCC 1685
DB 1841 AlaGlyValGlyArgThrGlyValPheIleThrLeuSerIleValIleuGlnArgPheArg 1860
QY 1686 TATGAGGCGGTGGTGCACATGTTTCAGACCGCTGAAGACCCCTGCTACACAGCGTCCGCC 1745
DB 1861 TyrGlnGlyValIleValAspPheThrGlnThrValLysThrLeuArgThrGlnArgProAla 1880
QY 1746 ATGGTGCAGACAGAGGACCATGATACGCTGTGCTACCGCGCGCCCTGGAGTACCTCGCC 1805
DB 1881 MetValGlnThrGlnAspGlnTyrGlnLeuGlyTyrArgAlaAlaLeuGlnTyrLeuGly 1900
QY 1806 ACCTTGACCACTATGCAAGC 1826
DB 1901 SerPheAspHisTyrAlaThr 1907
RESULT 9
AAR71726
ID AAR71726 standard; Protein; 1911 AA.
XX
AC AAR71726;
XX
DT 17-OCT-1995 (first entry)
XX
DE Human PTP-OB.
XX
KW PTP-OB; protein tyrosine phosphatase; osteoblast; differentiation;
KW osteoclast; osteoporosis; bone; cancer; osteosarcoma.
XX
OS Homo sapiens.
XX
FH Key
FH Peptide 1..29 Location/Qualifiers
FT /label= Sig-peptide
FT Modified-site 250
FT /label= N-glycosylation_site
FT Modified-site 721
FT /label= N-glycosylation_site
FT Modified-site 919
FT /label= N-glycosylation_site

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FT Domain 1253..1277
FT /label= Extracellular_domain
PN WO9507935-A.
XX
PD 23-MAR-1995.
XX
PF 09-SEP-1994; 94WO-US10166.
XX
PR 14-SEP-1993; 93US-0122032.
XX
PA (MERI ) MERCK & CO INC.
XX
PI Rodan GA, Rutledge SJ, Schmidt A;
XX
DR WPI: 1995-131318/17.
DR N-PSDB; AA086478.
XX
XX
XX Protein tyrosine phosphate protein ptp-ob specifically expressed
PT in bone cells - modulators of which are used to treat, e.g.
PT osteoporosis, and prevent and treat bone loss and cancer.
XX
PS Claim 1: Page 44-45; 63pp; English.
XX
XX PCR amplification of cDNA derived from human osteosarcoma
CC Saos-2/B10 using primers based on conserved regions of protein
CC tyrosine phosphatases and subsequent screening of a human
CC brain cDNA library yielded a cDNA-clone (sequence given in
CC AA086473) that encoded a novel human protein, PTP-OB (AAR71726).
CC Recombinant PTP-OB was expressed in E. coli, yeast, insect
CC and mammalian cells.
XX
XX
SQ Sequence 1911 AA;
Alignment Scores:
Pred. No.: 1.2e-227 Length: 1911
Score: 2880.00 Matches: 530
Percent Similarity: 94.32% Conservative: 35
Best Local Similarity: 88.48% Mismatches: 34
Query Match: 44.69% Indels: 0
Gaps: 0
US-09-743-492-1 (1-3467) x AAR71726 (1-1911)
QY 30 CACTCCTGTGACCCCTGTGGAGATGGGAGGCTCACTACACAGCCAGATGCGAGAC 89
DB 1313 HisProLysAspProValGlnMetAlaArgIleAsnPheGlnThrProGlyMetLeuSer 1332
QY 90 CACCCACCCATCCCATCACAGCCTGGCGGACCAACATGAGCGCGCTCAACCCACGAT 149
DB 1333 HisProIleProIleProIleAlaAspMetAlaGlnHisThrGlnArgLeuLysAlaAsnAsp 1352
QY 150 GGCCTCAAGTTCTCCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 209
DB 1353 SerLeuLysLeuSerGlnGlnTyrGlnSerIleAspProGlyGlnGlnPheThrTrpGlu 1372
QY 210 AATTCAAACTGGAGGTGAACAAGCCCAAGAACCCCTATGCCAATGTCTGCTCCTACGAC 269
DB 1373 HisSerAsnLeuGlnValAlaAsnLysProLysAsnAlaGlyTyrAlaAsnValIleAlaTyrAsp 1392
QY 270 CACTCTGAGTCATCCTTACTCTATCGATGGCGTCCCGGAGTGAATCAATCAATGCC 329
DB 1393 HisSerArgValIleLeuGlnProIleGlnGlyIleMetGlySerAspTyrIleAsnAla 1412
QY 330 AACTCATCTGATGGCTACCCGACAGCAAGATGCTTACATGCGCACGAGGCGCCCTGCC 389
DB 1413 AsnTyrValAspGlyTyrArgArgGlnAsnAlaTyrIleAlaThrGlnGlyProLeuPro 1432
QY 390 GAGCAATGGGCGGATTTCTGGAGAAATGGGTGGGAAACGCGACGCGACCTGTGGTCA 449
DB 1433 GluThrPheGlyAspPheThrParGmetValTrpGlnGlnArgSerAlaThrIleValMet 1452
QY 450 ATGACACGGCTGGAGAGAGATCCCGGGTAATATGTGATCACTACTGGCCAGCCGCTGGC 509

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Db 1453 MetThrArgLeuclnIuLysSerArgIleLysCysAspGlnTrpProAsnArgGly 1472
QY 510 ACCGAGACCTGGGCTTATTCAGGTGACCCCTTTGGACACAGTGGAGCGGCACATAC 569
Db 1473 ThrGlnThrTyrGlnPheIleGlnValThrLeuLeuAspThrIleGlnLeuAlaTrpPhe 1492
QY 570 ACTGTGCGACCTTTCACCTCCACAGAGTGGCTCCAGTGGAGAGAGGTGAGCGCTGAC 629
Db 1493 CysValArgThrPheSerLeuHisLysAsnGlySerSerGlnLysArgGlnValArgGln 1512
QY 630 TTTCAGTTTCATGCGCTGGCCAGACACATGAGTTCCTGAGTACCCAACTCCATCTGGCC 689
Db 1513 PheGlnPheThrAlaTrpProAspHisGlyValProGlnTrpProThrProPheLeuAla 1532
QY 690 TTTCCTACGACGGGTCAAGCGCTTCGAACCCCTTAGACGACGAGGCCATGGTGTGCACTGC 749
Db 1533 PheLeuAlaArgValLysThrCysAsnProProAspAlaGlyProIleValAlaHisCys 1552
QY 750 AGCGGCGGGGTGGCGCCGACCGCTGTCATGTCATGATGATGATGATGATGATGATGATG 809
Db 1553 SerAlaGlyValAlaGlyThrGlyCysPheIleValIleAspAlaMetLeuGlnValArgIle 1572
QY 810 AAGCAGAGAGAGCGGTGACATCTATGCGCCACGTGACCTGACCTGACATGACAGAGAAC 869
Db 1573 LysProGlnLysThrValAspValTyrGlnHisValThrLeuMetArgSerGlnArgAsn 1592
QY 870 TACATGTGTCCAGACGAGGACCACTAGTGTTCATCCATGAGGCGCTGTGAGCTGCC 929
Db 1593 TyrMetValGlnThrGlnAspGlnTyrSerPheIleHisGlnValLeuLeuGlnAlaVal 1612
QY 930 AGGTGGCGGCACACAGAGTGGCTGCGCCGACCTGATGCGCCACATCCAGAAAGTGGGC 989
Db 1613 GlnCysGlnAsnThrGlnValProAlaArgSerLeuTyrAlaLysIleGlnLysLeuAla 1632
QY 990 CAAGTGCCTCCAGGAGAGAGTGTGACCGCATGAGCTGAGTTCAGTTCGTCGCGCAGC 1049
Db 1633 GlnValGlnProGlnLysIleHisValThrGlnMetGlnLeuGlnPheLysArgLeuAlaAsn 1652
QY 1050 TCCAGAGGCCACACAGTCCCGCTTCATCAGCGCCACCTCCCTGCACAAAGTTCAAGAAC 1109
Db 1653 SerLysAlaHisThrSerArgPheIleSerAlaAsnLeuProCysLysLysPheLysAsn 1672
QY 1110 GCGGTGTGATCATGATGCGCTTACGAAATGACCCGCTGCTGCTGACGCCATCCCTGGT 1169
Db 1673 ArgLeuValAlaAsnIleMetProTyrGlnSerThrArgValCysLeuGlnProIleArgGly 1692
QY 1170 GTGAGAGCGCTGACTATCATATGACCAATGCGCAGCTTCGTTATGACAGCAGAGAGGC 1229
Db 1693 ValGlnGlySerAspTyrIleAsnAlaSerPheIleAspGlyTyrArgGlnGlnLysAla 1712
QY 1230 TACATAGCTTACACAGGCGCTTGGCAGAGACACCGAGACTTCTGGCCATGCTATGG 1289
Db 1713 TyrIleAlaThrGlnGlnTyrProLeuAlaGlnThrThrGlnAspPheTrpArgMetLeuTrp 1732
QY 1290 GAGCACAATTCACCATATCTCTCATGCTGACCAAGCTTCGGGAGATGGCGGAGGAA 1349
Db 1733 GlnAsnAsnSerThrIleValIleValMetLeuThrLysLeuAlaGlnMetLysArgGlnLys 1752
QY 1350 TCCGACACAGTACTGGCGCAGCAGAGCGCTGCTGCTACAGTACTTCTTGTGACCGC 1409
Db 1753 CysHisGlnTyrTrpProAlaGlnLysSerAlaArgTyrGlnTyrPheValAlaAspPro 1772
QY 1410 ATGCTGAGTACACATGCGCCAGATATATCTGCTGATTCAGGTCAGGATGCCCGG 1469
Db 1773 MetAlaGlnTyrAsnMetProGlnTyrIleLeuArgGlnPheLysValThrAspAlaArg 1792
QY 1470 GATGGGAGATCAAGGACATCCGGAGTCCAGTTCACAGATGGCCAGAGAGCGCGG 1529
Db 1793 AspGlnGlnSerArgThrValArgGlnPheGlnPheThrAspTrpProGlnGlnVal 1812
QY 1530 CCCAAGACAGGCGAGGATTCATTGACTTCATGCGGCGAGGTCCATTAAGACCAAGAGCAG 1589

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Db 1813 ProlysSerGlyGlnGlyPheIleAspPheIleGlyGlnValHisLysThrLysGlnGln 1832
QY 1590 TTTCGACAGATGGGCTTATCACGGTGCACCTGCAGTGTGCGTGGCGCGCAGCGGGTG 1649
Db 1833 PheGlyGlnAspGlyProIleSerValHisCysSerAlaGlyValAlaIleArgThrGlyVal 1852
QY 1650 TTTCATCAGTCTGAGCATCGCTCGGAGCGCATGCGCTATGAGAGGCGGTCGACATGTT 1709
Db 1853 PheIleThrLeuSerIleValIleGlnValArgMetArgTyrGlnValValAspIlePhe 1872
QY 1710 CACAGCGTGAAGACCTCGGTATCACAGCGCTCTGCCATGGTGCAGACAGAGCAAGTAT 1769
Db 1873 GlnThrValLysMetLeuArgThrGlnArgProAlaMetValGlnThrGlnAspGlnTyr 1892
QY 1770 CAGCTGTGCTACCGTCGCGCGCTGAGATCACTGCGACGCTTTGACCACTATGCAACG 1826
Db 1893 GlnPheCysTyrGlnAlaIleLeuGlnTyrLeuGlySerPheAspHisTyrAlaThr 1911

RESULT 10
AAM27225
ID AAM27225 standard; Protein: 1911 AA.
XX
AC AAM27225;
XX
DT 19-DEC-1997 (first entry)
XX
DE Human protein tyrosine phosphatase PTP-OB.
XX
KW Protein tyrosine phosphatase' PTP-OB; PTPrepsilon; osteoblast;
KW recombinant protein; growth; differentiation; brain; human.
XX
OS Homo sapiens.
XX
PN US5658756-A.
XX
PD 19-AUG-1997.
XX
PF 14-SEP-1993; 93US-0122032.
XX
PR 01-DEC-1994; 94US-0348006.
PR 14-SEP-1993; 93US-0122032.
XX
PA (MERI ) MERCK & CO INC.
XX
PI Rodan GA, Rutledge SJ, Schmidt A;
XX
DR WPI: 1997-424232/39.
XX
DR N-PSDB; AAT85389.
XX
PT DNA encoding protein tyrosine phosphatase PTP-OB - isolated from
XX human osteoblasts and useful for production of recombinant PTP-OB
XX
PS Claim 1; Column 23-34; 34pp: English.
XX
CC The present sequence represents human protein tyrosine phosphatase
CC (PTP-OB) protein. The DNA encoding this protein is useful for the
CC production of the recombinant protein, which is a protein tyrosine
CC phosphatase which may be involved in the growth and differentiation
CC of osteoblasts and brain cells and is useful for identifying compounds
CC that modulate PTP-OB activity and as a therapeutic agent for treating
CC PTP-OB-related diseases.
XX
SQ Sequence 1911 AA;
XX
Alignment Scores:
Pred. No.: 1,2e-227 length: 1911
Score: 2880,00 Matches: 530
Percent Similarity: 94,32% Conservative: 35
Best Local Similarity: 88,48% Mismatches: 34
Query Match: 44,69% Indels: 0
DB: 18 Gaps: 0

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us-09-743-492-1 (1-3467) x AAM27225 (1-1911)

QY	30	CACTCTCTGACACCTGTGTGGAATCTGGAGCTCAACTACCAACCCCAAGTATGGAGAC	89
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QY	90	CACCCACCACTATCCCATCACCAGCTGGCGAGCAACATCGACGGCTCAAGCAACGAT	149
Db	1333	HAAProDlIerProDlIeAlAsMeTAleGInThIshIcInuTgUeuLyAsAlAsnAsP	1355
QY	150	GGCCTCAAGTCTCCACAGAGTATGATCGATCGACACCTGGACAGCAAGTTCACGTGGAG	209
Db	1353	SeTleuLySeTserGInuTgUeIuserTleAsProlYInGInPherThrTgU	1372
QY	210	AATTCAAACCTGGAGGTGAACAACCCCAACACCCGATATCCGAATGTCTATGCCCTTACAC	269
Db	1373	HAAProLyAsnLeuGInuAlAsnLyProlYAsnAsnTgUeAlAsnAlIleAlaTyrAsP	1392
QY	270	CACCTCGAGTCATACCTTACCTGTATGATGAGGGCTCCCGAGAGTACATCATCATGCG	329
Db	1393	HAAProLyAlIeLeuGInProDlIeGInuTgUeMeClyserAsPryTleAsnAla	1412
QY	330	AACATCATGATGGCTACCGACAGACAGATCCCTACATCGCCACGAGGGCCCTGGCC	389
Db	1413	AsnTyrValAsPglTyrATgATgAGInAlAsnAlATgTleAlaThrGInuTgProlAsnPro	1432
QY	390	GAGACCATGGCGCATTTCTGGAGAAATGGTGTGGACAGCGGACGGCCACTGGTGCATG	449
Db	1433	GUThrPheGlyAsPheTgPrtATgMeTValTgProluInATgSerAlaThrIleValMet	1453
QY	450	ATGACACAGCGGTGAGAGAAATCCCGGATAAATGTGATAGTACATGACCTGACCCGTGAC	509
Db	1453	MeThrATgLeuGInuTgUeLyserATgIleuLyCysAsProluTgTgProlAsnTgGly	1472
QY	510	ACCGAGACCTGTGGCTTATTCAGGTGACCCCTGTGGACACAGTGGAGCTGGCCATATC	569
Db	1473	ThrGUThrTgUeGlyPheIleGInuAlaThrLeuAsnThrIleGInuAlaThrPhe	1492
QY	570	ACGTGGCCACCTTGCCACTCCAAACAAGAGGCTCCGATGAGAAAGCTGATGGCGGTGAG	629
Db	1493	CysValATgThrPheSerLeuInuLyAsnGlySerSerGInuLyAsnTgGInuAlaTgGIn	1512
QY	630	TTTCAGTTCATGGCTGGCCACAGACCATGATTCCTGTAGTACCCAACTCCATCCCTGGCC	689
Db	1513	PheGInPherThrAlaTgProlAsPnIsglyAlaProluTgTgProlAsPnIleuAla	1532
QY	690	TTTCTTACACAGGGGTCAAGCTGGACACCCCTAGACGACGAGGCCATGGTGGTGCATGTC	749
Db	1533	PheLeuATgATgValuLyshTgCysAsnProDlAsPAlaGlyProlleValAlaThIcys	1553
QY	750	ACCGGGGCGTGGCGCGACCGGCTGTTATGCTGATGGATTCATGATCCATGTGGAGCGGATG	809
Db	1553	SeTAlaGlyValuTgIATgThrGlyCysPheIleValIleAsPAlaMeTleuInuTgIle	1572
QY	810	AAGCAGAGAAAGAGGTGGATGTATGGCCAGCTGACCTGCATGCGATCAGACAGAGAC	869
Db	1573	LySProluLyshThrValAsPValTgUeIshIvalThrIleuMeTATgserGInuTgAsn	1592
QY	870	TTACATGGTGCAGAGGAGGACCAAGTACGTGTATATCCATGAGGGCTGCTGGAGCTGCC	929
Db	1593	TyrMeTValGInThrGInuAsPGLnTyrSerPheIleHisGInuAlaLeuMeuInuAlaVal	1612
QY	930	ACGTGGGCGCACAGAGAGTCCCTGGCCGACACCTGTATGCCACATCCAGAAAGCTGGGCG	989
Db	1613	GlyCysGlyAsnThrGInuAlaProluATgSerLeuTyrAlATyrIleGInuLyseuAla	1632
QY	990	CAAGTGCCTCCAGGGAGAGTGTACCGCCATGAGACTGCATGATTCAAAGTTCCTGGCCAGC	1049
Db	1633	GInuAluTgProluTgUeIshIvalThrGlyMeTGIuGInuTgPheLyAsnTgGInuAlAsn	1652
QY	1050	TGCCAAGGCCACACGCTCCGCTTATATAGCGCCACACCTGCTGCACAAAGTTCAAGAC	1109
Db	1653	SeTlyAsAlaThIshTserATgPheIleSerAlaAsnLeuProlCysLyAsPheLyAsn	1672

QY	1110	CGCGTGGGACATCATGCGCCCTACGATTGACCCGCTGCTGCAGCCCATCCGTGTG	1165
QY	1110	CGCGTGGGACATCATGCGCCCTACGATTGACCCGCTGCTGCAGCCCATCCGTGTG	1165
Db	1673	AGGLeuValaInnIleMePProTyrGlnSerThrArValaCysLeuInProIleArgGly	1692
QY	1170	GTGAGGGCTCTGCATCATCATATGCACGCTTCTGGATGCTTATAGACAGCAGAACCC	1239
Db	1693	ValIgluIysSerAspTyrIleasnAlaSerPheIleaspolyTyrArgGlnGlnIlysnAla	1712
QY	1230	TACATAGCTAACACAGGGGGCTCTTG6GACAGACAGACCGAGAGATTCTTG6GCACTGATAG	1289
Db	1713	TyrIleAlaThrGlnGlnGlyProLeuAlaGlnThrThrGlnAspPheThrPArgMetLeuTrp	1732
QY	1290	GAGCACAATTCCACACATCATGCTCATGCTGATCCACCAAGCTTCGGAGATGGGCGAGAGAA	1349
Db	1733	GluAsnAsnSerThrIleValaIValMetLeuThrLysLeuArgGlnMetCylArgGlnIlyuys	1752
QY	1350	TGCCACCAAGTACTG6GACAGACAGACCGCTCTGCTGCTACCAAGTACTTGTGTTGACCCG	1409
Db	1753	CysHisGlnTyrTrpProAlaGlnArgSerAlaArgTyrGlnTyrPheValIValAspPro	1772
QY	1410	ATGGCTAGTACAAACATGCCCGAGTATATCCGCTGCGAGTCAAGTCAAGGATCCGATCCGG	1469
Db	1773	MetAlaGlnTyrAsnMetProGlnTyrIleLeuArgGlnPheLysValThrAspAlaArg	1792
QY	1470	GATGGGCGAGTCACAGACAAATCCGGCAGATTCCAGTTCCAGACTGGCCACAGACGCGCTG	1529
Db	1793	AspGlyInserArgThrValArgGlnPheGlnPheThrAspTrpProGlnIlyal	1812
QY	1530	CCCAAGACAGCGAGGGATTCATTGACTTATGGGCGAGTGCGATAAACCAAGAGCAG	1589
Db	1813	ProLysSerGlyGlnGlyPheIleAspPheIleGlnIValaHisLysThrLysGlnIn	1832
QY	1590	TTTGACAGGATGGGCTATCACGCTGCATCGTGCATGTCAGTGGCGGTGGCCGACCCGGGGTG	1649
Db	1833	PheGlyGlnAspGlyProIleSerValHisCysSerAlaGlyAlaGlyArgThrIlyal	1852
QY	1650	TTCATCACTGTGACATCGCTCTTGAGAGCGATCGCTATGAGGGCGTGTCACATGTTT	1709
Db	1853	PheIleThrLeuSerIleValaLeuGlnArgMetArgTyrGlnIlyalValaIAspIlePhe	1872
QY	1710	CAGACCGGAGACCGCTCGCGTACACAGACCGCTCGCATGGTCAGACAGAGACAGCAT	1769
Db	1873	GlnThrValIlysnMetLeuArgThrGlnArgProAlaMetValaGlnThrGlnAspIlyuTr	1892
QY	1770	CAGCTGTGCTACCGCTGGCGCCCTGGAGTACCTGGCAGGCTTGGACCATATGCAACG	1826
Db	1893	GlnPheCysTyrGlnAlaIalaLeuGlnTyrLeuGlySerPheAspIlysnIleThr	1911
RESULT 11			
AAW94027			
ID	AAW94027	standard; Protein; 1911 AA.	
XX	AAW94027;		
AC	AAW94027;		
XX			
XX	01-APR-1999	(first entry)	
XX			
DE		Human protein tyrosine phosphatase (PTP-OB).	
XX			
KW		Protein tyrosine phosphatase; PTP; PTP-OB; bone; brain; cancer;	
KW		osteoporosis.	
KW			
XX			
OS		Homo sapiens.	
XX			
PN		US5866397-A.	
XX			
PD		02-FEB-1999.	
XX			
PF		14-FEB-1997;	97US-0808025.
XX			
PR		01-DEC-1994;	94US-0348006.
PR		14-SEP-1993;	93US-0120302.
PR		14-FEB-1997;	97US-0808025.

DB 1673 ArgLeuValAlaSnIleMetProTyrGluSerThrArgValCysLeuGlnProIleArgGly 1692
QY 1170 GTGGAGGCGCTCTACATCATCGCAGCTTCTGATGCTATATGACAGCAAGGCC 1229
DB 1693 ValGIuGlySerAspTyrIleAsnAlaSerPheIleAspLysTyrArgGlnGlnVal 1712
QY 1230 TACATGATCAACAGAGGCGCTGCGAGAGAGCAGCAGAGCTTCTGGCCATGCTATGG 1289
DB 1713 TyrIleAlaThrGlnGlyProLeuAlaGluThrThrGluAspPheThrPargMetLeuTTP 1732
QY 1290 GAGCACAATTCACCATCATCGTCATCGTACCAAGCTTCGGAGATGGCGCAGGAGAAA 1349
DB 1733 GluAsnAsnSerThrIleValIleMetLeuThrLysLeuArgGluMetGlyArgGluLys 1752
QY 1350 TGGCACCAGTACTGGCCAGCAGAGCGCTGCTGCTGCTACCACTTGTGTGGACCCG 1409
DB 1753 CysHISgluTyrTrpProAlaGluArgSerAlaArgTyrGlnTyrPheValAlaAspPro 1772
QY 1410 ATGGGCTGAGTACACATGCCCCAGTATATGCTGCTGAGTTCAGAGGTCACGAGCCCGG 1469
DB 1773 MetAlaGluTyrAsnMetProGlnTyrIleLeuArgGluPheLysValThrAspAlaArg 1792
QY 1470 GATGGCAGTCAAGACAATCCGCGAGTTCACATTCACAGACTGGCCAGAGCGCGTG 1529
DB 1793 AspGlyGlnSerArgThrValArgGlnPheGlnPheThrAspTrpProGluGlnGlyVal 1812
QY 1530 CCCAAGACAGCGGAGGATTCATTGACTTCATCGGCGAGGTGCATTAAGACCAAGAGCAG 1589
DB 1813 ProLysSerGlyGluGlnPheIleAspPheIleGlyGlnValHisLysThrLysGluGln 1832
QY 1590 TTTGGCAGAGTGGGCGCTTCACAGGTCAGTGCAGTGCAGTGGCGGCGCCAGCGGGTG 1649
DB 1833 PheGlyGlnAspLysProIleSerValHisCysSerAlaGlyAlaLysArgGlnGlyVal 1852
QY 1650 TTCATCACTCTGAGCATCTCTGAGCGCATGCGCTATGAGGCGCTGTGTCGATGTTT 1709
DB 1853 PheIleThrLeuSerIleValLeuGluArgMetArgTyrGluGlyValValAspIlePhe 1872
QY 1710 CAGACCGTCAAGACCTCGGTACACAGCGTCTGCGCATGGTGCAGACAGAGCAAGTAT 1769
DB 1873 GlnThrValLysMetLeuArgThrGlnArgProAlaMetValGlnThrGluAspGluTyr 1892
QY 1770 CAGCTGTGCTACCGTGGCCCTCGAGTACCTGCGAGCTTTGACCACTATGCAAGG 1826
DB 1893 GlnPheCysTyrGlnAlaIleAlaLeuGluTyrLeuGlySerPheAspHisTyrAlaThr 1911
RESULT 13
AAR75201
ID AAR75201 standard; Protein; 1291 AA.
XX
AC AAR75201;
XX
DT 10-MAY-1996 (first entry)
XX
DE Tyrosine phosphatase MPTP-delta.
XX
KW Tyrosine phosphatase MPTP-delta; murine; brain tissue;
KW glutathione-S-transferase; fusion protein; E. coli; differentiation;
KW activation; information transmission; nervous system; immune system;
KW carcinogenesis.
XX
OS Mus musculus domesticus.
XX
PN JP07236487-A.
XX
PD 12-SEP-1995.
XX
PF 28-FEB-1994; 94JP-0054726.
XX
PR 28-FEB-1994; 94JP-0054726.
PA (TOKS-) TOKYOTO SHINKEI KAGAKU SOGO KENKYUSHO ZH.
XX

DR WPI: 1995-347455/45.
DR N-PSDB; AA094311.
XX
PT DNA encoding tyrosine phosphatase MPTP delta - useful for
PT elucidation of signal transmission mechanisms.
XX
PS Claim 1; Page 5-11; 14pp; Japanese.
XX
CC This sequence represents murine tyrosine phosphatase MPTP-delta. The
CC cDNA sequence encoding this protein was isolated from murine brain
CC tissue and was cloned, for expression, into the downstream region of a
CC glutathione-S-transferase sequence and expressed as a fusion protein
CC in E. coli. MPTP-delta proteins regulate differentiation and
CC activation of cells. This sequence can be used in the elucidation of
CC the molecular mechanism for information transmission in cells,
CC regulation mechanisms in the nervous system or immune system, or in
CC the mechanism of carcinogenesis.
XX
SQ Sequence 1291 AA:
Alignment Scores:
Pred. No.: 2, 77e-227 Length: 1291
Score: 2874.50 Matches: 534
Percent Similarity: 95.16% Conservative: 36
Best Local Similarity: 89.15% Mismatches: 26
Query Match: 44,618 Indels: 3
DB: 16 Gaps: 3
US-09-743-492-1 (1-3467) x AAR75201 (1-1291)
QY 30 CACTCCTCTGACCTGTGGAGATGCGGAGGCTCACTACCAAGCCAGGTATCCGAGAC 89
DB 696 HisProthrAspProValGluLeuArgArgLeuAsnPheGlnThrProGluMetAlaSer 715
QY 90 CACCAACCCATCCCATCACCGACCTGGCGAGACATCCAGCGCCCTCAAGCCAAACGAT 149
DB 716 HisProIleProIleProIleLeuGluLeuAlaAspHisIleLeuArgLeuLysAlaAsnAsp 735
QY 150 GGCCTCAAGTTTCCACAGAGATGATGATCCATGACCCCTGAGACAGCATTCACGTGGAG 209
DB 736 AsnLeuLysPheSerGlnGluTyrGluSerIleAspProGlyGlnGlnPheThrProGlu 755
QY 210 AATTCAACCTGGAGGAGGAAACAGCCCAAGACCGGTATCGAATGATCCAGCTACGAC 269
DB 756 HisSerAsnLeuGluValAsnLysProLysAsnArgTyrAlaAsnValIleAlaTyrAsp 775
QY 270 CACTCTGAGTCACTCTTACCTCTATCGATGGCGGCTCCCGAGTGCATCATATGCC 329
DB 776 HisSerArgValLeuLeuSerAlaIleGluGlyIleProGlySerAspTyrValAlaSer 795
QY 330 AACTACATGATGGCTTACCGCAGAGCAAGATGCTTACATGCGCAGAGGCGCCCTGGCC 389
DB 796 AsnTyrIleAspGlyTyrArgLysGlnAsnAlaTyrIleAlaThrGlnGlySerLeuPro 815
QY 390 GAGACCATGGCGATTTCTGAGATGCGTGGAGACAGCGCAGCGCACTGTGCATC 449
DB 816 GluThrPheIleLysPheThrPargMetIleTropGluGlnLys--AlaThrValIleMet 834
QY 450 ATGACAGCGCTGAGAGGAGGAGTCCCGGTTAAATGTGATGATGATGAGGACCGCCCTGGC 509
DB 835 MetThrLysLeuGluGluArgSerArgValLysCysAspLysIleTyrTrpProSerArgGly 854
QY 510 ACCGAGACCTGTGGCTTATTCAGGTGACCTGTGGACACAGTGCAGTGCACATATAC 569
DB 855 ThrGluThrHisGlyLeuValGlnValThrLeuLeuAspThrValGluLeu--ThrTyr 873
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QY 630 TTTCACTTCATGCGCTGGCGCAGACCATGAGTTCCTGATGATGATGATGATGATGATGATG 689
DB 894 PheGlnPheThrAlaTrpProAspHisGlyValProGluHisProThrProPheLeuAla 913

QY	150	GGCTCAAGTTCCTCCACAGGATGATGATGCATGACCTTGACAGACATGTCACGTGGAG	209
Db	943	serLeuylsLeuSerGlnGluTyrGlnSerLLeaSProlGlnInPheThrProL	962
QY	210	AATTCAACCCGGAGGATGACCAAGCCCAAGAACCGGTATGGCAATGTCAATGCCCTACAG	269
Db	963	HisSerAsnLeuGlnAalaAsnLysProlLysAsnArgTyrAlaAsnValLLeaLysAsp	982
QY	270	CACCTCTGAGCACTCTTACCCTCATGATGAGGGGCTCCCGGAGGATCACTCAATGCC	329
Db	983	HisSerArgValLLeuGlnProLeuGlnGlyLLeuGlySerAspTyrLLeuSnaL	1002
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Db	1003	AsnTyrValAspGlyTyrArgTargLAsnAlaTyrLLeaLathGlnGlyProLeuPro	1022
QY	390	GAGACATGGCCGATTTCTGGAAATGGTGTGGGAACAGCCAGCGCCACTGTGGTCATG	449
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QY	870	TACATGGTGCAGACGACGACAGCACTAGTCAGTTCATCATCAGAGGCGCTGTGGAGGCTGCC	929
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QY	1170	GTGAGAGGCTCTGACTCATCATATGCCAGCTTCTGTGGATGGTTATAGACAGCAAGGCC	1229
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QY	1230	TACATAGCTACACAGGGGCGCTTGCCAGAGACACCCAGAGACTTCTGGCGCATGCTATGG	1289
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QY	1290	GAGCAACAATCCACCATCATCTGTCATGCGTGCACCAAGCTCGGGAGATGGGAGGGAGAA	1349
QY	1323	GUAAAnAsrSerThrTrlLeValValMetLeuThrLysLLeuArgGluMetLysArgGluLys	1342
QY	1350	TGCCACCACTAGTGGCCACACAGAGCGCTGCTCCGTACCACTAGCTTTGTTTGACCCG	1409
Db	1343	CysHISGlnIntYrTrpProAlaGlnArgSerAlaArgYrGlnTrpPheValValAspPro	1362
QY	1410	ATGCGTAGTACACACATGCCCCCAGTATATCTGCGCTGAGTTCACAGTCACGAGATGCCCG	1469
Db	1363	MetaIaGlnTyrAsnMetProGlnIntYrTrlLeuArgGlnPheLysValTrhAspAlaArg	1382
QY	1470	GATGGGCGACATCAAGAGCAATCCGGCAGATTCCAGTTCCACAGACTGGCCAGAGAGGCGTG	1529
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QY	1530	CCCAAGACAGGAGGAGGATTCATATGACTCATCGGGCAGGCGCATTAAGACCAAGAGCAG	1589
Db	1403	ProLysSerGlyGlnGlyPheLleAspPheIleGlyGlnValHisLysThrLysGlnGln	1422
QY	1590	TTTGACACAGATAGGCGCTATCAACGGTGCACACTGCATGCTGCGCGGCGCCGACCGGGTG	1649
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QY	1650	TTTCATCAGCTCTAGACATCGTCTCTGGAGCGCATAGCGCTATGAGGGCGGTGCGACATGTT	1709
Db	1443	PheIleTrhLeuSerTrlLeValLeuGlnArgMetArgTrgYrGlnGlyValValAspTrlePhe	1462
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Db	1463	GlnTrhValLysValLeuArgTrhGlnArgProAlaMetValGlnTrhGlnAspGlnTyr	1482
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AC	07-MAR-2002	(first entry)	
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XX		vasospastic ischaemia; ischaemic condition; ischaemic disease.	
XX		Mus musculus.	
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PD	22-NOV-2001.		
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PF	18-MAY-2001; 2001WO-JP04192.		
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FR	18-MAY-2000; 2000JP-0145977.		
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PA	(UNINT.) UNIV NIHON SCHOOL JURIDICAL PERSON.		
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PI	Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;		
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DR	WPI: 2002-034733/04.		
XX	N-PSDB; ABI99344.		
XX			
PT	Examining the ischemic condition (e.g. occlusive ischemia) by measuring		
PT	expression levels of particular genes defined in the specification or		
PT	by determining the expression profile of a gene group comprising these		

PT genes -
XX
PS Claim 2; Page 636-644; 2690pp; English.

XX
CC The present invention describes a method for examining ischemic
CC conditions, comprising measuring the expression levels of particular
CC genes (1) in a test sample or determining the expression profile of a
CC gene group in the sample comprising genes selected from (1). The method
CC is useful for examining the ischemic condition (e.g. compressive
CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
CC expression levels of particular genes (AB199202 to AB199912, encoding
CC the protein sequences in AB199202 to AB199912) or by determining the
CC expression profile of a gene group comprising these genes. The
CC expression levels or expression profiles produced by these genes are
CC used as an indicator when screening for ischemic condition-improving
CC drugs or therapeutics for ischemic diseases. AB199913 and AB199914
CC represent PCR primers for a mouse ischemic condition related sequence,
CC which are used in the exemplification of the present invention.

XX
SQ Sequence 1904 AA:

Alignment Scores:

Pred. No.: 5,336-223 Length: 1904
Score: 2823.50 Matches: 520
Percent Similarity: 93.49% Conservative: 40
Best Local Similarity: 86.81% Mismatches: 36
Query Match: 43.82% Indels: 3
DB: 23 Gaps: 1

US-09-743-492-1 (1-3467) x ABB57100 (1-1904)

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QY 150 GGCCCTGAGTCTCCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 209
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QY 270 CACTCTGAGTCATCTTACTCTATCGATGGCGCTCCCGGAGTGAATCTATCATGCGC 329
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Search completed: January 17, 2003, 10:03:42
Job time : 237 secs

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GenCore version 5.1.3
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OM nucleic - protein search, using frame_plus_n2p model

Run on: January 17, 2003, 10:12:20 ; Search time 25 Seconds
(without alignments)
5513.505 Million cell updates/sec

Title: US-09-743-492-1

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Searched: 120991 seqs, 19878514 residues

Total number of hits satisfying chosen parameters: 241982

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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Database : Published Applications-AA:*

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Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	2880	44.7	1502	9	US-09-808-602-54 Sequence 54, Appl
2	2856	44.3	1948	3	US-09-808-602-55 Sequence 55, Appl
3	2347	36.4	442	10	US-09-925-300-950 Sequence 950, App
4	1335	20.7	306	10	US-09-788-626-8 Sequence 8, Appl1

ALIGNMENTS

RESULT 1
US-09-808-602-54
; Sequence 54, Application US/09808602
; Patent No. US20020155115A1
; GENERAL INFORMATION:
; APPLICANT: Vermet, Corine A
; APPLICANT: Fernandes, Elma
; APPLICANT: Shinkets, Richard A
; APPLICANT: Herrman, John L
; APPLICANT: Majumder, Rumud
; APPLICANT: Mishra, Vishnu
; APPLICANT: Mezes, Peter S
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: No. US20020155115A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-697 CIP
; CURRENT APPLICATION NUMBER: US/09/808, 602
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 09/800, 198
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/186, 596
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 1502
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-808-602-54

Alignment Scores:

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US-09-743-492-1 (1-3467) x US-09-808-602-54 (1-1502)

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DB 1064 THRGLUTRITYGLYPHEILEGLVALTHRLEULASPTHLRILEULVALATHRPE 1083
OY 570 ACTGTGCGACCTTGCGACTCCCAAGAGTGGTCCAGTGAAGACGTTGAGTGGCTGAC 629
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1084 CYSVALATGTHPHESETLEULHISYASNGLYSERSEGLULYSARGGLUVALARGLIN 1103
OY 630 TTTTCAGTTTCATGGCTGGCCAGACCATGAGATTCCTGAGTACCAACCTCCATCCTGGCC 689
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1104 PHEGLNPHERTHALATRPPOASPHISGLYVALPROGLUTYRPROTHRPROHELEULA 1123
OY 690 TTTCAGACAGGGGTGAAGCCTGCAACCCCTAGACGACGAGGCCCATGGTGGTGCATGTC 749
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1124 PHELEULATGATVALYLTHTCYSSANPROPRASPAIAGLYPROILEVALVALHISCS 1143
OY 750 AGCGGGCGGTGGCGGCGACCGGCTTCATCGATGATTGAGCCATGTTGGAGGGGATG 809
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1144 SERIALAGLYVALATGATHTCICYSPHEILEVALIILEASPAIAMELEULENLIURGILE 1163
OY 810 AAGCAGAGAGAGCGGTGACATCTATGCGCCAGCTGACCTGATCGATACAGAGAAC 869
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1164 LYSPTROGLULYSTHVALASPAIATYRGLYHISVALTHRLEUMELARGSERLINRYSN 1183
OY 870 TACATGTGTCAGACGAGACCATGATGCTGTTATCATATGAGCGCGTGTGAGGCTGCC 929
    *||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1184 TYRMEIVATGINTHGLUASPLINTYRSERPHEILEHISGLUALALEULENLIUVAL 1203
OY 930 ACGTGGCGGCACACAGAGAGTGCCTGCCGCAACCTGTATGCCACATTCAGAAAGCTGGGC 989
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

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DB 1204 GLYCYSGLYASPTHGLUVALPROIALATGSERLTYRATYRILEGLNLYSEULAL 1223
OY 990 CAAGTCCCTCCAGGAGAGATGTGACCCCATAGAGACTCGAGTTCAAGTTGCTGGCCAC 1049
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1224 GLINVALGUPROGLYGLIHISVALTHRGLYMETGLULEGLUPHEULYSARGLEULASNP 1243
OY 1050 TCCAGGGCCCAACAGCTCCCGCTTCATCACCGCCCAACCTGCCCTGCACAAAGTTCAAGAAC 1109
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1244 SERLYSALAHISTHSEARPHLEIESERIALASNPLEUPROCYLSLYSLEULYSASN 1263
OY 1110 CGGTGTGATCATATGCGCTTACGAAATGACCCGCTGTGCTGAGCCCATCGCTGCT 1169
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1264 ARGLEULVALSNLILEMETRPTGYGLUSERTHRARGVALCYSEULINPROILEATGELY 1283
OY 1170 GTGGAGGCTGTGATCATATGACCCAGCTTCTGGATGATTATAGACAGAGAGGCC 1229
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1284 VALGULGYSERASPYRILLESNALSERPHLEIASPGLTYTARGLNGLINLYSALA 1303
OY 1230 TACATPACTACACAGGCGCTGTGGCAGACAGACCCAGAGACTTGTGGCGCATGCTAGC 1289
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1304 TYRILEALATHGGLNGIYPROLEULAGIUTHTHGLUASPHETRPARGYMETLEUTRP 1323
OY 1290 GAGCAAAATTCACCATCATGCTCATGCTGACCAAGCTTGGGAGATGGCGAGAGAA 1349
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1324 GLUASASNSETRTHLEVALVALMETLEUTHRLYSLEUATGGLUMETGLYARGGLULYS 1343
OY 1350 TGCACCAATGCTGCGCCACAGAGCGCTGCTGCTGCTACATGCTTGTGTGACCGC 1409
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1344 CYSHISGLINTYTRPROIALGIMATGSERLATATGYTGLINTYRPHLEVALVALASNP 1363
OY 1410 ATGCTGATACACATGCGCCAGATATATCTGCGTGAATTCAGGTCAAGTACGATGCCG 1469
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1364 METALAGIUTYRASNMEPRGINTYRILEULATARGGLUPHEULYSVALTHRASPAIATRG 1383
OY 1470 GATGGGCAATCAAGGACATCCGCGCATGCTCACAGTCCAGACTGGCGACAGAGGGCGTG 1529
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1384 ASPGLYGLINSEARTRTHVALARGLINPHEGLINPHERTHASPTRPPOIUDINGLYVAL 1403
OY 1530 CCCAAGACAGCGGAGATTCATGATCTTCATGCGGAGTGCATATAGACCAAGAGAGCAG 1589
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1404 PROLYSSEGLYGLUGLYPHEILEASPHLEILEGLYGLVALHISLYSTHRLYSGLUGLN 1423
OY 1590 TTTGCACAGAGATGGGCTTATCACGGTGCACCTGACATGCTGGCGGTGGCCGCGGCTG 1649
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1424 PHEGLYGLINASPGLYPROLIESERVALHISCYSESERIALAGLYVALGTYARGTHRGLYVAL 1443
OY 1650 TTTCATCATCTGAGCATGCTGCTGGAGGCGCATGCGCTATGAGGGGTGGTGCACATGTT 1709
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1444 PHEILETHRLEUSERLILEVALLEUGLUMATGEMETARGTYRGLUVALVALASPLIEPHE 1463
OY 1710 CAGACCGTGAAGACCCCTGCGTACACAGCGTCCCTGCCATGTTGCACAGAGAGCATGAT 1769
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1464 GLINTHVALLYMETLEULARGHGINATGPROIALAMEVALGINTHGLUASPLINTYR 1483
OY 1770 CAGCTGTGCTACCGTGGCGGCTGGAGTACCTGCGCAAGCTTTGACCAATATGCAACG 1826
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1484 GLNPHECYSTYGLIALALALEUGLUTYRLEUGLYSERPHEASPHISLYATLATHR 1502
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
RESULT 2
US-09-808-602-55
; Sequence 55, Application US/09808602
; Patent No. US2002015115A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corline A
; APPLICANT: Fernandes, Elma
; APPLICANT: Shimkets, Richard A
; APPLICANT: Herrman, John L
; APPLICANT: Majumder, Kumud
; APPLICANT: Mishra, Vishnu
; APPLICANT: Mezes, Peter S
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: NO. US2002015115A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-697 CIP
```

[illegible]

Db	1574	YALLYSTH	Cysasnp	Protoas	Palag1	ProtoLeval	Valn1	Scysse	ra1	ag1	Yal	1595											
Qy	762	GGCCGACCCGCGTGGTTCATGCGTATGATGGAGCCATGTCGAGCGGATGAGGACGACGAG	821																				
Db	1594	GLYATGTHrGLY	Cys	Phel	LeVal1	Leas	Pal	MeLeu	GLu	Arg1	GLys	Pro	GLu	1613									
Qy	822	ACGGTGACATCTATGGCGACGAGTCGACCGATGCGATCAGAGAGAACTACATGGTGCAG	881																				
Db	1614	THrVal	Asp	Val	GLY	GLY	His	Val	Thr	Leu	Me	Arg	Se	GLu	Arg	sn	Thy	Me	Val	GLn	1633		
Qy	882	AGGAGAACCAAGTACGTTTCATCCATGAGAGCCGCTGCTGGAGGCTGCACATGGCGGAC	941																				
Db	1634	THrGLu	Asp	GLn	Thy	Ser	Phel	Leu	His	GLu	Al	Leu	Leu	GLu	Al	Val	GLu	Arg	sn	1653			
Qy	942	ACAGAGGCGCTGGCGCGGACCTGATGGCCATCCAGAAAGTCGGGCGCAATGGCTGCA	1001																				
Db	1654	THrGLu	Al	Pro	Ala	Arg	Se	Leu	Thy	Al	Arg	Thr	Leu	His	Leu	Al	Val	GLu	Arg	sn	1673		
Qy	1002	GGGGAGAGTGTACCGCCCATGGACCTCGATTAAGTTCGTGGCCAGCTCCAAAGGCCAC	1061																				
Db	1674	GLYGLu	His	Val	Thr	GLu	Me	GLu	GLu	Arg	Leu	Phel	Arg	Leu	Ala	sn	Arg	His	1693				
Qy	1062	ACGTCCCGCTTCATCAGCGCCACACTCCCTGCAACAAGTTCACAGACCGGCTGTGAC	1121																				
Db	1694	THrSer	Arg	Phel	Leu	Se	Ala	sn	Leu	Pro	Cys	Ala	sn	Thy	Phel	sn	Arg	Leu	Ala	sn	1713		
Qy	1122	ATCATGGCCCTGAGAAATGACCCGCGTGTCTGCACGCCATCCGCGTGTGGAGGGGCT	1181																				
Db	1714	ILMe	Tr	Pro	Thy	GLu	Ser	Thr	Arg	Val	Cys	Leu	GLu	Pro	Leu	Arg	GLu	Val	GLu	GLu	1733		
Qy	1182	GACTCATCAATATGCGACGCTTCCTGATGAGTAAATAGACAGACAGAGCCATACCTACA	1241																				
Db	1734	Asp	Thy	ILe	sn	Ala	Se	Arg	Phel	Leu	Arg	GLu	Arg	GLu	Arg	GLu	Arg	GLu	Arg	GLu	1755		
Qy	1242	CAGGGCGCTTGCGACAGAGACCCGAGACTTGTGGCGATGCTATGGAGCAATTCC	1301																				
Db	1754	GLn	GLy	Pro	Leu	Ala	GLu	Thr	Thr	GLu	Asp	Phel	Trp	Arg	Me	Leu	Trp	ILu	sn	sn	1773		
Qy	1302	ACCATCATGTCATGCGACCAACACTTCGGGAGATGGCGAGGAGAAATGCCACCACTAG	1361																				
Db	1774	THr	ILe	Val	Ala	Me	Leu	Thr	Lys	Leu	Ala	Arg	Me	GLu	Val	Arg	GLu	sn	Arg	sn	1793		
Qy	1362	TGGCCACAGAGACCGCTGCTGCTGCGTACCACTATTGTGTGGACCCGATGGCTAGTAC	1421																				
Db	1794	Trp	Pro	Ala	GLu	ILu	Arg	Se	Ala	Arg	Thy	GLn	Thy	Phel	Val	Ala	Asp	Trp	Me	Leu	Arg	1813	
Qy	1422	AACATGCCCCAGTATATCTGTGCGTGAATTCAAAGTCACGAGATGCCGGATGGGACATCA	1481																				
Db	1814	Asn	Me	Tr	Pro	GLn	Thy	ILe	Val	Arg	GLu	Arg	Leu	Val	Thr	Asp	Arg	sn	Arg	sn	1833		
Qy	1482	AGGAAATCCGGGAGTTCGAGTTCACAGATGGCGACAGACGAGCGTGCCTCAAGACAGC	1541																				
Db	1834	Arg	Thy	Tr	Val	Ala	Arg	GLu	Pro	Leu	Phel	Thr	Asp	Trp	Pro	GLu	GLu	Val	Ala	Pro	Thy	Arg	1853
Qy	1542	GAGGATTCATGACTTCATCCGCGAGAGTGCATAAACCAAGAGACAGTTTGGACAGGAT	1601																				
Db	1854	GLu	GLy	Phel	Leu	Asp	Phel	Leu	GLu	Val	His	GLu	Thy	Lys	Se	ILu	Arg	Phel	GLu	Arg	1873		
Qy	1602	GGGCGCTATCAGGTGCACATGCACTGTGCGTGGGCGGACCGGGGTGTTATCACTGTG	1661																				
Db	1874	GLY	Pro	ILe	Se	Tr	Val	His	Cys	Se	Arg	ILu	Val	GLu	Arg	Thr	GLu	Val	Phel	Leu	1893		
Qy	1662	AGCATCGCTCGAGAGCCATGCGGTATAGAGGCGGTGGTGCACATGTTTCAAGCCTGAAG	1721																				
Db	1894	Ser	ILe	Val	Leu	GLu	Arg	Me	Arg	Thy	GLu	ILu	Val	Val	Asp	ILe	Phel	GLu	Thr	Val	1913		
Qy	1722	ACCGTGCCTACACAGCGCTCGGCATGCGTGCACACAGAGACAGATAGATGCTGTAC	1781																				
Db	1914	Me	Leu	Ala	Arg	Thr	GLu	Arg	Pro	Ala	Me	Val	GLn	Thr	GLu	Asp	ILu	Arg	sn	Thy	1933		
Qy	1782	CGTGGCGCCGTGAGTACTCGGACGTTTGCACATATGCAACG	1826																				

Db 1934 GlnAlaAlaLeuGluTyrLeuGlySerPheAspHisTyrAlaThr 1948

RESULT 3
US-09-925-300-950
: Sequence 950. Application US/09925300
: Patent No. US20020151681A1
: GENERAL INFORMATION:
: APPLICANT: Craig Rosen,
: APPLICANT: Steve Ruben
: TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
: FILE REFERENCE: PA101
: CURRENT APPLICATION NUMBER: US/09/925,300
: PRIOR FILING DATE: 2001-08-10
: PRIOR APPLICATION NUMBER: PCT/US00/05998
: PRIOR FILING DATE: 2000-03-08
: PRIOR APPLICATION NUMBER: 60/124,270
: PRIOR FILING DATE: 1999-03-12
: NUMBER OF SEQ ID NOS: 1890
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 950
: LENGTH: 442
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-925-300-950

Alignment Scores:
Pred. No.: 1,37e-150 Length: 442
Score: 2347.00 Matches: 442
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 36.42% Indels: 0
Gaps: 10

US-09-743-492-1 (1-3467) x US-09-925-300-950 (1-442)

QY 501 GCCCGTGGCAGGAGACCTGTGGCTTATTCAGGTGACCCCTTTGGACACATGGAGCTG 560
Db 1 AAlaA9GgLyThrGluThrCysGlyLeuIleGlnValThrLeuAlaSprThrValGluLeu 20
QY 561 GCCACATACACTGTGCGACACTTCCGACATCCACAGAGAGTGCCTCCAGTGAAGCGTGA 620
Db 21 AAlaThrTyrThrValAlaThrThrPheAlaLeuHisLysSerGlySerGlnLysArgGlu 40
QY 621 CTGGCTGAGTTTCAGTTCATGGCTGGCCGACAGCATGGAGTTCGAGTACCAACTGCC 680
Db 41 LeuAlaGlnPheGlnPheMetAlaThrProAspHisGlyValProGluTyrProThrPro 60
QY 681 ATCCGGGCTTCCTAGACGGGCTCAAGGCTTCACACCCCTAGAGCGAGGCCCATGGTG 740
Db 61 IleLeuAlaPheLeuAlaArgValLysAlaCysAsnProLeuAspAlaGlyProMetVal 80
QY 741 GTGCACTGACGGCGGGGCTGGCGGCGCACCGGCTTCATGATGATGGATGCAATGGTG 800
Db 81 ValHisCysSerAlaGlyValGlyArgThrGlyCysPheIleValIleAspAlaMetLeu 100
QY 801 GAGCGGATGAACACGAGAAAGCGGTGAACATCTATGGCCACGTGACCTGCATGCGATCA 860
Db 101 GlnArgMetLysHisGlyLysThrValAspIleTyrGlyHisValThrCysMetArgSer 120
QY 861 CAGAGAGACTACATGCTGACAGCGAGGAGCGAGTACGTGTTCATGCAAGAGCGCTGCTG 920
Db 121 GlnAlaGlnTyrMetValGlnThrGlnAspGlnTyrValPheIleHisGlnAlaLeuLeu 140
QY 921 GAGCGTGGCAGGCGGGCGACACAGAGGTGCTGCCCAACCTGTATGCCACATGCCAG 980
Db 141 GluAlaAlaThrCysGlyHisThrGlnValProAlaAlaArgAsnLeuTyrAlaHisIleGln 160
QY 981 AAGCTGGGCAAGTGCCTCCAGGGGAGAGTGTGACCGGCATGAGCTGAGTTCAAGTTG 1040
Db 161 LysLeuGlyGlnValProProGluLysSerValThrAlaMetGlnLeuGlnPheLysLeu 180
QY 1041 CTGGCGACGTCGAGGCCACACAGCTCCGCTTCATCAGCGCCCAACCTGCCGCAACAG 1100
|||||

Db 181 LeuAlaSerSerLysAlaHisThrSerAlaPheIleSerAlaAsnLeuProCysAsnLys 200
QY 1101 TTCAGAAACCGCGTGGTGAACATCATGCCCTACGAATTGACCCGTTGTGCTGGACGCC 1160
Db 201 PheLysAsnArgLeuValAsnIleMetProTyrGlnLeuThrAlaValCysLeuGlnPro 220
QY 1161 ATCCGTGTGTGGAGGCTGTGATCATCATCAATGCGACGCTTCGATGGATTATGACAG 1220
Db 221 IleArgGlyValGlnGlySerAspTyrIleAsnAlaSerPheLeuAspLysTyrArgGln 240
QY 1221 CAGAAAGCTACATAGCTACACAGGGGCTCTGGCAGAGACGACGAGACTTCTGGCGC 1280
Db 241 GlnLysAlaTyrIleAlaThrGlnGlnProLeuAlaGlnSerThrGlnAspPheThrArg 260
QY 1281 ATGCTATGGAGCACAAATTCACCAATCATCATGATGCTGACCAAGCTTCGGAGATGGGC 1340
Db 261 MetLeuThrPrgLinhAsnSerThrIleIleValMetLeuThrLysLeuArgGlnMetGly 280
QY 1341 AGGGAATAATGCCACAGTACGTGGCCAGACAGAGCGCTGTGCTACAGTACTTTGTT 1400
Db 281 ArgGlnLysCysHisGlnTyrThrProAlaGlnArgSerAlaArgTyrGlnThrPheVal 300
QY 1401 GTTGACCGGATGGCTGAGTACACATGCCCGGCTATATCTCTGCTGAGTTCAAGTCAAG 1460
Db 301 ValAspProMetAlaGlnTyrAsnMetProGlnTyrIleLeuAlaGlnPheLysValThr 320
QY 1461 GATGCCCGGATGGGCGACGTCAAGACAAATCCGCGAGTTCCAGTTCAAGACTGGCCAGAG 1520
Db 321 AspAlaAlaArgAspGlyGlnSerArgThrIleArgGlnPheGlnPheThrAspThrProGlu 340
QY 1521 CAGGCGGTGCCCAAGACAGCGGAGGATTCATTCATTCATTCGAGGCGAGTGCATTAAGCC 1580
Db 341 GlnGlyValProLysThrGlyGlnGlyPheIleAspPheIleGlyGlnValHisLysThr 360
QY 1581 AAGGACGAGTTTGGACAGAGATGGGCTATCACAGGTGACACTGAGAGTGTGGCTGGCCGCC 1640
Db 361 LysGlnGlnPheGlyGlnAspGlyProIleThrValHisCysSerAlaGlyValGlyArg 380
QY 1641 ACCGGGCTTCATCACTCTGAGCATCTGCTGCTGCGAGCCGATCGCTATGAGGCGCTGTC 1700
Db 381 ThrGlyValPheIleThrLeuSerIleValIleGlnAlaArgMetAlaTyrGlnLysValVal 400
QY 1701 GACATGTTTCAGACCGGTGAAGACCTGCGTACACAGCGTCTGCCATGCTGCGACAGAG 1760
Db 401 AspMetPheGlnThrValLysThrLeuArgThrGlnArgProAlaMetValGlnThrGln 420
QY 1761 GACGATATCAGCTGTGCTACCGGTGCGGCGCGGTGAGTACCTGGGAGCTTGACCACTAT 1820
Db 421 AspGlnTyrGlnLeuCysTyrArgAlaAlaLeuGlnTyrLeuGlySerPheAspHisTyr 440
QY 1821 GCAACG 1826
Db 441 AlaThr 442

RESULT 4
US-09-788-626-8
: Sequence 8. Application US/09788626
: Patent No. US20020009762A1
: GENERAL INFORMATION:
: APPLICANT: Flint, Andrew J.
: APPLICANT: Cool, Deborah E.
: TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE
: FILE REFERENCE: 200125,401
: CURRENT APPLICATION NUMBER: US/09/788,626
: PRIOR FILING DATE: 2001-02-13
: NUMBER OF SEQ ID NOS: 40
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 8
: LENGTH: 306
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-788-626-8

Alignment Scores:

Pred. No.:	1,73e-82	Length:	306
Score:	1335.00	Matches:	232
Percent Similarity:	93.41%	Conservative:	3
Best Local Similarity:	92.31%	Mismatches:	4
Query Match:	20.72%	Indels:	14
DB:	10	Gaps:	2

US-09-743-492-1 (1-3467) x US-09-788-626-8 (1-306)

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QY 195 CAGTTCACGTGGAGAAATTCAAACCTGGAGGTGAACAGCCCAAGACCGCTATGCCAAT 254
    |||
Db 1 GlnPheThrTrpGlnuSerInleuGluValAsnLysProLysInArgYrAlaAsn 20
QY 255 GTTCATGCCCTAGACCACTCTGTGAGTCATCTTACCTATAGCATGGCCGCCGGAGT 314
    |||
Db 21 ValIleAlaTyrAspHisSerArgValIleLeuThrSerIleAspGlyValProGlySer 40
QY 315 GACTACATCAATGCCAATCAATCAATGCTACCGCAACAGAGATCCCTACATCCGCACG 374
    |||
Db 41 AspTyrIleAsnAlaSerInleuAspGlyTyrArgLysGlnAsnAlaTyrIleAlaThr 60
QY 375 CAGGGCCCCCTGCCGAGACCAATGGCGATTTCTGGAGAATGGTGGGAGACGCCAGC 434
    |||
Db 61 GlnGlyProLeuProGlnThrMetGlyAspPheTrpArgMetValTrpGlnAlaGlnThr 80
QY 435 GCCACTGTGTGATCATGTAGACAGCGCTGAGAGAGATCCCGGTAATGTGATCAGTAC 494
    |||
Db 81 AlaThrValValMetMetThrArgLeuGlnGlnLysSerArgValLysCysAspGlnTyr 100
QY 495 TGGCCAGCCCGTGGCCAGACCTGTGGCTTATTCAGTACCTGTGGACACAGT 554
    |||
Db 101 TrpProAlaArgGlyThrIleThrCysGlyLeuIleGlnValThrLeuLeuAspThrVal 120
QY 555 GAGCTGGCCACATACACTGTGGCACCCTTGGCACTCCACAGAGTGGTCCAGTGAAG 614
    |||
Db 121 GlnLeuAlaThrTyrThrVal-----PheAlaLeuHisLysSerGlnLysSerGlnLys 138
QY 615 CGTGAACCTCGTACGTTTCACTGATGCTGCGCCAGACCCATGAGTTCCTGAGTACCA 674
    |||
Db 139 ArgGlnLeuAlaArgGlnPheGlnPheMetAlaTrpProAspHisGlyValProGlnTyrPro 158
QY 675 AATCCCATCGTGGCTTCTTCTAGTACAGCGGTCAAGGCTTGAACCCCTTAACGAGAGGCC 734
    |||
Db 159 ThrProIleLeuAlaPheLeuAlaArgValLysAlaCysAsnProLeuAspAlaGlyPro 178
QY 735 ATGTGTGTCACCTGACGAGCGGGCGTGGCCGACCGGCTGCTCATCGATTTGATGCC 794
    |||
Db 179 MetValValHisCysSerIleAlaGlyValGlyArgThrGlnCysPheIleValIleAspAla 198
QY 795 AATGTGGAGCGGATGAAGCAGAGAGAGCGTGGACATGTATGGCCACGCTGACCTGATG 854
    |||
Db 199 MetLeuGlnArgMetLysHisGlnLysThrValAspIleTyrGlnLysIleValThrCysMet 218
QY 855 CGATACCAAGGAAGTACTACTGTGGTGGAGAGGAGGAGCAATAGTGTTCATCCATGAGGG 914
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Db 219 ArgSerGlnArgAsnTyrMetValGlnThrGlnAspGlnTyrValPheIleHisGlnAla 238
QY 915 CTGTGTGAGGCTGCGACGTCGGCGCCACAGAGAGT----- 950
    |||
Db 239 LeuLeuGlnAlaAlaThrCysGlnThrGlnValValIleAspAlaMetLeuGlnAlaArg 258
QY 951 -----CCTGCCCGCAACCTGTATGCCCAATC 977
    |||
Db 259 MetLysHisGlnLysThrValAspIleTyrGlnLysIleVal 271

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RESULT 5

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US-09-788-626-27
; Sequence 27, Application US/09788626
; Patent No. US20020009762A1
; GENERAL INFORMATION:
; APPLICANT: Flint, Andrew J.

```

```

; APPLICANT: Cool, Deborah E.
; TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE
; FILE REFERENCE: 200125.401
; CURRENT APPLICATION NUMBER: US/09/788,626
; CURRENT FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 294
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-788-626-27

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Alignment Scores:

Pred. No.:	8.44e-80	Length:	294
Score:	1295.00	Matches:	245
Percent Similarity:	99.19%	Conservative:	0
Best Local Similarity:	99.19%	Mismatches:	0
Query Match:	20.10%	Indels:	2
DB:	10	Gaps:	1

US-09-743-492-1 (1-3467) x US-09-788-626-27 (1-294)

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QY 1062 ACCTCCCGCTTTCATCAGCCCAACCTGCGCTGCAACAAGTTCAAAGACCGGCTGTGAC 1121
    |||
Db 1 ThrSerArgPheIleSerAlaAsnLeuProCysAsnLysPheLysAsnArgLeuValAsn 20
QY 1122 ATCATCCCTTACGAATTCACCCGCTGTGTCTGCACGCCATCCGCTGGTGGAGGCTCT 1181
    |||
Db 21 IleMetProTyrGlnLeuThrArgValCysLeuGlnProIleArgGlyValGlnGlySer 40
QY 1182 GACTACATCAATGCCAGCTTCTGTGATGGTTATAGACACAGAGGCTACATAGTACTAC 1241
    |||
Db 41 AspTyrIleAsnAlaSerPheLeuAspGlyTyrArgGlnGlnLysAlaTyrIleAlaThr 60
QY 1242 CAGGGCCCTGGCAGAGACACCGAGACTTCTGGCGATGCTATGGAGACCAATTCG 1301
    |||
Db 61 GlnGlyProLeuAlaGlnSerThrGlnAspPheTrpArgMetLeuTrpLysHisAsnSer 80
QY 1302 ACCATCATCGTACGTGACCAAGCTTCCGGAGATGGCAGAGAGAAATGCCACCACTGC 1361
    |||
Db 81 ThrIleIleValMetLeuThrLysLeuAlaArgGlnMetGlyArgGlnLysCysHisGlnTyr 100
QY 1362 TGGCAGCAGAGCGCTCTCTGCTACACAGTACTTGTGTCACCGATGGCTGAGTAC 1421
    |||
Db 101 TrpProAlaGlnArgSerAlaArgTyrGlnTyrPheValValAspPrometAlaGlnTyr 120
QY 1422 AACATCCCCCAGATATCTGCTGCTGAGTTCMAAGTACAGGATGCCGGATGGGACGTCA 1481
    |||
Db 121 AsnMetProGlnTyrIleLeu-----PheLysValThrAspAlaArgAspGlnGlnSer 138
QY 1482 AGGACAATCCGCGAGTTCACGATTCACAGACTGGCCAGACGAGGCTGCCCAGACAGCG 1541
    |||
Db 139 ArgThrIleArgGlnPheGlnPheThrAspTrpProGlnGlnLysAlaTrpLysThrGly 158
QY 1542 GAGGATTCATGACTTTCATCGGGCAGGTGCATAGACCAAGAGGAGATTGGACAGGAT 1601
    |||
Db 159 GlnGlnPheIleAspPheIleGlnValHisLysThrLysGlnGlnPheGlnGlnAsp 178
QY 1602 GGGCCATACAGTGCATGCAATGCTGCTGGCGCGGCGGACCGGGTGTTCATCACTGTG 1661
    |||
Db 179 GlnProIleThrValHisCysSerIleAlaGlyValGlyArgThrGlnLysAlaPheIleThrLeu 198
QY 1662 AACATGCTCTGGAGGCGCATGGCTATGAGGCGGTGGTGCATGTTTCAGACCGGAGAG 1721
    |||
Db 199 SerIleValLeuGlnArgMetArgTyrGlnGlnValValValAspMetPheIleThrValLys 218
QY 1722 ACCCTGCTGACACAGCGCTCTGCCATGTGACACAGAGACCAAGTATGATGCTGTGCTAC 1781
    |||
Db 219 ThrLeuAlaArgThrGlnArgProAlaMetValGlnThrGlnLysAspGlnTyrGlnLeuCysTyr 238
QY 1782 CGTGGCGCCCTGGAGTACCTC 1802

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Db 239 ArgAlaAlaLeuGluTyrLeu 245

RESULT 6
US-10-087-993-34

Sequence 34, Application US/10087993
Patent No. US20020169303A1

GENERAL INFORMATION:

APPLICANT: Ullrich, Axel

Aoki, Naohito

Kim, Yeong Moon

Mang, Hong Yang

Chen, Zhengjun

Naylor, Oliver

Kharitonov, Alexei Igorevich

TITLE OF INVENTION: NOVEL PRP20, PCP-2, BDP1, CLK,
AND SIRP POLYPEPTIDES AND RELATED

PRODUCTS AND METHODS

NUMBER OF SEQUENCES: 38

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: FASTSEQ for Windows 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/087,993

FILING DATE: 05-Mar-2002

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/877,150

FILING DATE: June 17, 1997

APPLICATION NUMBER: U.S. 60/019,629

FILING DATE: June 17, 1996

APPLICATION NUMBER: U.S. 60/023,485

FILING DATE: August 9, 1996

APPLICATION NUMBER: U.S. 60/030,860

FILING DATE: No. US20020169303A1ember 13, 1996

APPLICATION NUMBER: U.S. 60/034,286

FILING DATE: December 19, 1996

APPLICATION NUMBER: U.S. 60/030,964

FILING DATE: No. US20020169303A1ember 15, 1996

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 225/298

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 34:

SEQUENCE CHARACTERISTICS:

LENGTH: 1430 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 34:

US-10-087-993-34

Alignment Scores:

Pred. No.: 1,54e-69

Score: 1145.50

Percent Similarity: 58.44%

Best Local Similarity: 40.73%

Length: 1430

Matches: 246

Conservative: 107

Mismatches: 231

Query Match: 17.78% Indels: 20
DB: 9 Gaps: 10

US-09-743-492-1 (1-3467) x US-10-087-993-34 (1-1430)

QY	17	CTCTCTGCTGGCCCACTCTCTGACCTGTGAGATGGGAGGCTCAACTACAGACCC	76
DB	833	LeuLeuGlyGlySerProArgArgProGlyGly-ArgGlyGlySerProTyrHisThrG1	852
QY	77	AGGTATGGAGACCCACCCATCCATCCATCCATCCATCCATCCATCCATCCATCCAT	136
DB	852	YGLNLeu-----HisProAlaValAlaValAlaValAlaValAlaValAlaValAla	870
QY	137	CAAGCCCAAGATGGCCCTCAAGTCTCTCCAGAGATGATGATGATGATGATGATGAT	196
DB	870	tlYsthrAlaGluGlyTyrGlyPheGlyGluGlyTyrGlySerPhePheGlyGly-----	888
QY	197	GTTCACTGGGAGAAATTCAAACCTGGAGGTGAACAAAGCCCAAGACCCATGCGAATGT	256
DB	889	-----TyrAspAlaThrLysLysLysAspLysValLysGlySerArgGlnGluProMe	906
QY	257	CATGGCCCTACGACCACTCTGAGTCATCTTACCTCTGATGCGCTCCCGGAGATGA	316
DB	906	TrpAlaLysAspArgHisArgValLysLeuHisProMetLeuGlyAspProAsnAlaAs	926
QY	317	CTACATCAATGCAACTACATGATGATGATGATGATGATGATGATGATGATGATGATG	376
DB	926	PtyrLileAsnAlaAsnTyrLileAspGlyTyrHisArgSerAsnHisPheLileThrG1	946
QY	377	GGGCCCCCTCCCGAGACCAATGGCGGATTTCTGAGAATGTTGGGAGAACCCGACGCG	436
DB	946	nglyProLysProGluMetValTyrAspPheTrpArgMetValTrpGlnGlnHisCysSe	966
QY	437	CACGTGTGATGATGACGCGCTGGAGAGAACGCCGGTAAAGTGTGATGATGATGATG	496
DB	966	rSerLileValMetLileThrLysLeuValGlyValGlyValLysCysSerArgTyrTr	986
QY	497	GCCAGCCCGTGGACGAGACCTGTGGCTTATTCAGGTGACCTGTGGACAGATGGA	556
DB	986	Pro-----GlnAspSerAspThrTyrGlyAspLysLysLysLysLysLysLysLys	1005
QY	557	GCTGGCCATACACTGTGGCCGACCTTGGCACTCCACAGAGTGGCTCACTGAGAACGG	616
DB	1005	rLeuAlaGluTyrValAlaArgThrPheAlaLeuGluArgGlyTyrSerAlaAlaGln1	1025
QY	617	TGAGCTGGCTAGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATG	676
DB	1025	sgluValArgLysSerHisPheThrAlaTrpProGluHisGlyValProTyrHisAlaThr	1045
QY	677	TCCCATCTGCTGCTTCTACGACGGGTCAAGCCCTGCAACCCCTAGACGAGGCGCAT	736
DB	1045	rGlyLeuLeuAlaLheLileArgArgValLysAlaSerThrProProAsnAlaGlyPro11	1065
QY	737	GGTGATGATGACGACGCGGCGGTGGCCGACGCGCTGTCATCGTATGATGATGAT	796
DB	1065	eValLileHisCysSerAlaGlyThrGlyArgTyrArgTyrLysLysLysLysLysLys	1085
QY	797	GTTGAGGCGGATGAAGCAG	856
DB	1085	rLeuAspMetAlaGluCysGluGlyValAlaAspLysLysAsnGlyValLysThrLecy	1105
QY	857	ATCAGAGAGAACTACATGTCAGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	916
DB	1105	sSerArgArgValAsnMetLileGlnThrGluGluGlnTyrLilePheLileHisAspAla11	1125
QY	917	GCTGAGGCTGCCACAGTGGCGGACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	976
DB	1125	eLeuGluAlaCysLeuGlyGluThrThrLileProValSerGluPheLysAlaThrTy	1145
QY	977	CCAGAGCTGGGCCAAGTGGCTCCAGGGAGAGTGAACCCCATGAGCTGAGTTCAA	1036
DB	1145	rLysGluMetLileArgLileAspProGlnSerAsnSerSerGlnLeuArgGluGluPheG1	1165

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QY 1037 GTTGTGCGCCAGC-----TCAAGGCCACACAGTCGCCCTTCATGACGGCCACCTGCC 1090
   :      |||      |||
Db 1165 nThrLeuAnSerValThrProProLeuAspValGluGluCysSerIleAlaLeuLeuP 1185
QY 1091 CTGCACAAGATTCAGAACCCGGCTGTGAACATCATGCCCCCTACGAATTGACCCGCTGTG 1150
   :      |||      |||      |||      |||      |||      |||      |||
Db 1185 oArgAsnArgAspLysAsnArgSerMetAspValLeuProProAspArg-----Cy 1202
QY 1151 TCTGCAGCCATCCGCGGTGGTGGAGGC-----TCTGACTACATCAATGACCGACTTCC 1204
   |||      |||      |||      |||      |||      |||      |||      |||
Db 1202 sleuProPheLeuIleSerThraSpLysSerAsnAsnTyrIleAsnAlaIleLeuTh 1222
QY 1205 GGATGGTTATAGACACAGCAGAGGCCCTACATAGCTACACAGAGGCCCTGTGCAGACAG 1264
   |||      |||      |||      |||      |||      |||      |||      |||
Db 1222 rAspSerTyrThrArgArgSerAlaPheMetValThrLeuHisProLeuGlnSerThr 1242
QY 1265 CAGAGACTTGTGGCCATCTTATGGAGCAATTCACCATCATGTCATGCTGACCAA 1324
   :      |||      |||      |||      |||      |||      |||      |||
Db 1242 rProAspPheTyrArgLeuValTyrAspTyrGlyCysThrSerIleValMetLeuAsnG 1262
QY 1325 GCTTGCGGAGATGGGAGGAGG---AAATGCCACAGTACTGCCCGCAGAGCGCTCTGC 1381
   :      |||      |||      |||      |||      |||      |||      |||
Db 1262 nLeuAsnGlnSerAsnSerAlaTyrProCysLeuGlnTyrTyrProGluProGlyArgG 1282
QY 1382 TCGCTACAGTACTTGTGTGTGACCCGAGTGGCTGAGTACAACATGCCCAATATCT 1441
   :      |||      |||      |||      |||      |||      |||      |||
Db 1282 nGlnTyrGlyLeuMetGluValGluPheMetSerGlyThrAlaAspGluAspLeuVal 1302
QY 1442 GCGTAGATTCAAGGTCACGAGATCCCGGGATGGGAG-----TCAAGGACATCCGCGCA 1495
   |||      |||      |||      |||      |||      |||      |||      |||
Db 1302 aArgValPheArgValGlnAsnIleSerArgLeuGlnGluGlyAspLeuLeuValArg 1322
QY 1496 GTTCAGTCCACAGACTGGCCAGAG---CAGGCGCTGCCCAACAGACGGGAGGATTCAT 1552
   |||      |||      |||      |||      |||      |||      |||      |||
Db 1322 SPheGlnPheLeuArgTyrSerAlaTyrArgAspThrProAspSerLysAlaIle 1342
QY 1553 TGACTTCATCGGCGAGGTCATAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1612
   :      |||      |||      |||      |||      |||      |||      |||
Db 1342 uHisLeuLeuAlaGluValAspLysTyrPheGlnAlaGlnSerGly---AspGlyArgThr 1361
QY 1613 GGTGACATGACAGTGGCTGGCGGCGGCGGAGCGGGGTTCATCACTGAGAGAGTGGCT 1672
   |||      |||      |||      |||      |||      |||      |||      |||
Db 1361 eValHisCysLeuAsnGlyGlyArgSerGlyThrPheCysAlaCysAlaThrVal 1381
QY 1673 GGAGGGCAGTGGCGGTATGAGGGGGTGGTGCATGTTTGACAGCCGGAACACCTGGGTAC 1732
   |||      |||      |||      |||      |||      |||      |||      |||
Db 1381 uGlnMetIleArgCysHisAsnLeuValAspValPhePheAlaAlaGlnThrLeuArgAs 1401
QY 1733 ACAGCGCTCGCCATGTCAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1792
   :      |||      |||      |||      |||      |||      |||      |||
Db 1401 nTyrLysProAsnMetValGluThrMetAspGlnTyrHisPheCysTyrAspValAla 1421
QY 1793 GGAGTACTTC 1802
   |||      |||      |||      |||      |||      |||      |||      |||
Db 1421 uGlnTyrLeu 1424

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RESULT 7

US-10-000-954-2

Sequence 2, Application US/10000954

Patent No. US2002012726A1

GENERAL INFORMATION:

APPLICANT: Schlessinger, Joseph

Barnea, Giliad

Grunet, Martin H.

Margolis, Richard U.

TITLE OF INVENTION: A NEW CLASS OF RPTPases: THEIR

STRUCTURAL DOMAINS AND LIGANDS

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSSEE: PENNIE & EDMONDS

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

```

? COUNTRY: U.S.A.
? ZIP: 10036
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/10/000,954
? FILING DATE: 04-Dec-2001
? CLASSIFICATION: <unknown>
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 09/644,293
? FILING DATE: 23-Aug-2000
? APPLICATION NUMBER: 08/081,929
? FILING DATE: <unknown>
? ATTORNEY/AGENT INFORMATION:
? NAME: Coruzzi, Laura A.
? REGISTRATION NUMBER: 30742
? REFERENCE/DOCKET NUMBER: 7683-041-999
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 212 790-9090
? TELEFAX: 212 869-8864/9741
? TELEX: 66141 PENNIE
? INFORMATION FOR SEQ ID NO: 2:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 2308 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: unknown
? MOLECULE TYPE: protein
? SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-000-954-2

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Alignment Scores:
Pred. No.: 9,22e-68 Length: 2308
Score: 1120.00 Matches: 245
Percent Similarity: 57.00% Conservative: 105
Best Local Similarity: 39.90% Mismatches: 216
Query Match: 17.38% Indels: 48
DB: 12 Gaps: 15

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US-09-743-492-1 (1-3467) x US-10-000-954-2 (1-2308)

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QY 72 ACCCCAGATATCCGAGACACCACCACCCATCCCATACCCGACCTGGCGGAC----- 122
   :      |||      |||      |||      |||      |||      |||      |||
Db 1678 SerProArgValIleSerThrProThrProIlePheProIleSerAspValGly 1697
QY 123 -----AACATCGAGCGGCTCAAGGCCAACAGATGGCCTC 155
   :      |||      |||      |||      |||      |||      |||      |||
Db 1696 AlaIleProIleLysHisPheProLysHisValAlaAspLeuHisAlaSerGly--- 1716
QY 156 AAGTCTCCACAGAGATATGAG-----TCCATGACCCCTGGACAGCAGTTC 200
   |||      |||      |||      |||      |||      |||      |||      |||
Db 1717 ---PheThrGluGluPheGlnGluValGlnSerCysThrValAspLeuGly----- 1733
QY 201 ACCTGGAGAAATTCAAACCTGGAGGTGAACAACCCCAAGACCCGATATGCAATGTCATC 260
   |||      |||      |||      |||      |||      |||      |||      |||
Db 1734 ThrAlaAspSerSerAsnHisProAspAsnLysHisLysAsnArgTyrIleAsnIleVal 1753
QY 261 GCCTAGACCACTGTCGAGTATCTCTATCCCTATATCGATGGCGTCCCGCG-----AGT 314
   |||      |||      |||      |||      |||      |||      |||      |||
Db 1754 AlaTyrAspHisSerArgValLysLeuAlaGlnIleAlaGluLysAspLysLeuThr 1773
QY 315 GACTACATCAATGCCACATGATCGATGCGTACCCGACAGACAGAAATGCTATCGCCACG 374
   |||      |||      |||      |||      |||      |||      |||      |||
Db 1774 AspTyrIleAsnAlaAsnTyrValAspGlyTyrAsnArgProLysAlaTyrIleAla 1793
QY 375 CAGGGCCCCCTGCCGAGACATGGCGGCGATTTCTGAGAGANTGTGGAGACAGCGCAGC 434
   |||      |||      |||      |||      |||      |||      |||      |||
Db 1794 GlnGlyProLeuLysSerThrAlaGluAspPheTyrArgMetIleTyrPheGlnHisAsnVal 1813
QY 435 GCCACTGTGCTATGATGACACAGCGCTGGAGGAGGAGTCCCGGGTAAATGTGATCAGTAC 494

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Db	1814	GIUValIIEValIMetIIEthraSLneValIGIuLysGlyAraGArgLysCysaspIInTr	1833
Qy	495	TGGCCAGCCCGCTGGCACCAGACCTGTGGCCTTAATTCAGGTGACCCTGTGTGGACACAGTG	554
Db	1834	TTrProIaaSPrgLysSerGIuLGIuTYGlyAaSPheLeuValThrClnLysSerValGln	1855
Qy	555	GAGCTGGCCACATACACTGTGTGGCACTTGTGGCACTCCAC-----AAGAGTGGC	602
Db	1854	ValLeuValaTYTrTYTrThValaIArgaSPheThLeuValaGAsnThLysIleLysLysGly	1873
Qy	603	TCCAGTGGAGAGCCTGAG-----CTGCGTCAGTTTCAGTTTCAGTTGCTGGCCGGCA	650
Db	1874	SerGlnLysGIaArgProSerGIaArgValaValThGIInTYHisTYTrhClnTrPro	1893
Qy	651	GACCATGAGAGTTCTGTGATGCCAACATCCCATCTGGCTCTTACGAGCGGTCAAGGCC	710
Db	1894	AspMetGIaValProGIuTYTrSerLeuProValLeuThrPheValaArgLysAlaIaIaTr	1913
Qy	711	TGCAACCCCTAGACGAGGGCCATGTGTGTCTACTGCACGCGGGCGGTGGCCGACC	770
Db	1914	AlaIysArgHisAlaValGIaProValaValaHisCysSerValGIaLGIaLGIaArgThr	1933
Qy	771	GAGCTCTTCATCGTATTAAGCCATGTTGGACGGATGACAGACGAGAGAGCGGTGGAC	830
Db	1934	GIuThrTYTrIIEValaILeuaspSerMetLeuGlnGlnIleGlnHisGIuLGIuThrValaSPn	1953
Qy	831	ATCTATGAGCCAGTACCTGATGCATGCATACAGAGAGAACTATACATGTCGACAGCAGAC	890
Db	1954	IlePheGIaPheLeuLysHisIleArgSerGIaArgaSPnTYLeuValGIaThrClnIuLGIu	1973
Qy	891	CAGTACGTGTTCATTCATAGAGCGCTGTGTGAGCGCTGCCACGTGGCGCCACAGAGGTG	950
Db	1974	GIuTYTrValaPheIIEHisaspThrIIEuValaGIuAlaIleLeuSerLysGIuThrGIuVala	1993
Qy	951	CGTGCCGACACGTTATGGCCACATCCCAACACTGGGCCAAGTGTCTCCAGGGAGAGT	1010
Db	1994	LeuaspSerHisIIEHisAlaTYTrValaSPnaIaLeu---LeuIleProGIaProIaGly	2012
Qy	1011	GTGACCGCATGAGATCGATGATTCAGATTGTCTGGCCAGTCCCAAGGCCACAGCTCCGCG	1070
Db	2013	LysThrTYLeuGIuLysGlnPheGlnLeuLeuSerGIaSerAsnIleGlnIaSerasp	2032
Qy	1071	TTCATCAGCGCCAACTGCCCCGTGCACAACTTCAGAACCGCGGTGTGATCATCTGCC	1130
Db	2033	TYSerIaIaIaIaLeuLysGlnCysAsnArgGIuLysaArgTYHisSerSerIIEIlePro	2052
Qy	1131	TACCAATTGACCCGTGTGTGTCTGACGCCCATCCGTGTGTGTGGAGGGCTGTGACTACATC	1190
Db	2053	ValGIaArgSerAlaValaGIuLysSerLeuSerGIu---GIuGIuThrasPYTrIIE	2071
Qy	1191	AATGCAAGCTTCCTGGATGTGTTATAGACACAGAAAGGCTACATATGCTACAGAGGGCT	1250
Db	2072	AsnaIaSerTYTrIIEMetGIuTYTrGIuInSerAsnGIuPheIIEIleThrClnHisPro	2092
Qy	1251	CTGGCAGAGACACACGAGGACTTGTGGCGATGCTATGGAGACACAAATTCACATATC	1310
Db	2092	LeuLeuHisThrIIELysaSPheThraPrgMetIIETrPAspHisAsnaIaGIuLeuVal	2111
Qy	1311	GTCACTGTGACCAACGTTCCGGAGATGGCAGGGAGAAATGCCACCAGTACTGGCCA--	1367
Db	2112	ValMetIIEProaSPrgLysGlnaSPmetAlaGIuLysGIu---PheValTYTrProaSPn	2130
Qy	1368	GCAGCGCGCTGTGCTGCTCTACAGTACTTGTGTGTGGACCCGACGGAGCTGGAG--	1418
Db	2131	LysaSPgIuProIIEaSPnCYsGIuSerPheLysValaThrLeuMetAlaGIuIuHisLys	2150
Qy	1419	-----TACAAACATGCCCCAGTATATCTGTGCTGATTCAGGTCAAGGTACAGGATCCCGGAT	1472
Db	2151	CysLeuSerAsnGIuLGIuLysLysLeuIIEGlnaSPpHeIIELeuGIuAlaIaThrClnaSP	2170
Qy	1473	GGGAGTCAAGAGCAATCCGGCAGCTTCACAGTTCACAGACTGGCCAGAGCAGGGCGTGGCC	1532

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Db      2171 AspryValIleuGlValAlArgHisPheGlnCysProLysTrpProAsnProAspSerPro   2190
Qy      1533 -----AAGACAGCGCGAGGGCATTCATTGCATCTCCGCCAGCGTCCATGAACCAAGAG   1586
           ||||| ||| ||| |||
Db      2191 IleSerLystrPheGlu---LeuIleSerValIle-----LysGluInu    2204
Qy      1587 CAGTTTGACAGKATGGGCGCTATCACCGGTGCATCGACAGTCGTGGCTGGCGCCGACGGG   1646
           :::::|||||:::||||| |||
Db      2205 AlaAlaasArGaSpGlyPrometIleValHisAspGlnHisGlyValThrAlaGly   2224
Qy      1647 GNGTCATCATCTCGACATCGTCGTGGACGCGGTGCGATGCGGTATGAGCGCGGTGTCACATG   1708
           ||| ||::::: ||::::: ||| |||||:::
Db      2225 ThrPheCySaLaLeuThrThrIleMetHisGlnHeuGlnLysGlnAsnSerValAspAl   2244
Qy      1707 TTTCGACCGCTGGAAGACCCTGCGTACACAGCGTCCTCCATGCTGTGCACAGAGAGCAG   1766
           ::||| || |::: ||||| |||
Db      2245 TyrGlnValAlaLysMetIleAsnLieuMetArgProGlyValPheAlaSplLeuGln   2264
Qy      1767 TATCATCGTGTCTACCGTGGCGCGCTGGAGTCCGACG   1808
           ||||| ||::: ||| :::
Db      2265 TyrGlnPheLeuYrLysValIleLeuSerLeuValSerThr   2278

RESULT 8
US-09-788-626-9
; Sequence 9, Application US/09788626
; Patent No. US2002009762A1
; GENERAL INFORMATION:
; APPLICANT: Flint, Andrew J.
; APPLICANT: Cool, Deborah E.
; TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATES
; FILE REFERENCE: 200125.401
; CURRENT APPLICATION NUMBER: US/09/788,626
; CURRENT FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-626-9

Alignment Scores:
Pred. No.:          2.9e-43              Length:        305
Score:              752.50               Matches:       144
Percent Similarity: 72.69%               Conservative:  37
Best Local Similarity: 57.83%            Mismatches:   65
Query Match:         11.68%              Indels:       3
DB:                  10                   Gaps:         2

US-09-743-492-1 (1-3467) x US-09-788-626-9 (1-305)

Qy      204 TGCGGAGATTTCAAACCTCGAGGCTGGAACAACCCCAAGAACCCTATGCCGATTCATGCC   263
           ||:::|||||::: ||::: ||||| ||||| |||:::|||||
Db      4 TrpAspSerAlaLysLysAspRgJAsnArgMetLysAsnArgGlyTolLysAsnIleAla   23
Qy      264 TAGACACCACTGCTCAGTCACATCTTACCTATGATGAGAGCGGCTCCCGGAGCAGTAACATC   323
           ||||| ||||| ||| |||:::||||| ||||| ||||| |||||
Db      24 TyrAspHisSerArgValAlaArgLeuGlnThrIleGlnGlyAspThrAsnSerSprlytle   43
Qy      324 AATGCCAATACTACATCGATGGCTACCCGACAGACAGAAATGCTTACATGCGACAGAGGCCCC   383
           ||| ||||| ||||| ||| ||| ||||| ||||| ||||| |||||
Db      44 AsnGlnLysGlyTleAspRglYtYrGlnHisArgProAsnHisTyrlIleAlaThrclnGlypro   63
Qy      384 CTGCCCCAGACATAGGGCGATTTCTGGAGAAATGTTGGTGGAAACAGCGCACGGCCACTGTG   443
           ::: |||||::: ||||| ||||| ||||| ||||| ||||| |||||
Db      64 MetGlnGlnThrIleTyrAspPheThrPatGmetValTyrHisGlnHisThrAlaSerIle   83
Qy      444 GTCATCATGACACGCGCTGCGAGAGAAAGTCCCGGCTAAATGTGATCAGTACGTGCGCCACC   503
           :::::||||| ||| ||| ||||| ||||| ||||| ||||| |||||
Db      84 IleMetValThrAsnLeuValGlnValAlaGlyValLysCysCysLysTyrTyrPro---   102
Qy      504 CGTGACACCGGACGACTGTGGCTTTATTCAGAGTAGTACCCTTGTGACACAGTGGAGCTGGCC   563
```



```

Db      103  ASPTFTGluIleTyrLysAspIleLysValThrLeuIleGluThrGluLeuLeuAla 122
QY      564  ACATACACTGTGGCGCCTTCGCACCTCCACAGAGTGGCTCCAGTGAAGAAGCTGAGCTG 623
Db      123  GltTyrValIle-----PheAlaValGluLysArgGlyValHisGluIleLeuArgGluIle 140
QY      624  CGTCAGTTTCAGTTCATGGCGCTGGCCAGACCATGAGAGTTCGAGATCCAGATCCCATC 683
Db      141  ATGGINPheHisPheThrGluTyrProAspHisGlyValAlaProTyrHisAlaThrGlyLeu 160
QY      684  CTGGCCCTTCCTTACAGAGGCTCAAGGCTCCAAACCCCTCAGACAGCAGGCGCCATGCTGTG 743
Db      161  LeuGlyPheValArgIleValLysSerLysSerProProSerAlaGlyProLeuVal 180
QY      744  CACTGACGGCGGGCGCTGGCGCCGACCGGCTGCTCATGCTGATGATGATGATGAG 803
Db      181  HisCysSerAlaGlyValGluValArgThrGlyCysPheIleValIleAspIleMetLeuAsp 200
QY      804  CGGATGAACGACGAGAGAGCGGTCATGTATGCGCAGTGCATGCGATGCGATCAG 863
Db      201  MetAlaGluArgGluGluValValAlaAspIleTyrAsnCysValArgGluLeuArgSerArg 220
QY      864  AGGAACCTACATGATGTCAGAGCAGGACGACGATGCTTCATGCTAGAGCGCTGCTGAG 923
Db      221  ArgValAsnMetValGluThrGluGluGluGluGluGluGluGluGluGluGluGlu 240
QY      924  GCTGCCACGCTGGCGCCACACAGAGGTG 950
Db      241  AlaCysLeuGlyCysGlyAspThrSerVal 249

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RESULT 9

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US-09-788-626-10
; Sequence 10, Application US/09788626
; Patent No. US2002009762A1
; GENERAL INFORMATION:
; APPLICANT: Flint, Andrew J.
; APPLICANT: Cool, Deborah E.
; TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE
; FILE REFERENCE: 200125.401
; CURRENT APPLICATION NUMBER: US/09/788,626
; CURRENT FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-626-10

```

```

Alignment Scores:
Pred. No.: 2.07e-41 Length: 310
Score: 725.00 Matches: 140
Percent Similarity: 71.48% Conservative: 43
Best Local Similarity: 54.69% Mismatches: 67
Query Match: 11.25% Indels: 6
Db: 10 Gaps: 2

```

US-09-743-492-1 (1-3467) x US-09-788-626-10 (1-310)

```

QY      195  CAGTTCACCTGGGAGAAATTCAAACCTGGAGGTGACAAACCCCAAGACCGCTATGCGAAT 254
Db      1  GlnAlaThrCysGluAlaIleSerLysGluGluAsnLysGluLysAsnArgTyrValAsn 20
QY      255  GTCATCGCTAGACGACACTCTGAGTCACTTACCTCATGAGTGGCGCTCCCGGAGT 314
Db      21  IleLeuProTyrAspHisSerArgValHisLeuThrProValGluGluValProAspSer 40
QY      315  GACTACATGAATGCACTACATGATGCTACCGGACAGAGATGCTACATGCGCAGG 374
Db      41  AspTyrIleAsnAlaSerPheIleAsnGlyTyrGluGluLysAsnLysPheIleAlaIle 60

```

```

QY      375  CAGGGCCCGCTGGCCGAGACCATGGCCATTCCTGAGAAATGGTGGGAGACAGCCGACG 434
Db      61  GlnGlyProLysGluGluThrValAsnAspPheThrArgMetIleThrGluGluAsnThr 80
QY      435  GCCACTGTGTCATGATGACACGCGTGGAGAGAAAGTCCCGGATAAATGATCAGTAC 494
Db      81  AlaThrIleValMetValThrAsnLeuLysGluArgLysGluCysLysCysAlaGluTyr 100
QY      495  TGGCCAGCCCGTGGACCGACGACCTGTGCTTATTCAGGTGACCTGTGACACAGTGC 554
Db      101  TyrProAspGlnGlyCysThrTyrGlyAsnIleArgValSerValGluAspValIleThr 120
QY      555  GAGCTGGCAACATACACTGTGGCGCACCTGGCATCCCAAGAGTGGCGTCCAGTAGAAG 614
Db      121  ValLeuValAspTyrThrVal-----PheCysIleGlnGlnValGluLysPheThrAsn 138
QY      615  CGTGAG-----CTGGCTCAGTTTCAGTTTCATGCGCCGCGCAACCATGAGATT 662
Db      139  ArgLysProGlnArgLeuIleThrGlnPheHisPheThrSerTyrProAspPheGlyVal 158
QY      663  CCTGAGTACCAACTCCATCCTGCGCTTCTTACGACGAGGTCAGAGCCCTGCAACCCCTA 722
Db      159  ProPheThrProIleGlyMetLeuLysPheLeuLysValLysValLysAlaCysAsnProGln 178
QY      723  GACGCGAGGCGCCATGTTGGTGCACCTGACGCGCGGCTGGCGCCAGCCGCTGCTCATC 782
Db      179  TyrAlaGlyAlaIleValAlaHisCysSerAlaGlyValGlyThrGlyThrPheVal 198
QY      783  GTGATGATGCCATGTTGGAGCGGATGAAGCAGAGAACGTCATGATGCGCCAC 842
Db      199  ValIleAspAlaMetLeuAspMetMetHisThrGluArgLysValAlaPalaIlyrGlyPhe 218
QY      843  GTGACCTGCATCGCATCACAAGAGAACTACATGTCGACAGGAGGACGACGATGCTTC 902
Db      219  ValSerArgIleArgAlaGlnArgCysGlnMetValGlnThrAspMetGlnTyrValPhe 238
QY      903  ATCCATGAGGCGCTGTGGAGCGTGCACGCTGCGGCCACACAGAGGTG 950
Db      239  IleTyrGlnAlaLeuLeuGluHisTyrLeuTyrGlyAspThrGluLeu 254

```

RESULT 10

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US-09-788-626-6
; Sequence 6, Application US/09788626
; Patent No. US2002009762A1
; GENERAL INFORMATION:
; APPLICANT: Flint, Andrew J.
; APPLICANT: Cool, Deborah E.
; TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE
; FILE REFERENCE: 200125.401
; CURRENT APPLICATION NUMBER: US/09/788,626
; CURRENT FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-626-6

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Alignment Scores:
Pred. No.: 5.85e-40 Length: 319
Score: 703.50 Matches: 140
Percent Similarity: 65.57% Conservative: 39
Best Local Similarity: 51.28% Mismatches: 79
Query Match: 10.92% Indels: 15
Db: 10 Gaps: 3

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US-09-743-492-1 (1-3467) x US-09-788-626-6 (1-319)

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QY      201  ACCTGGAGAAATTCAAACCTGGAGGTGAAACCCCAAGACCGCTATGCGAATGCTATC 260
Db      3  ThrAlaGlnHisSerAsnHisThrProGluAsnLysHisLysAsnArgTyrIleAsnIleLeu 22

```

```
OY 261 GCCTAGCAGCACTCTGAGTCACTTACCTCTATCATGAGCGCTCCCGG-----AGT 314
|||
Db 23 AATATGASPHISSErATGVallyLysleuArProleuProGlyLysAspserLyshSser 42
|||
OY 315 GACCTACATACGCAATGCACTACATGCTACCGCAGACAGAAATGCTACATCCGCACG 374
|||
Db 43 AspyrTlleasnaAlaAsnTyValAspGlyTyAsnLysAlaLysAlaTyTlleaLaThr 62
|||
OY 375 CAGGCGCCCTGCGCCGAGACCATGGCGATTTCTGAGATGATGTTGGAGACAGCGCACG 434
|||
Db 63 GlnGlyProLeuLysSerThrPheGluAspPheTrpArgMetLleTrpGlnGlnsnThr 82
|||
OY 435 GCCACTGTGTCATGATGACAGCTGAGAGAGAGATCCCGGAAATGTGATCAGTAC 494
|||
Db 83 GlyTlleValMetLleThrAsnLeuValGluLysGlyArgArgLysCysAspLntyr 102
|||
OY 495 TGGCAGCCCGGTGGCAGCAGACCTGTGGCTTATTCAGAGTACCTGTGGACACAGTG 554
|||
Db 103 TrpProThrGluAsnSerGlnGlnTyrGlyAsnLleValThrLeuLysSerThrLys 122
|||
OY 555 GAGCTGGCCACATACACTGTGGCAGCTTTCGCACTCCACAAGAGT----- 599
|||
Db 123 IleHisAlaCysTyThrVal-----PheSerIleArgAsnThrLysValLysGly 140
|||
OY 600 -----GCTCCAGTAGAGAGAGCTGAGCTGCGTCACTTCATTCATTCATG 641
|||
Db 141 GlnLysGlyAsnProLysGlyArgGlnAsnGlnuArgValIleGlnTyHisTyThr 160
|||
OY 642 GCGTGGCCAGACATGAGAGTTCCTGATACCACTCCCATCTGCGCTTCCTACAGAGG 701
|||
Db 161 GlnTrpProAspMetGlyValProGlnTyThrAlaLeuProValLeuThrPheValArgArg 180
|||
OY 702 GTCAAGGCTGCAACCCCTGAGACGAGCCCATGTGTGCTGACTGACGAGCGGCGTG 761
|||
Db 181 SerSerAlaIleArgMetProGlnTyThrGlyProValIleValHisCysSerAlaGlyVal 200
|||
OY 762 GCGCCAGCCGCGTCTTCATCGTGAATGATGCGCATGTTGGAGCGGATGAACGACGAG 821
|||
Db 201 GlyArgThrGlyThrTyThrIleValIleAspSerMetLeuGlnIleLysAspLysSer 220
|||
OY 822 ACCGTGACATCTATGCGACGCTGACGTCATGCGATCACAGAGAACTACATGCTGACG 881
|||
Db 221 ThrValAsnValLeuGlyPheLeuLysHisIleArgThrGlnArgAsnTyTlleuValGln 240
|||
OY 882 ACCGAGACAGATACGTGTTTCATCCATGAGCGCTGTGAGAGCTGCCACGCGGCGCAC 941
|||
Db 241 ThrGlnGlnGlnTyThrIlePheLleHisAspAlaLeuLeuGlnAlaIleLeuGlyLysGlu 260
|||
OY 942 ACAGAGTGCCTGCCCGCAACCTGTATGCCACATCCAG 980
|||
Db 261 ThrGluValIleAspSerMetLeuGlnGlnIleLys 273
|||
RESULT 11
US-09-788-626-7
: Sequence 7, Application US/09788626
: Patent No. US20020009762A1
: GENERAL INFORMATION:
: APPLICANT: Flint, Andrew J.
: APPLICANT: Cool, Deborah E.
: TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE
: FILE REFERENCE: 200125.401
: CURRENT APPLICATION NUMBER: US/09/788.626
: NUMBER OF SEQ ID NOS: 40
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 7
: LENGTH: 313
: TYPE: PRT
: ORGANISM: Drosophila melanogaster
US-09-788-626-7
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Alignment Scores:
Pred. No.: 9,26e-40 Length: 313
Score: 700.50 Matches: 131
Percent Similarity: 69.32% Conservative: 52
Best Local Similarity: 49.62% Mismatches: 76
Query Match: 10.87% Indels: 5
Db: 10 Gaps: 3
US-09-743-492-1 (1-3467) x US-09-788-626-7 (1-313)
OY 207 GAGATTCGAACCTGGAGAGTGAAGCAAGCCCAAGACCCGTATGCGATGTCATGCCCTAC 266
|||
Db 5 GlnHisSerGlnHisProGlnuAsnTyArgLysAsnArgTyTlleuAsnIleThrLaTyThr 24
|||
OY 267 GACCACTCTCGAGTATCCTTCTACTCTATGCAATGCGCGTCCCGGAGT--GACTACATC 323
|||
Db 25 AspHisSerArgValHisIleuHisProThrProGlnGlnLysLysAsnLeuAspTyTlle 44
|||
OY 324 AATGCCAATCATGATGATGCTACCGCAGACAGAAATGCTTACATGCGCACAGCGGCCCC 383
|||
Db 45 AsnAlaAsnPheIleAspGlyTyGlnLysGlnHisAlaPheIleGlyThrGlnGlyPro 64
|||
OY 384 CTGCCCCGAGACCATGGCGGATTTCTGAGAAATGCTGTGGAAACAGCGACGCGCACTGTG 443
|||
Db 65 LeuProAspThrPheAspCysPheTrpArgMetLleTrpGlnGlnArgValAlaIleLe 84
|||
OY 444 GTCATGATGACAGCGCTGAGAGAGTCCCGGTAATGATGATCAGTACGTGCGCACGCC 503
|||
Db 85 ValMetIleThrAsnLeuValGlnuArgGlyArgArgLysCysAspMetTyTrpProLys 104
|||
OY 504 CGTGGCACCAGACCTGTGGCCTTATTCAGATGACGCTGTGGACACAGATGAGAGCTGGCC 563
|||
Db 105 AspGlyValGlnTyThrTyGlyValIleGlnValLysLeuIleGlnGlnGlnuValMetSer 124
|||
OY 564 ACATGCACTGCG-----CGCACCTTCGCACTCCACAAGAGTGGCTCCAGTAGAGAG 614
|||
Db 125 ThrTyThrValLeuGlnIleLysHisLeuLysLysLysLysLysGlnCysAsnThr 144
|||
OY 615 CGTGAGCTG---CGTCACTTCATGATGAGCGCTGGCCAGACAGATGCTGAGTAC 671
|||
Db 145 GlnLysLeuValTyGlnTyThrHisTyThrAsnTrpProAspHisGlyThrProAspHis 164
|||
OY 672 CCAACTCCCAATCTGCGCTTCTACGAGCGGTCAAGGCTGTGCAACCCCTAGACGAGG 731
|||
Db 165 ProLeuProValIleuAsnPheValLysLysSerSerAlaAlaAsnProAlaGlnuLacGly 184
|||
OY 732 CCCATGTTGAGCGATGAGAGCAGCAGAGAGAGTGTGACATCTATGCGTACGTGACTGC 791
|||
Db 185 ProIleValIleHisCysSerAlaGlyValGlyArgThrGlyThrTyTlleValLeuAsp 204
|||
OY 792 GCCATGTTGAGCGGATGAGAGCAGCAGAGAGAGTGTGACATCTATGCGTACGTGACTGC 851
|||
Db 205 AlaMetLeuLysGlnIleGlnGlnLysAsnIleValAsnValPheGlyPheLeuArgHis 224
|||
OY 852 ATGCGATCACAGAGATACATGCTGCGACAGCGAGAGACAGTACGTTCATCATGAG 911
|||
Db 225 IleArgAlaGlnArgAsnPheLeuValGlnThrGlnGlnGlnTyThrIlePheLeuHisAsp 244
|||
OY 912 GCGGTGCTGAGAGCGCCAGCGTGGCCACAGAGAGTGTGCGCGCCGCAACCTGATGCC 971
|||
Db 245 AlaLeuValGlnuAlaIleAlaSerGlyLutThrAsnLeuValLeuAspAlaMetLeuLys 264
|||
OY 972 CACATCCAGAG 983
|||
Db 265 GlnIleGlnGln 268
|||
RESULT 12
US-09-788-626-11
: Sequence 11, Application US/09788626
: Patent No. US20020009762A1
: GENERAL INFORMATION:
: APPLICANT: Flint, Andrew J.
: APPLICANT: Cool, Deborah E.
```



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Db 203 TyrIleValLeuAspSerMetLeuGlnGlnIleGlnHisGlnGlyThrValAsnIlePhe 222
QY 837 GGCCAGCTGACCTGCATGGCATCACAGAGAACTACATGAGCGAGAGCGACAGTAC 896
Db 223 GlyPheLeuLysHisIleArgSerGlnArgAsnTyrLeuValGlnThrGlnGlnGlnTyr 242
QY 897 GTGTCATCATGAGAGCGCTGCTGGAGCTGCCACGCTGGCCACACAGAGTGCCTGCC 956
Db 243 ValPheIleHisAspThrLeuValGlnAlaIleLeuSerGlnThrGlnValValLeu 262
QY 957 CGCAACCTGTATGCCACATCCAGAAAGCTGGCGCAAGTG 995
Db 263 AspSerMetLeuGlnGlnIleGlnHisGlnGlyThrVal 275

RESULT 14
US-09-788-626-26
; Sequence 26, Application US/09788626
; Patent No. US20020009762A1
; GENERAL INFORMATION:
; APPLICANT: Flint, Andrew J.
; APPLICANT: Cool, Deborah E.
; TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE
; FILE REFERENCE: 200125.401
; CURRENT APPLICATION NUMBER: US/09/788.626
; CURRENT FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-626-26

Alignment Scores:
Pred. No.: 4.73e-39 Length: 316
Score: 690.00 Matches: 138
Percent Similarity: 63.74% Conservative: 36
Best Local Similarity: 50.55% Mismatches: 91
Query Match: 10.71% Indels: 8
DB: 10 Gaps: 2

US-09-743-492-1 (1-3467) x US-09-788-626-26 (1-316)
QY 201 ACGTGGAGAAATTCAAACTGGAGGTGAACAGCCCAAGACCGGTATGCGATGTCATC 260
Db 3 ThrAlaAspSerSerAsnHisProAspAsnLysHisLysAsnArgTyrIleAsnIleVal 22
QY 261 GCCTAGCAACACTGTCGATGTCATCCTTACCTTATGATGAGGCTCCCGGCGG-----ACT 314
Db 23 AlaTyrAspHisSerArgValLysLeuAlaGlnLeuAlaGlnLysAspLysLeuThr 42
QY 315 GACTCATCAATAGCCAACTACTACATGAGTGCCTACCCAGACAAATGCCATCATCCGCACG 374
Db 43 AspTyrIleAsnAlaAsnTyrValAspArgTyrAsnArgProLysAlaTyrIleAla 62
QY 375 CAGGCCCCCTGCCGAGCATGGGCGCATTTCTGGAGAAAGTGGGGAACAGCGCACG 434
Db 63 GlnGlyProLeuLysSerThrAlaGlnAspPheArgMetIleArgPheIleAsnVal 82
QY 435 GCCACTGTGTCATGATGATGACAGCGCTGGAGAGAGATCCCGGGTAAATGATGATGATAC 494
Db 83 GluValIleValMetIleThrAsnLeuValGlnLysGlnArgArgLysLysAspGlnTyr 102
QY 495 TGGCCAGCCCGTGGCAGCAGACACTGTCGCTTATTCAGGTGACCCCTGTTGACACAGTG 554
Db 103 TyrProAlaAspGlySerGlnGlnTyrGlnAsnPheLeuValThrGlnLysSerValGln 122
QY 555 GAGCGGGCCACATACATGCTGGCGACCTTCGACATCCACAAAG----- 596
Db 123 ValLeuAlaTyrTyrThrValPheThrLeuArgAsnThrLysIleLysGlnSerGln 142
```

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QY 597 AGTGAGTCCAGTGAAGAGCGTGAAGCTGCTCACTTTCAGTTTCAGTGGCCGACCAT 656
Db 143 LysGlyArgProSerGlnArgValValThrGlnTyrHisIleTyrThrGlnThrProAspMet 162
QY 657 GGAGTTCCTGAGTACCAGCAACTCCATCCCTGCGCTTCTACAGAGGTCACAGGCTCAAC 716
Db 163 GlyValArgGlnTyrSerLeuProValLeuThrPheValArgLysAlaTyrAlaLys 182
QY 717 CCCCTGAGACGACGACCCATGCTGCTGACATGCTGACAGCGCGCGCTGGCCGACCGCTGC 776
Db 183 ArgHisAlaValAlcLysProValValAlaHisCysSerAlaGlyValGlnArgThrGln 202
QY 777 TTCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 836
Db 203 TyrIleValLeuAspSerMetLeuGlnGlnIleGlnHisGlnGlyThrValAsnIlePhe 222
QY 837 GGCCAGCTGACCTGCATGGCATCACAGAGAACTACATGAGCGAGAGCGACAGTAC 896
Db 223 GlyPheLeuLysHisIleArgSerGlnArgAsnTyrLeuValGlnThrGlnGlnGlnTyr 242
QY 897 GTGTCATCATGAGAGCGCTGCTGGAGCTGCCACGCTGGCCACACAGAGTGCCTGCC 956
Db 243 ValPheIleHisAspThrLeuValGlnAlaIleLeuSerGlnThrGlnValValLeu 262
QY 957 CGCAACCTGTATGCCACATCCAGAAAGCTGGCGCAAGTG 995
Db 263 AspSerMetLeuGlnGlnIleGlnHisGlnGlyThrVal 275

RESULT 15
US-09-788-626-4
; Sequence 4, Application US/09788626
; Patent No. US20020009762A1
; GENERAL INFORMATION:
; APPLICANT: Flint, Andrew J.
; APPLICANT: Cool, Deborah E.
; TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE
; FILE REFERENCE: 200125.401
; CURRENT APPLICATION NUMBER: US/09/788.626
; CURRENT FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-626-4

Alignment Scores:
Pred. No.: 2.41e-38 Length: 317
Score: 679.50 Matches: 138
Percent Similarity: 63.50% Conservative: 36
Best Local Similarity: 50.36% Mismatches: 91
Query Match: 10.34% Indels: 9
DB: 10 Gaps: 3

US-09-743-492-1 (1-3467) x US-09-788-626-4 (1-317)
QY 201 ACGTGGAGAAATTCAAACTGGAGGTGAACAGCCCAAGACCGGTATGCGATGTCATC 260
Db 3 ThrAlaAspSerSerAsnHisProAspAsnLysHisLysAsnArgTyrIleAsnIleVal 22
QY 261 GCCTAGCAACACTGTCGATGTCATCCTTACCTTATGATGAGGCTCCCGGCGG-----ACT 314
Db 23 AlaTyrAspHisSerArgValLysLeuAlaGlnLeuAlaGlnLysAspLysLeuThr 42
QY 315 GACTCATCAATAGCCAACTACTACATGAGTGCCTACCCAGACAAATGCCATCATCCGCACG 374
Db 43 AspTyrIleAsnAlaAsnTyrValAspArgTyrAsnArgProLysAlaTyrIleAla 62
QY 375 CAGGCCCCCTGCCGAGCATGGGCGCATTTCTGGAGAAAGTGGGGAACAGCGCACG 434
Db 63 GlnGlyProLeuLysSerThrAlaGlnAspPheArgMetIleArgPheIleAsnVal 82
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QY 435 GCCACTGTGGTCATGATGACAGCGGTGGAGAGAAGTCCCGGTAAATGTGATCACTAC 494
Db 83 GluValIleValMetIleThrAsnLeuValGlnLysGlyArgLysCysAspGlnTyr 102
QY 495 TGG---CCAGCCCGGTGACACCGAGACCTGTGCCCTTATTGACGTCACCCGTGGACACA 551
Db 103 TrpProProAlaAspGlnSerGlnGluTyrGlyAsnPheLeuValThrGlnLysSerVal 122
QY 552 GTGGACCTGGCCACATACACTGTGGCACCTTGCCACTCCACAAG----- 596
Db 123 GlnValLeuAlaTyrTyrThrValPheThrLeuArgAsnThrLysIleLysLysGlySer 142
QY 597 ---AGTGGCTCCAGTGAAGAAGCTGAGCTGCGACGTTTCAGTTCATGGCTGCCAGAC 653
Db 143 GlnLysGlyArgProSerGlyArgValValThrGlnTyrHisTyrThrGlnTrpProAsp 162
QY 654 CATGAGATTCTGTGATACCCAACTCCATCCCTGACCTTCTTACGACGAGGTCAAGGCTGC 713
Db 163 MetGlyValProGlnTyrSerLeuProValLeuThrPheValArgLysAlaAlaTyrAla 182
QY 714 AACCCCTAGACGACGAGGCCCATGTGTGCTGACGACGCGGGCGTGGGCCGACCGGC 773
Db 183 LysArgHisAlaValAlaGlyProValValValHisCysSerAlaGlyValGlyArgThrGly 202
QY 774 TGGTTCATGTGATGTGATGCCATGTGGAGCGGATGACACGACGAGAAGCGGTGGACATC 833
Db 203 ThrTyrIleValLeuAspSerMetLeuGlnGlnIleGlnHisGlnGlyThrValAsnIle 222
QY 834 TATGGCCACGTGACCTGCATGCGATGCATGACAGAGAACTACATGCTGCAGACGAGACCA 893
Db 223 PheGlyPheLeuLysHisIleArgSerGlnArgAsnTyrLeuValGlnThrGlnGluGln 242
QY 894 TACGTGTTCATGCATGAGCGGCTGTGAGAGGTCGCCACGTGCGGCCACACAGAGTGCTT 953
Db 243 TyrValPheIleHisAspThrLeuValGlnAlaIleLeuSerLysGlnThrGlnValVal 262
QY 954 GCCCGCAACCTGTATGCCACATCCAGAAAGCTGGGCCAAGTG 995
Db 263 LeuAspSerMetLeuGlnGlnIleGlnHisGlnGlyThrVal 276
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OM nucleic - protein search, using frame_plus_n2p model

Run on: January 17, 2003, 09:57:19 ; Search time 35.5 Seconds

(without alignments)
5747.001 Million cell updates/sec

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Delop 6.0 , Delext 7.0

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 525148

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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-MODE=LOCAL -OUTFMT=pic -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=6 -ICPU=3
-USER=US09743492 -ECGN_1_1_45 -runat.17012003.093837.11560 -MCP=6 -ICPU=3
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-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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4: /cgn2_6/prodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/prodata/1/1aa/6C.COMB.pep:*
6: /cgn2_6/prodata/1/1aa/6D.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	2880	44.7	1911	2	US-08-800-825A-5
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6	2850	44.2	1501	2	US-08-716-679-3
7	1553	24.1	289	1	US-08-036-210-13
8	1553	24.1	289	2	US-08-449-609-13
9	1552	24.1	793	1	US-08-015-985-3
10	1551	24.1	802	1	US-08-015-985-3
11	1423	22.1	699	1	US-08-348-006B-7
12	1423	22.1	699	2	US-08-800-825A-7

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17	1307	20.3	1452	2	US-08-991-258A-4	Sequence 4, Appl1
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20	1306	20.3	1452	2	US-08-449-644-8	Sequence 8, Appl1
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22	1295	20.1	245	2	US-08-685-992-26	Sequence 26, Appl1
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26	1243	19.3	1457	2	US-08-652-971-3	Sequence 3, Appl1
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ALIGNMENTS

RESULT 1
US-08-348-006B-5
Sequence 5, Application US/08348006B
Patent No. 5658756
GENERAL INFORMATION:
APPLICANT: RODAN, GIDEON A.
APPLICANT: SCHMIDT, AZRIEL
APPLICANT: RUTLEDGE, SU JANE
TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: J. MARK HAND
STREET: 126 E. LINCOLN AVE., P. O. BOX 2000
CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/348,006B
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/122,032
FILING DATE: 14-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: HAND, J., MARK
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 189921A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3905


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: TELEFAX: 908-594-4720
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1911 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
:
US-08-348-006B-5

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Alignment Scores:

Pred. No.:	5,03e+240	length:	1911
Score:	2880.00	Matches:	530
Percent Similarity:	94.32%	Conservative:	35
Best Local Similarity:	88.48%	Mismatches:	34
Query Match:	44.69%	Indels:	0
DB:	1	Gaps:	0

US-09-743-492-1 (1-3467) x US-08-348-006B-5 (1-1911)

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QY	150	GGCCCTCAAGTTCTCCAGAGATAGATGCCATGACCCGTGACAGCAGCTTCACTGAGAG	209
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QY	210	AATTCACAACCTGGAGGCTGAACACGCCAGAACCCGTATGCGATGTCAATGCCCTTACGC	269
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QY	270	CACCTGTGAGCATCCTTACTCTATGCGATGGGGTCCCGGAGATGACTACATCATATGCC	329
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QY	330	AACFACATCGATGGCTGACCCGACAGCAAAAGCTTACATGCGCACGAGGCGCCCGCCGCC	389
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QY	690	TTTCTTACGAGGGGTCAAGGCTCTCAACCCCTTGAGACGACGGCCCATGGTGGTGTGCATGC	749
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QY	990	CAAGTGCCTCCACAGGAGAGGTGACCGCATCGCATGAGCTGAGTCAAAAGTGTGGCCAGC	1049
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QY	1050	TCCAAAGCCCAACAGCTCCCGCTTCATCAGCGCCACACCTGCCCTGCACAAAGTTCAAGAC	11099
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QY	1410	ATGGCTGAGTCAACATGCCCCAGATATATCTGCTGATTCACAGTTCACAGATCCCGG	1469
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: Sequence 5, Application US/08800825A			
: Patent No. 5866397			
: GENERAL INFORMATION:			
: APPLICANT: RODAN, GIDEON A.			

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APPLICANT: SCHMIDT, AZRIEL
APPLICANT: RUTLEDGE, SU JANE
TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASE
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESSES:
ADDRESSEE: J. MARK HAND - MERCK & CO., INC.
STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,825A
FILING DATE: 14-FEB-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HAND, J. MARK
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 18992DA
TELEPHONE: 732-594-3905
TELEFAX: 732-594-4720
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1911 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-800-825A-5

Alignment Scores:
Pred. No.: 5,03e-240 Length: 1911
Score: 2880.00 Matches: 530
Percent Similarity: 94.32% Conservative: 35
Best Local Similarity: 88.48% Mismatches: 34
Query Match: 44.69% Indels: 0
DB: 2 Gaps: 0

US-09-743-492-1 (1-3467) x US-08-800-825A-5 (1-1911)
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QY 90 CACCCACCCATCCCATCACCGACCTGGCGGAGACATCGAGCGCTCAAGCCAAAGCAT 149
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DB 1353 SerLeuLYLeuSerGlnIuTyrgIuSerIleAspProGlyGlnInPheThrTrpGlu 1372
QY 210 AATTCGAACCTGTGAGTGAACAAGCCCAAGAACCCGTATGCGAATGCTCATGCGCTACGAC 269
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QY 390 GAGACCATGGGCGATTTCGAGAAATGTGTGGAGACAGCGCACCTGTGTCATG 449
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DB 1453 MetThrArgLeuGluGlnIuYsSerArgIleTyCysAspIeInTyraProAsnArgGly 1472
QY 510 ACCGAGACCTGTGCGCTTATTCAGGTGAGCCCTGTGGACACGACATGGAGCGGCCACATAC 569
DB 1473 ThrGluThrTyGllPheIleGlnValThrLeuAsnSPThrIleGluLeuAlaThrPhe 1492
QY 570 ACTGTGCGCACCTTTCGCACATCCACAAGAGTGGCTCCAGTAGAAGAGCGTAGTGCCTCAG 629
DB 1493 CysValaArgThrPheSerLeuHisTylSaSnGlySerSerGluYsArgValaArgGln 1512
QY 630 TTTCACTTCACTGCGCTGGCGCACACCATGAGATTCTGAGTACCACCAATCCCATCTGGCC 689
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DB 1593 TyraMetValaGlnThrGluSPGlnTyraSerPheIleHisGluIleuLeuGluAlaVal 1612
QY 930 ACGTGGCGCCACACAGAGTGGCTGCCACCGCATCTGATGCTCCACATCCAGAACTGGGC 989
DB 1613 GlyCysGlyAsnThrGluValaProAlaArgSerLeuTyraIleGlnIuSleuAla 1632
QY 990 CAAATGCTTCACAGGAGAGTGTGACCCCATGAGAGCTGCATGTTCAAGTTGCTGGCCAGC 1049
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QY 1050 TCCAAAGGCCACAGCGTCCGCTTCATCAGAGGCCAACCTGGCCGCAACAAAGTTCAGAAC 1109
DB 1653 SerLYsaIaHisThrSerArgPheIleSerAlaAsnLeuProCysIuSlysIuSPhelyAsn 1672
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DB 1673 ArgLeuValaSnIleMetProGlyrgIuSerThrArgValaCysLeuGlnProIleArgGly 1692
QY 1170 GTGGAGGCTCTGACTACATCAATGCCAGCTTCTGGATGGTTATAGACAGCAAGAGCC 1229
DB 1693 ValGluGlySerAspTyraIleAsnAlaSerPheIleAspIuTyraArgGlnGlnIuSaIa 1712
QY 1230 TACATGCTACACAGGCGCTCGGACAGAGAGACCGAGGAGGAGGAGGAGGAGGAGGAG 1289
DB 1713 TyraIleAlaThrGlnGluProLeuAlaGluThrThrGluSPThrPheArgMetLeuTrp 1732
QY 1290 GAGCACAATTCACATCATCTGATGCTGACCAAGCTTCCGGAGATGGGACAGAGAA 1349
DB 1733 GluAsnAsnSerThrIleValaValMetLeuThrLysLeuArgGluMetGlyArgGluIuYs 1752
QY 1350 TGGCACCAGTACTGGCGCAGAGAGCGCTGCTGCGCTACCAAGTATTTGTGTGGACCG 1409
DB 1753 CysHisGlnIuTyraProAlaGluArgSerAlaArgTyraGlnTyraPheValaIaSPPro 1772
QY 1410 ATGCGTGAAGTACAAATGCCCCAGTATATCTTCGCGAGTTCAAAGGACAGAGTGGCCCG 1469
DB 1773 MetAlaGluTyraSPMetProGlnTyraIleLeuArgGluPheYsValaIuAspAlaArg 1792
QY 1470 GATGGCAGTCAAGAGCAATCCGAGATTCCACTTACAGACACTGGCCAGAGCGGCGTG 1529
DB 1793 AspGlyGlnSerArgThrValaArgGlnPheGlnPheThrAspTrpProGluGlnIuYal 1812

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OY 1530 CCGAAGACGGGAGGATTCATTGATTCATCGCGCAGGTGCATTAAGACCAAGAGCAG 1589
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 Db 1833 PheGlyGlnAspGlyProIleSerValHisCysSerAlaGlyValGlyArgThrGlyVal 1852
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 Db 1853 PheIleThrIleSerIleValIleuGlnIleuArgTyrGlyGlyValValAspIlePhe 1872
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 Db 1873 GlnThrValLysMetIleuArgThrGlnArgProAlaMetValGlnThrGlnAspGlyTyr 1892
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 Db 1893 GlnPheCysTyrGlnAlaIleuGlnIleuGlySerPheAspHisTyrAlaThr 1911

RESULT 3

US-09-158-657-5
 : Sequence 5, Application US/09158657
 : Patent No. 6214564

GENERAL INFORMATION:

APPLICANT: RODAN, GIDEON A.
 APPLICANT: SCHMIDT, AZRIEL
 APPLICANT: RUTLEDGE, SU JANE
 TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
 NUMBER OF SEQUENCES: 7
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: J. MARK HAND - MERCK & CO., INC.
 STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
 CITY: RAHWAY
 STATE: NEW JERSEY
 COUNTRY: USA
 ZIP: 07065-0900

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/158,657
 FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/800,825
 FILING DATE: 14-FEB-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: HAND, J. MARK
 REGISTRATION NUMBER: 36,545
 REFERENCE/DOCKET NUMBER: 18992DA
 TELEPHONE: 732-594-3905
 TELEFAX: 732-594-4720
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1911 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-158-657-5

Alignment Scores:

Pred. No: 5.03e-240 Length: 1911
 Score: 2880.00 Matches: 530
 Percent Similarity: 94.32% Conservative: 35
 Best Local Similarity: 88.48% Mismatches: 34
 Query Match: 44.69% Indels: 0

DB:	4	Gaps:	0
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Db 1313 HisProIleAspProValGluMetArgTyrGlyLeuSerPheGlnThrProGlyMetLeuSer 1332			
OY 90 CACCCACCCATCCCATCAGCCAGCTGGCGGCAACATCGAGCGGCTCAACAGCAT 149			
Db 1333 HisProIleProIleProIleAlaAspMetAlaGlnHisThrGluArgLeuLysAlaAsp 1352			
OY 150 GCGCTCAAGTCTCCAGAGATATAGTTCATGCAACCTGAGACACAGTCTCAGTGGAG 209			
Db 1333 SerLeuLysLeuSerGlnGlyTyrGlnThrIleSerIleAspProGlyGlnGlnPheThrProGlu 1372			
OY 210 AATTCAACCTGAGGTATACACAGCCCAAGAACCTGTATGCAATGTATGCTCCTACGAC 269			
Db 1373 HisSerAsnLeuGlnValAsnLysProLysAsnAlaGlyTyrAlaAsnValIleAlaTyrAsp 1392			
OY 270 CACTCTGAGTCATCTTATCTATGATGCGGTCCCGGAGTACTACATCAATGCC 329			
Db 1393 HisSerArgValIleIleuGlnProIleGlnGlyIleMetGlySerAspTyrIleAsnAla 1412			
OY 330 AACTACATCGATGCTACCCGACAGCAAGATGCTTACATGCGCAGCGGCGGCTGCC 389			
Db 1413 AsnTyrValAspGlyTyrArgArgGlnAsnAlaTyrIleAlaThrGlnGlyProLeuPro 1432			
OY 390 GAGACATGGGGATTTCTGGAGATGGTGGGAACGCGGCGGCGGCGGCGGCGGCGGCGG 449			
Db 1433 GlnThrPheGlyAspPheThrArgMetValTyrGlnGlnArgSerAlaThrIleValMet 1452			
OY 450 ATGACACGGCTGGAGAGAAAGTCCCGGTTAAATGTATGATGCTGCGCAACCGCTGGC 509			
Db 1453 MetThrArgLeuGlnGlyLysSerArgIleLysCysAspGlnTyrTrpProAsnArgGly 1472			
OY 510 ACCGAGACCTGTGCTTATTCAGGTGACCTGTGGACACAGTGGAGCTGGCCATAC 569			
Db 1473 ThrGlnThrTyrGlyPheIleGlnValThrLeuAspThrIleGlnLeuAlaThrPhe 1492			
OY 570 ACTGTGCGACCTTGCGCTCCACAGAGTGGCTGCATGAGAACGCGAGCGTGGCTAG 629			
Db 1493 CysValArgThrPheSerLeuHisLysAsnGlySerSerGlnLysArgGlnValArgGln 1512			
OY 630 TTTCACTTCATGCTGCTGCGCAGACCATGAGTCTTCTGAGTACCCCACTCCCTGCC 689			
Db 1513 PheGlnPheThrAlaThrProAspHisGlyValProGluTyrProThrProPheLeuAla 1532			
OY 690 TTCTACGACGGGTGAAGGCTGCAACCCCTAGACGACGAGGCGCATGTGTGACTGCC 749			
Db 1533 PheLeuArgArgValLysThrCysAsnProProAspAlaGlyProIleValValHisCys 1552			
OY 750 AGCGGCGGCTGGCGGCGGCGGCGGCTTCAATCGATGATGCGCATGTTGAGCGGATG 809			
Db 1553 SerAlaGlyValGlyArgThrGlyCysPheIleValIleAspAlaMetLeuGlnArgIle 1572			
OY 810 AAGCAGCAAGAGACGCTGATGATGATGAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 869			
Db 1573 LysProGluLysThrValAspValTyrGlnHisValThrLeuMetArgSerGlnArgAsn 1592			
OY 870 TACATGTGTCAGACGAGGAGGACAGTACGTGTCATGCAATGAGCGGCTGAGGCTGCC 929			
Db 1593 TyrMetValGlnThrGlnAspGlnTyrSerPheIleHisGlnAlaLeuGlnVal 1612			
OY 930 ACGTGGCGGCGCACACAGAGTGGCTGCGGCAACCTGTATGCGCAATGCGACAGAGTGGCG 989			
Db 1613 GlyCysGlyAsnThrGlnValProAlaArgSerLeuTyrAlaTyrIleGlnLysLeuAla 1632			
OY 990 CAAGTGCCTCAGGAGGAGATGTGACCCGATGAGTGTGATGATGCTGCTGCGCAGC 1049			
Db 1633 GlnValGlnProGlyGlnHisValThrGlnMetGlnLeuGlnPheLysArgLeuAlaAsn 1652			
OY 1050 TCCAAAGGCCCAACGCTCCCGCTTCTATCAGCGCAACCTGCGCTGCAACAAGTTCAAGAAC 1109			

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Db      1653 SerLysAlaHisThrSerArgPheIleSerAlaAsnLeuProCysLysPheLysAsn 1672
      1110 CGGCTGGTGAACATCATGCCCTACGAATTGACCCGCTGTCTGTCCAGCCCATCCGTGT 1169
      1673 ArgLeuValAsnIleMetProTyrGluSerThrArgValCysLeuGlnProIleArgGly 1692
      1170 GTGGAGGGCTCTACTATCATCAATGCCAGCTTCTGTGATGTATTAGACAGCAGAGGCC 1229
      1693 ValGlnGlySerAspTyrIleAsnAlaSerPheIleAspIlyTyrArgGlnGlnLysAla 1712
      1230 TATATAGCTACACAGGGGCTGTGGCAGAGACAGCAGGAGCTTGGGCGCATGCTATGG 1289
      1713 TyrIleAlaThrGlnGlyProLeuAlaGluThrThrGlnAspPheThrPargMetLeuTyr 1732
      1290 GAGCACAATTCCACATCATCTGCTATGCTGACCAAGCTTCGGGAGATGGGAGAGAGAAA 1349
      1733 GluAsnAsnSerThrIleValValMetLeuThrLysLeuArgGluMetGlyArgGlnLys 1752
      1350 TGGCCACGACTACTGGCCAGCAGAGCCGCTGTCTGCTACCAAGTCTTGTGTGACCCG 1409
      1753 CysHisGlnTyrTrpProAlaGluArgSerAlaArgTyrGlnTyrPheValAlaAspPro 1772
      1410 ATGGCTGAGTACACATGCCCGCATATCTGCGTGAAGTTCAGAGGTCCAGGATGCCCGG 1469
      1773 MetAlaGlnTyrAsnMetProGlnTyrIleLeuArgGlnPheLysValThrAspAlaArg 1792
      1470 GATGGCAGTCAAGACAATCCGCGAGTTCAGATTCACAGATGCGCAGAGAGGCGGTG 1529
      1793 AspGlyGlnSerArgThrValArgGlnPheGlnPheThrAspTrpProGlnGlnGlyVal 1812
      1530 CCCAACAAGGCGAGGATTCATTGACTTTCATGGCGCAGCTGCATTAAGCAAGAGCAG 1589
      1813 ProLysSerGlyGlnLysPheIleAspPheIleGlyAlaHisLysThrLysGlnGln 1832
      1590 TTGGACAGAGTGGCTATACAGGTCAGTGCATGAGTGCCTGGGCGCCAGCCGCGGTG 1649
      1833 PheGlnGlnAspIleProIleSerValHisCysSerAlaGlyAlaGlyArgThrGlyVal 1852
      1650 TTCATCACTGTGAGCATGCTGCTGAGAGCGCATGCGGTATGAGGGCGGTGTGCATGTTT 1709
      1853 PheIleThrLeuSerIleValIleuGluArgMetArgTyrClnGlyValValAlaPhe 1872
      1710 CAGACCGTGAAGACCTGCTTACACAGCTCTCTGCCATGTGTGACAGACAGGACAGTAT 1769
      1873 GlnThrValLysMetLeuArgThrGlnArgProAlaMetValGlnThrGlnAspGlnTyr 1892
      1770 CAGCTGTGCTACGCTGGCGCCGCGAGTACCTGGGCGAGCTTGACCATATGCAAGC 1826
      1893 GlnPheCysTyrGlnAlaAlaLeuGlnTyrLeuGlySerPheAspHisTyrAlaThr 1911

RESULT 4
PCT-US94-10166-5
: Sequence 5, Application PC/TUS9410166
: GENERAL INFORMATION:
: APPLICANT: RODAN, GIDEON A
: APPLICANT: SCHMIDT, AZRIEL
: APPLICANT: RUTLEDGE, SU JANE
: TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
: TITLE OF INVENTION: TYROSINE PHOSPHATASE
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: JOHN W. WALLEN III
: STREET: P.O. BOX 2000, 126 E. LINCOLN AVE.
: CITY: RAHWAY
: STATE: NJ
: COUNTRY: USA
: ZIP: 07065
: COMPUTER READABLE FORM:
: MEDIUM TYPE: FLOPPY disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25

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: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US94/10166
: FILING DATE: 09-SEPT-1994
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/122,032
: FILING DATE: 14-SEP-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: WALLEN, JOHN W III
: REGISTRATION NUMBER: 35403
: REFERENCE/DOCKET NUMBER: 18992
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 908-594-3905
: TELEFAX: 908-594-4720
: TELEX: 138825
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1911 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: PCT-US94-10166-5

Alignment Scores:
Pred. No.: 5.03e-240 Length: 1911
Score: 2880.00 Matches: 530
Percent Similarity: 94.32% Conservative: 35
Best Local Similarity: 88.48% Mismatches: 34
Query Match: 44.69% Indels: 0
DB: 5 Gaps: 0

US-09-743-492-1 (1-3467) x PCT-US94-10166-5 (1-1911)
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: 90 CACCCACCATCCCATCACCGACCTGGCGAGCAACAATCGAGGCGCTCAAGCCACAGAT 149
: 1333 HisProIleProIleAlaAspMetAlaGlnHisThrGlnArgLeuLysAlaAsnAsp 1352
: 150 GGCCTCAAGTTCCTCCAGAGATGATGATCCATGACCTGAGACAGCTTACGTGGAG 209
: 1353 SerLeuLysLeuSerGlnGlyArgGlnSerIleAspProGlnGlnPheThrProGln 1372
: 210 AATTCAACCTGGAGGAGCAAGCCCAAGACCGGTATGCAATGATCGCTAGAC 269
: 1373 HisSerAsnLeuGlnValAsnLysProLysAsnArgTyrAlaAsnValIleAlaTyrAsp 1392
: 270 CACTCTGAGTCACTTACTTATCGATGCGGTCCCGGAGTGAATCATCAATGCC 329
: 1393 HisSerArgValIleLeuGlnProIleGlnGlyIleMetGlySerAspTyrIleAsnAla 1412
: 330 AACTACTCATGCTGCTACCCAGCAAGATGCTCATCATGCGCAGCGAGGCCCTGCCC 389
: 1413 AsnTyrValAspGlyTyrArgArgGlnAsnAlaTyrIleAlaThrGlnGlyProLeuPro 1432
: 390 GAGACCATGGCGATTTCTGAGAAATGCTGGAGACGCGCAGCGCATGCTGTCATG 449
: 1433 GlnThrPheGlnAspPheThrPargMetValTrpGlnGlnArgSerAlaThrIleValMet 1452
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: 510 ACCGAGACCTGTGGCTTATTCAGGTGACCTGTGGACACAGTGGAGCTGGCCACATAC 569
: 1473 ThrGlnThrTyrGlnPheIleGlnValThrLeuLeuAspThrIleGlnLeuAlaThrPhe 1492
: 570 ACTGTGGCAGCTTGGCACTCCACAGAGTGGCGCTGAGTGAAGAGCTGAGCGTGGCAG 629
: 1493 CysValArgThrPheSerLeuHisLysAsnGlySerSerLysArgGlnValArgGln 1512

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 Db 963 HisSerAsnLeuIleAlaAsnLysProLysAsnArgTyrIleAsnValIleAlaTyrAsp 982
 QY 270 CACTCTGAGTACATCCCTTACTCATGAGGCGCCCGGAGTGACTACATCAATGCC 329
 Db 983 HisSerArgValIleLeuGlnProLeuGlnGlyIleMetIleSerAspTyrIleAsnAla 1002
 QY 330 AACTACATGATGGCTACCGCAAGACAGAAATGCTACATGCGCCACGAGGCCCTGCGCC 389
 Db 1003 AsnTyrValAspGlyTyrArgArgGlnAsnAlaTyrIleAlaThrGlnGlnProLeuPro 1022
 QY 390 GAGACATGGCGCATTTCTGAGAAATGGTGGAAACAGGCCGCGCATGTGGTATG 449
 Db 1023 GlnThrPheGlyAspPheTrpArgMetValTrpGlnGlnArgSerAlaThrValMet 1042
 QY 450 ATGACACGGCTGGAGAGAAATCCCGGTAATGTGATCATGACTGACGCGCCGTCGCG 509
 Db 1043 MetThrArgLeuGlnGluLysSerArgValLysCysAspGlnTyrTrpProAsnArgGly 1062
 QY 510 ACCGAGACCTGTGGCTTATTCAGGTGACCCCTGTGGACACAGTGGAGCTGCCCATAC 569
 Db 1063 ThrGlnThrTyrGlnPheIleGlnValThrLeuLeuAspThrMetGlnLeuAlaThrPhe 1082
 QY 570 ACGTGGCGGCACTTCGCACTCCACAGAGAGTGGCTCCAGTGAGAAAGCTGAGCTGCG 629
 Db 1083 CysValArgThrPheSerLeuHisLysAsnGlySerSerIleLysArgGlnValAlaGlnHis 1102
 QY 630 TTTCAGTTCATGCGCTGGCCGACAGCATGAGATTCCTGATGACCAATCCCATCTGGCC 689
 Db 1103 PheGlnPheThrAlaTrpProAsnHisGlyValProGlnTyrProThrProPheLeuAla 1122
 QY 690 TTCTCAAGACGGGTCAAGGCTCAACCCCTCAAGACGAGGCCCATGTTGGTGCACCTGC 749
 Db 1123 PheLeuArgArgValLysThrCysAsnProProAsnAlaGlyProValIleHisCys 1142
 QY 750 AGCGCGGCGCTGGCCGACACCGGCTGTTATGATGATTCATGCGATGGAGCGCATG 809
 Db 1143 SerIleGlyValIleTyrGlnThrGlyCysPheIleValIleAspAlaMetLeuGlnArgIle 1162
 QY 810 AACGACGAGAGAGCGGTGATCATGTGACGCTGACCTGCATGGCATGACAGAGAAC 869
 Db 1163 ArgThrGlnLysThrValAspValTyrGlyHisValThrLeuMetArgSerGlnAlaGln 1182
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 QY 990 CAAGTGCCTCCAGGGGAGATGTGACCGGCGAGCTGAGTTCAGTTCAGTGGCGGCGAC 1049
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 QY 1050 TCCAGAGCCACACGTCGCGCTTCATCAGCGCCACCTGCTGCACAAAGTTCAGAAC 1109
 Db 1243 SerTyrAlaHisThrSerArgPheIleThrAlaSerLeuProCysAsnLysPheLysAsn 1262
 QY 1110 CGGCTGGTGAACATCATGCCCTTACGAATTCACCGGTGTGTGTGCAGCCCATCGTGT 1169
 Db 1263 ArgLeuValAsnIleLeuProTyrGlnSerSerArgValCysLeuGlnProIleArgGly 1282
 QY 1170 GTGGAGGCGCTGCTACATACATGCACGCTTCGTGATGATGAGAGCGAGAGGCC 1229
 Db 1283 ValGlnGlySerAspTyrIleAsnAlaSerPheIleAspGlyTyrArgGlnGlnAla 1302
 QY 1230 TACATAGCTACAGAGGCGCTGTGGCAGAGAGACCGAGACTTGTGGCGCATGTATGG 1289
 Db 1303 TyrIleAlaThrGlnGlnProLeuAlaGlnThrThrGlnLysPheTrpArgAlaLeuTrp 1322

QY 1290 GAGCACAATTCCACCATCATGTCATGTCAGCAAGCTTCGGGAGATGGCGAGGAGAAA 1349
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 QY 1350 TGCCACGACTACTGGCCAGAGAGCGCTGCTGCTGCATACAGATCTTGTGTGTGACCG 1409
 Db 1343 CysHisGlnTyrTrpProIleGlnArgSerAlaArgTyrGlnTyrPheValValAspPro 1362
 QY 1410 ATGGCTAGTACAAATGCCCCAGTATATCTGCGTGAAGTTCAGAGTTCACGAGATGCCCG 1469
 Db 1363 MetAlaGlnTyrAsnMetProGlnTyrIleLeuArgGlnPheLysValThrAspAlaArg 1382
 QY 1470 GATGGGAGGTCAGCAAGAAATCCCGGACTTCAGTTCACAGCTGCGCAGACGAGCGTG 1529
 Db 1383 AspGlyIleSerArgThrValArgGlnPheGlnThrAspTyrProGlnGlnGlyAla 1402
 QY 1530 CCCAAGACAGGCGGAGATTCATTCATTCATGATGCGGAGGTGATAGACCAAGAGACAG 1589
 Db 1403 ProLysSerGlnGlnGlyPheIleAspPheIleGlyIleValHisLysThrLysGlnGln 1422
 QY 1590 TTTCGACAGATGGCGCTATTCAGCGTGCACCTGACGTGCGCGTGGCCGCGAGGCTG 1649
 Db 1423 PheGlyIleAspGlyProIleSerValHisCysSerAlaGlyValGlyArgThrGlyVal 1442
 QY 1650 TTTCATCCTGACATGCGCTTCGAGCGCATGGCGCATAGAGGCGGTGCGACATGTT 1709
 Db 1443 PheIleThrLeuSerIleValIleGlnArgMetArgTyrGlnGlyValIleAspIlePhe 1462
 QY 1710 CAGACCGTGAAGACCTGCTCATACAGCGTGCCTGCATGGTGCAGACAGAGACAGTAT 1769
 Db 1463 GlnThrValLysValLeuArgThrGlnArgProAlaMetValGlnThrGlnAspGlnTyr 1482
 QY 1770 CAAGTGTCTACCGTGGCGGCTGGAGTACCTCGGCACTTTCAGCACTATGCAACG 1826
 Db 1483 GlnPheCysPheGlnAlaIleAlaLeuGlnTyrLeuGlnCysPheAsnIleTyrAlaThr 1501

RESULT 6
 US-08-716-679-3
 ; Sequence 3, Application US/08716679
 ; Patent No. 5846800
 ; GENERAL INFORMATION:
 ; APPLICANT: Schlessler, Joseph
 ; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PROTEIN
 ; TITLE OF INVENTION: PHOSPHOTYROSINE PHOSPHATASE-SIGMA
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/716,679
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/130,570
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mistrock, S. Leslie
 ; REGISTRATION NUMBER: 18,872
 ; REFERENCE/DOCKET NUMBER: 7683-043
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-790-9090
 ; TELEFAX: 212-869-8864/9741

TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1501 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-716-679-3

Alignment Scores:
 Pred. No.: 1,73e-237 Length: 1501
 Score: 2850.00 Matches: 523
 Percent Similarity: 93.99% Conservative: 40
 Best Local Similarity: 87.31% Mismatches: 36
 Query Match: 44.23% Indels: 0
 Gaps: 2
 DB: 0

US-09-743-492-1 (1-3467) x US-08-716-679-3 (1-1501)

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 Db 923 HSPProProlleProIleThrAspMetAlaGluHisMetGluArgLeuLysAlaAsnAsp 942
 QY 150 GGCCTCAAGTTCTCCAGAGATGATGATCATGACCCCTGAGCAGAGATTCACGTTGAGGAG 209
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 QY 210 AATTCAAACTGGAGGTGAACAAGCCCAAGAACCGCTATGCGAATGCTATGCGCTACGAC 269
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 QY 270 CACTCTGAGTATGCTTACCTCTATGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 329
 Db 983 HSPSerAlaGluAlaIleLeuGluInProLeuGluGlyIleMetGlySerAspTyrIleAsnAla 1002
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 Db 1003 AsnTyrValAspGlyTyrArgArgGlnAsnAlaTyrIleAlaThrGlnGlnIleProLeuPro 1022
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 Db 1023 GluThrPheGlyAspPheThrArgMetValTyrGluGlnArgSerAlaThrValIleMet 1042
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 Db 1043 MetThrArgLeuGluGluIleuSerArgValLysCysAspGlnTyrTrpProAsnArgGly 1062
 QY 510 ACCGAGACCTGTGCTTATTCAGGTGACCTGTTGACACAGTGGAGAGTGGCCACATAC 569
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 QY 570 ACTGTGGCAGCTTGGCAGCTCCACAAGAGTGGCTCCAGTGAAGAGCGTGAAGTGGCTGAC 629
 Db 1083 CysValArgThrPheSerLeuHisLysAsnGlySerSerGlnLysArgGluValAlaArgHis 1102
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 Db 1123 PheLeuAlaArgValLysThrCysAsnProProAsnAlaGlyProValValAlaHisCys 1142
 QY 750 AGCGGCGCGTGGCGCGACCGGCTTCATGCTGATGATGATGATGATGATGATGATGATGATGATG 809
 Db 1143 SerAlaGlyValGlyArgThrGlyCysPheIleValIleAspAlaMetLeuGluIleArgIle 1162
 QY 810 AAGCAGGAGAGAGCGGTGACATCTATGCGCCAGTGAAGTGGATGATGATGATGATGATGATGATGAT 869

Db 1163 ArgThrGluLysThrValAspValTyrGlyHisValThrLeuMetArgSerGlnArgAsn 1182
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 Db 1203 GlyCysGlyAsnThrGluValProAlaArgSerLeuTyrThrTyrIleGlnLysLeuAla 1222
 QY 990 CAAGTCCCTCCAGGAGGAGTGGACCGGACCTGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 1049
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 QY 1050 TCCAAAGCCCAACAGCTCCCGCTTCATCAGCGCCACACCTGCCCTGCAACAAGTTCAGAAAC 1109
 Db 1243 SerLysAlaHisThrSerArgPheIleThrAlaSerLeuProCysAsnLysPheLysAsn 1262
 QY 1110 CGGCTGGTACATCATGCTGCTACGAATTCAGAACCCGTTGCTGTGACGCCATCGTGT 1169
 Db 1263 ArgLeuValAsnIleLeuProTyrGluSerSerArgValCysLeuGlnProIleArgGly 1282
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 Db 1283 ValGluGlySerAspTyrIleAsnAlaSerPheIleAspGlyTyrArgGlnGlnLysAla 1302
 QY 1230 TACATGCTACACAGAGGCTGCTGCGAGAGACACCGAGAGCTTGTGCGCATGTATG 1289
 Db 1303 TyrIleAlaThrGlnGlnIleProLeuAlaGluThrThrGluAspPheThrArgAlaLeuTrp 1322
 QY 1290 GAGCACAATTCACATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1349
 Db 1323 GluAsnAsnSerThrIleValAlaMetLeuThrLysLeuArgGluMetGlyArgGluLys 1342
 QY 1350 TGGCAGCAGTACCTGCGCAGCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1409
 Db 1343 CysHisGlnTyrTrpProAlaGluIleuArgSerAlaArgTyrGlnTyrPheValAlaAspPro 1362
 QY 1410 ATGCTGATGATACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1469
 Db 1363 MetAlaGluTyrAsnMetProGlnTyrIleLeuArgGluPheLysValThrAspAlaArg 1382
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 QY 1710 CAGACCGTGAAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1769
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 QY 1770 CAGCTGTGCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1826
 Db 1483 GlnPheCysPheGlnAlaIleAlaLeuGluIleuGlySerPheAspHisTyrAlaThr 1501

RESULT 7
 US-08-036-210-13
 ; Sequence 13, Application US/08036210
 ; Patent No. 558523
 ; GENERAL INFORMATION:
 ; APPLICANT: Moller, Niels P.H.
 ; APPLICANT: Moller, Karin B.


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OY 321 ATCAATGCCAATACATCGATGCTACCGCAGACAGATGCTATCGCCAGCAGGCG 380
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 287 ILeasnlaserpelleasnglyTYrglnclulysasnlyspheilleaialagngly 306
OY 381 CCCCTGCCGAGACCATGGGCGATTTCTGAGAAATGCTGGGAGACGCGCGCCACT 440
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 307 ProLYsglnclulthrvalasnaspheletrpargmellertprgluglnasntrhlaThr 326
OY 441 GTGGTATATGACACGGCTGGAGAGAAAGTCCCGGGTAAATGTGATCGTACTGGCCA 500
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 327 ILeValmetvalthrnsnleulysgluArglysglucysysalaglnTYrtrpPro 346
OY 501 GCCCTGGCGCAGACCGCTGCTTATGAGTGCACCTGTTGGACACAGTGGAGCGTG 560
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 347 AspGlnGlycystrrphrlyrglyasnvalArgvalserValgluAspvalThrvalLeu 366
OY 561 GCCACATATACCTGGCGACCTTGCGACTGCACAGAGTGGCTCCAGTGAAGCGTGAG 620
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 367 ValAspTYrThrValArglyspheSerIleGlnGlnValgluAspvalThrAsnArgly 386
OY 621 -----CTGGCTGAGTTTCAGTTTCATGGCCCTGGCGACACCATGGATTCCTGAG 668
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 387 ProGlnArgleuIleThrGlnPheHisPheThrSertrpAsprrpHeGlyValProPhe 406
OY 669 TACCAACTCCCATCCCTGGCTTCTACGACGGGTCAAGGCTGCAACCCCTAGACGCA 728
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 407 ThrProIleGlymetleuysPheleuysLysValIlysalacysnProGlnTYrAla 426
OY 729 GGGCCCATGGTGGTGCATGTCAGCGCGGGCGGTGGCCGACCGGCTGCTCATCGTAT 788
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 427 GLYAlaIleValIValHisCysSerIlaGlyValGlyrhrGlyThrPheValIle 446
OY 789 GATGCGATGTTGAGCGGATGAAGCAGAGAAACGCTGACATCTATGCCACGTGACC 848
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 447 AspAlaMetleuAspmetleHisSerGluArglyValAspValTYrGlyPheValSer 466
OY 849 TGCATCGCATACAGAGAACTACATGTTGTCACAGGAGACAGATACGTTTCATCTCAT 908
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 467 ArgIleArgIlaGlnArgCysGlnMetValGlnThrAspMetGlnTYrAlaPheIleTYr 486
OY 909 GAGCGCTGCTGGAGCTGCGCACGCTGCGCACACAGAGCTGCTGCCCAACTGTAT 968
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 487 GlnAlaLeuendIunHsTYrleuTYrGlyAspThrGlnleuendIunAlThrSerleuGlu 506
OY 969 GCCCATATCCAGAGCTGGCGCAAGTGCCTCCAGGGAGAGTGTGACCCCATGAGAGCTC 1028
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 507 ThrHisleuGlnIlystIeTYrAsnLysIleProGlyThrSerAsnAsnGlyleuGln 526
OY 1029 GAGTTCAAGTTCCTGGCGCAGCTCCAGGGCCACAGCGTCCGCTTCATCAGCGCAACCTG 1088
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 527 GluPheLysLysleuThrSerIleLysIleGlnAsnAspLysMetLarghrGlnAsnleu 546
OY 1089 CCCTGACAGATTCAAGAAACGCGCTGGTGACATGATGCCCTACGAATTGACCCGTG 1148
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 547 ProAlaAsnMetLysLysAsnArgValleuGlnIleIleProTYrGluPheAsnArgVal 566
OY 1149 TGCTTCGACCCCATCGCTGCTGGAGGGCTCTGACTACTCACTCAATGCCAGCTTCGGAT 1208
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 567 IleIleProValLysArgGlygluGlnAsnThrAspTYrValAsnAlaSerPheIleAsp 586
OY 1209 GGTATAGACAGACAGAAAGCTACATAGCTACACAGGGCGCTGCGCAGACAGACCGAG 1268
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 587 GlyTYrArgGlnLysAspSerTYrIleAlaSerGlnGlyProleuendIunHsIleGlu 606
OY 1269 GACTTCTGGCGCATGCTAGAGGACACAAATCCACCATCTGCTCATGCTGACCAAGCTT 1328
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 607 AspPheTrpArgMetIletrpGluTYrLysSerCysSerIleValMetleuThrGlnleu 626
OY 1329 CCGGAGATGGCGAGGAGAAATCCACCATGCTACTGGCGCAGACGCGCTGCTCGCTAC 1388
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 627 GluGlnArgGlyGlnGlnLysCysAlaGlnTYrtrpProSerAspGlyleuValSerTYr 646
OY 1389 CACTACTTGTGTGACCGCATGGCTGAGTACACATGCCCAAGTATATCTCGCGTGA 1448

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Db 647 GlyAspIleThrValGlnleuLysLysGlnGlnLucysGlnSerTYrThrValArgAsp 666
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 1449 TTCAGGCTACAGATGCCCGGAGATGGGAGTCAAGACAAATCCGCGACTTCACATTCACA 1508
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 667 LeuValMetLysAsnThrArgGlnAsnLysSerArgGlnIleArgGlnPheHisPheHis 686
OY 1509 GACTGGCAGACAGAGCGCGTGGCCCAAGACAGCGGAGGATTCATGCTACTCATCGGCGAC 1568
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 687 GlyTrpProGlnValGlyIleProSerAspGlyLysGlnMetIleAsnIleAlaAla 706
OY 1569 GTCCATATACAGACAGACAGATGAGGCTTTCAGACAGGCGCTTTCAGGCGCTGAGTGC 1628
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 707 ValGlnLysGlnGlnGlnGlnGlnSerGly---AsnHisProIleThrValHisCysSerAla 725
OY 1629 GCGCTGGCGCAGACCGCGGTCTTCATCTGATCTGACATCTGCTGAGCGCATCCGCTAT 1688
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 726 GLYAlaGlyrhrGlyThrPheCysAlaLeuSerThrValleuGlnArgValIlyAla 745
OY 1689 GAGGCGCTGGTGCATGTTTCAGACCGTGAAGACCTGGCTGACAGCGCTCTGCCATG 1748
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 746 GluGlyIleLeuAspValPheGlnThrValLysSerleuArgleuGlnArgProHisMet 765
OY 1749 GTCCAGACAGAGACAGATATGACTGTGCTTACCGTGCAGCGCGCTGAGTACTCGGCGAC 1808
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 766 ValGlnThrleuGlnGlnTYrGlnPheCysTYrLysValValGlnGlnIlyrIleAspAla 785
OY 1809 TTTGACCATATGCA 1823
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 786 PheSerAspTYrAla 790

RESULT 10
US-08-015-985-1
: Sequence 1, Application us/08015985
: Patent No. 5538886
: GENERAL INFORMATION:
: APPLICANT: Schlessler, Joseph
: TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: PENNIE & EDMONDS
: STREET: 1155 AVENUE OF THE AMERICAS
: CITY: NEW YORK
: STATE: NEW YORK
: COUNTRY: U. S. A.
: ZIP: 10036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/015,985
: FILING DATE: 10-FEB-1993
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Coruzzi, Laura A.
: REGISTRATION NUMBER: 30,742
: REFERENCE/DOCKET NUMBER: 7683-020
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 790-9090
: TELEFAX: (212) 869-9741/8864
: TELEX: 66141 PENNIE
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 802 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-015-985-1

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Alignment Scores:
 Pred. No.: 2.03e-125 Length: 802
 Score: 1551.00 Matches: 298
 Percent Similarity: 67.35% Conservative: 96
 Best Local Similarity: 50.94% Mismatches: 185
 Query Match: 24.07% Indels: 6
 DB: 1 Gaps: 3

US-09-743-492-1 (1-3467) x US-08-015-985-1 (1-802)

QY 84 CGAGACCAACCCATCCATCCACGACCTGGGGGACACATGAGCGCTCAAGCC 143
 Db 216 ArglystyrProleuProvalAsplylsleuGlugluLileasnaArgyMeta 235
 QY 144 AACGATGGCCTCAAGTCTCCAGAGATAGTCCATCGACCTGGACAG--CAGTTC 200
 Db 236 AsparaAnlylsleuPhearglulubPheasnaLaleuProalacysProileglna 255
 QY 201 ACGTGGAGATTCAAACCTGGAGGTGAACAGCCCAAGAACCGCTATGCAATGTCATC 260
 Db 256 ThrCysGlnAlaLaserLysglulubAsnlylsGlnlylsAsnArgTyValAsnLileu 275
 QY 261 GCCTACGACCACTCGACGTCTCTTACCTATCGATGGGCTCCCGGAGTACTAC 320
 Db 276 ProTyraSPHsSerArgValHisleuThrProValGluGlyValPheAspSerAspTy 295
 QY 321 ATCAATGCCAATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 380
 Db 296 IleasnaLaserPheLileasnaLysglulubAsnlylsPheLilealaleglnly 315
 QY 381 CCCCTGCCCCAGACCATGGGCGATTTCTGGAGAAATGCTGGGAAACAGCGCGCCACT 440
 Db 316 ProLysglulubThrValAsnAspPheTrpArgMetLileTrpGluLileasnaThrLale 335
 QY 441 GTGGCAGATGACACGCGCTGGAGAGAAAGTCCCGGTAATGATGATGATGATGATGATGAT 500
 Db 336 IleValMetValThrAsnleuLysglulubArgLysGlnLysCysAlaGlnLileTrpPro 355
 QY 501 GCCCTGGACACGACCTGGGCTTATTCAGTACGACCTGGTGGACACAGTGGAGCTG 560
 Db 356 AspglnlyCysTrpThrTyrlCylasnlleatargValSerValGlnAspValThrLaleu 375
 QY 551 GCCACATCACTGTGACCTGCGACTCCACAAGAGTGGCTCCAGTGAAGGCTGAG 620
 Db 376 ValAspTyrlThrValArgLysPheCysLileglnGlnValGlyAspMetThrAsnArgLys 395
 QY 621 -----CTGGCGTCACTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 668
 Db 396 ProGlnArgLileuLileThrGlnPheHisPheThrSerTrpProAspPheGlyValProPhe 415
 QY 669 TACCCAACTCCCACTGGCTTCTACAGAGGATGACAGGCTTGAACCCCTAGACGA 728
 Db 416 ThrProileglnMetLileuLysPheLileuLysValLysAlaCysAsnProleInlyrha 435
 QY 729 GAGGCCATGTTGCTGCTGACGAGCGGCGCTGGCGCCGACCGCTGCTTCATGCTGAT 788
 Db 436 GlnAlaLileuValAlaHisCysSerAlaGlyValGlyArgThrGlnThrPheValAlile 455
 QY 789 GATGGCATGTTGGAGCGATGAAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 848
 Db 456 AsparaMetLileuAspMetMetHisThrLileuArgLysValAlaValLileuLysPheValSer 475
 QY 849 TGCATGCATCAACAGAGAACTACTATGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 908
 Db 476 ArgLileuArgLileuArgLileuArgLileuArgLileuArgLileuArgLileuArgLileu 495
 QY 909 GAGCGCTGCTGGAGGCTGACGAGCGGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 968
 Db 496 GlnAlaLileuLysGlnLileuLysLysLysLysLysLysLysLysLysLysLysLysLys 515
 QY 969 GCCACATCAACAG 1028
 Db 516 ThrHisLileuGlnLysLileuLysLysLysLysLysLysLysLysLysLysLysLysLys 535

QY 1029 GAGTTCAGTCTGCTGCGACCTCCAGAGCCACAGCTCCCGCTTCATGACGCCACCTG 1088
 Db 536 GluPheLysLysLileuThrSerLileLysLileGlnAsnaAspLysMetArgThrGlnLysLileu 555
 QY 1089 CCCTGCACAACTTCAAGACAGCGGCTGGTGAACATCATGCTCCATGACATGACCGCTG 1148
 Db 556 ProAlaAsnMetLysLysAsnArgValLileGlnLileLileProTyrlCylubPheAsnArgVal 575
 QY 1149 TGTCTGCACCCATCGCTGGGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1208
 Db 576 LileLileProValLysArgLileGlnLileGlnLileGlnLileGlnLileGlnLileGlnLile 595
 QY 1209 GCTTATGACAG 1268
 Db 596 GlyTyraGlnLysAspSerTyrlLilealaserGlnlyProleuLileHisThrLileGln 615
 QY 1269 GACTTCTGGCGCATGCTATGAGACACAAATTCACCATCATGCTCATGCTGACCAAGCTT 1328
 Db 616 AspPheTrpArgMetLileTrpLileLysSerCysSerLileValMetLileuThrGlnLileu 635
 QY 1329 CGGAGATGGCGAG 1388
 Db 636 GluGlnArgLileGlnLileLysCysAlaGlnTyrlTrpProSerAspLysLileuValSerTy 655
 QY 1389 CAGTACTTGTGTTGACCCGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1448
 Db 656 GlyAspLileThrValGlnLileuLysLysGlnLileGlnLileGlnLileGlnLileGlnLile 675
 QY 1449 TTCAGAGTCAAGAGATCCCGGAGTGGACAGTCAAGACAAATCCGCGATTCAGTTCACA 1508
 Db 676 LeuLileuValThrAsnThrArgLysLysSerArgGlnLileArgGlnPheHisPheHis 695
 QY 1509 GACTGGCAACAG 1568
 Db 696 GlyTrpProGlnLysLileLysLileProSerAspLysLysLysLysLysLysLysLysLysLys 715
 QY 1569 GTGCATATGACCAAG 1628
 Db 716 ValGlnLysGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 734
 QY 1629 GCGTGGCGCGACCGGCGCTGTCATCACTGACAGCATGCTCCGAGCGCATG 1688
 Db 735 GlnAlaGlnArgThrGlnTyrlPheCysAlaLileuSerThrValLileuGlnArgValAla 754
 QY 1689 GAGGCGTGGTGCAGATGTTTACAGCCGTGACAGCCGTGACAGCCGTGACAGCCGTGACAG 1748
 Db 755 GlnGlnLileLileuAspValPheGlnThrValLysSerLileuArgLileuGlnArgProHisMet 774
 QY 1749 GTGCACAG 1808
 Db 775 ValGlnThrLileuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 794
 QY 1809 TTTGACCACTATGCA 1823
 Db 795 PheSerAspTyraLale 799

RESULT 11
 US-08-348-006B-7
 ; Sequence 7, Application US/08348006B
 ; Patent No. 5658756
 ; GENERAL INFORMATION:
 ; APPLICANT: RODAN, GIDEON A.
 ; APPLICANT: SCHMIDT, AZRIEL
 ; APPLICANT: RUTLEDGE, SU JANE
 ; TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
 ; TITLE OF INVENTION: TYROSINE PHOSPHATASE
 ; NUMBER OF SEQUENCES: 7
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: J. MARK HAND
 ; STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
 ; CITY: RAHWAY
 ; STATE: NEW JERSEY


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OY 1248 CTTGGCAGAGAGACCCAGGAGCTTTGTGGCGCATGCTATGGGACAGACATTCACATTC 1307
Db 1248 |||||...:|||||...|||||...|||
OY 1308 ATCTCATGCTGACACAGCTTCCGGAGATGAGCGAGGAGAGAAATGGCCACCATGACGAGCA 1367
Db 1308 |||||...:|||||...|||||...|||||...:|||||...:|||||...:|||||...
OY 521 ILeValMeLleuThrGluValAlGlnGluValGlnGluValAspLysCysTyrGlnTyrPro 540
Db 521 |||...:|||||...:|||||...:|||||...:|||||...:|||||...:|||||...
OY 1368 GCAGAGCGCTCTGCTGGCTACACAGTACTTGTGTGTGTATGACCCGATGAGTCAACAATG 1427
Db 1368 |||||...:|||||...:|||||...:|||||...:|||||...:|||||...:|||||...
OY 1428 CCCAGATATTCCTGGCTGAGTTCAGAGTCAGC-----GATGCCGGGAT 1472
Db 1428 |||||...:|||||...:|||||...:|||||...:|||||...:|||||...:|||||...
OY 1473 GGGCAGTCAAGAGCAATCCCGCAGTTCCAGTTCCAGATCAGATCGGCACAGAGAGGCGCTGCC 1532
Db 1473 |||||...:|||||...:|||||...:|||||...:|||||...:|||||...:|||||...
OY 581 GluGlnValAlaArgMetValAlaGlnIlePheHisGlyTyrProGluValGlyIlePro 600
OY 1533 AAGACAGCGCAGGATTCATTGACTTCATATCCGGGACGTCATTAAGACAGAGCAGTTT 1592
Db 1533 |||||...:|||||...:|||||...:|||||...:|||||...:|||||...:|||||...
OY 1593 GGAGAGATGGGCTATACAGGTCAGTCAGTGCAGTGCCTGGCGGCGCAGCGGGGTGTC 1655
Db 1593 |||||...:|||||...:|||||...:|||||...:|||||...:|||||...:|||||...
OY 621 Gly---AsnHisProIleThrValHisCysSerAlaGlyAlaGlyAlaGlyThrGlyIle 639
Db 621 |||||...:|||||...:|||||...:|||||...:|||||...:|||||...:|||||...
OY 1653 ATCACTGTGAGCATCTGCTCGTGGAGCGCATGCGCTATGAGAGGCGCTGTCGACATGTTTCAG 1712
Db 1653 |||||...:|||||...:|||||...:|||||...:|||||...:|||||...:|||||...
OY 1713 ACCGTGAAGACCTGCGTATACAGCGCTCTGCCATGTGTCAACAGAGAGCAGATATAG 1772
Db 1713 |||||...:|||||...:|||||...:|||||...:|||||...:|||||...:|||||...
OY 660 AlaValLysSerLeuAlaArgLeuGlnAlaArgProHisIleMetValGlnThrLeuGlnIleTyrGlu 679
OY 1773 CTGCGTACCGTGGCGGCTCGAGTATCCGCGCAGCTGTGACCATTAAGCA 1823
Db 1773 |||||...:|||||...:|||||...:|||||...:|||||...:|||||...:|||||...
Db 680 PheCysTyrLysValValAlaGlnAspPheIleAspIlePheSerAspTyrAla 696

RESULT 13
US-09-158-657-7
: Sequence 7, Application us/09158657
: Patent No. 6214564
: GENERAL INFORMATION:
: APPLICANT: RODAN, GIDEON A.
: APPLICANT: SCHMIDT, AZRIEL
: APPLICANT: RUTLEDGE, SU JANE
: TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
: NUMBER OF SEQUENCES: 7
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: J. MARK HAND - MERCK & CO., INC.
: STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
: CITY: RAHWAY
: STATE: NEW JERSEY
: COUNTRY: USA
: ZIP: 07065-0900
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/158,657
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/800,825
: FILING DATE: 14-FEB-1997
: ATTORNEY/AGENT INFORMATION:
: NAME: HAND, J. MARK

```

:	36,545	REGISTRATION NUMBER:
:	18992DA	REFERENCE/DOCKET NUMBER:
:		TELECOMMUNICATION INFORMATION:
:	732-594-3905	TELEPHONE:
:	732-594-4720	TELEFAX:
:	7	INFORMATION FOR SEQ ID NO:
:		SEQUENCE CHARACTERISTICS:
:	699 amino acids	LENGTH:
:	single	TYPE: amino acid
:	linear	STRANDEDNESS:
:	peptide	TOPOLOGY:
:		MOLECULE TYPE:
:		US-09-158-657-7
Alignment Scores:		
Pred. NO.:	2.16e-114	Length:
Score:	1423.00	Matches:
Percent Similarity:	64.49%	Conservative:
Best Local Similarity:	47.07%	Mismatches:
Query Match:	22.08%	Indels:
DB:	4	Gaps:
US-09-743-492-1 (1-3467) x US-09-158-657-7 (1-699)		
OY	60 CTCACCTACGAGCCCGCAGATGCAGAGACCACCCCATCCCATCACCGACTTGGC	119
Dd	101 LeuSerArgSerProSerGlyProLysLysPhePheProIleProValIguHisLeuGlu	120
OY	120 GACACATCGAGCGGCTCAAGGCCAACAGATGGCTCAAGTTCTCCGAGAGTAGACTCC	179
Dd	121 GluGluIleArgValArgSerAlaAspAspCysLysArgPheArgGluGluIleAsnSer	140
OY	180 ATGCACCTTGACAAG--CAGTTACAGTGAGGAGAATTCAAACCTGAGGTGAACAACCCC	236
Dd	141 LeuProSerGlyHisIleGlnGlyThrPheGluIleuAlaAsnLysGluIuAsnArgGlu	160
OY	237 AAGAACCGCTTATGCGAATGTATGCGCTACGACCACTGTGAGTCATCTTAACTCTATC	296
Dd	161 LysAsnArgTYrProAsnIleLeuProAsnAspHisCysArgValIleLeuSerGlnVal	180
OY	297 GATGGCGTCCCCGGAGTAGACTACATCAATCAATCAATCAATGAGTGGCTACCGCAACAG	356
Dd	181 AspGlyIleProCysSerAspTYrIleAsnAlaSerTYrIleAspGlyTYrLysGluLys	200
OY	357 AATGCCCTATCGCGCACGACGAGCGCCCTCGCCACGACAACTGGCGCTTCTGGAGAAATG	418
Dd	201 AsnLysPheIleAlaIleGlnGlyProLysIleIuThrValAsnAspPheTrpArgMet	220
OY	417 GTGTGGACAGACGCGACGCGCACTGTGTGTCATGATGACACGCGTGAAGAGAACTCCGG	476
Dd	221 ValTrpGluGlnArgSerAlaThrIleValIleuThrAsnLysGluIuArgGlu	240
OY	477 GTAATAATGTATCACTACTGGCCGACCCGTVGGACCSAGACSTTGGCCTTATTCAGAGTG	536
Dd	241 GluLysCysTYrGlnTYrTrpProAspGlnGlyCysTrpThrTYrGluAsnIleArgVal	260
OY	537 ACCCGTTGGACACAGAGAGGACTGGCCACATACATACAGTGGACGACCTCCGCACTCCAC--	593
Dd	261 CysValGluAspCysValIleValIleValAspTYrThrIleArgLysPheCysIleHisPro	280
OY	594 -----AAGACTGGCTCCAGTAGAGAAAGCGTAGAGCTGGCTGAGTTTCAGTTTCAGGCTGG	647
Dd	281 GluLeuProAspSerCysLysAlaIleProAlaGluValIleArgGlnLeuHisIlePheTrpSer	300
OY	648 CCAGACCATGAGATTCTCTGACTACCCATCCATCCATCTGGCCTTCTTACAGACGGGTGAC	707
Dd	301 ProAspPheGlyValIleProIleThrProIleGlyMetLeuLysPheLeuLysValLys	320
OY	708 GCCTGCAACCCCTTAAGACGAGGGCCCATGGTGGTGGACAGCGGCGGCGTGGCGCGC	757
Dd	321 ThrLeuAsnProSerHisAlaGlyProIleAlaValHisCysSerAlaGlyValGlyArg	340
OY	768 ACAGCGCTTCATCGTGTATGATGAAGCCATGTTGGACGGAGATGAAGCAGGAGACGGTG	827

Db	341							360
QY	828	GACATCTATGGCCACATCCCTGCATCCGATCCACAGAGCAATCATGTGCAGACGAG	8875							
Db	361	AspValPheGluPheValSerArgGleArgGlnGlnArgProGlnMetValGlnThrAsp	380							
QY	888	GACCACTACAGCTTCATCCATGAGGCGCTGCTGAGAGCTGCCACGTGCGGCACACAG	9477							
Db	381	ValGlnTyrThrPheIleTyrGlnAlaLeuLeuGlnIleTyrTyrLeuTyrGlyAspThrGlu	400							
QY	948	GGCGCTGGCCGCAACCTGTATGCCCAATCCAGAGAGCTGGGCCCAAGTGGCTCCAGGGGAG	100							
Db	401	LeuAspValSerSerLeuGlnArgGlnIleuGlnIleuThrIleuHisSerThrAlaThrHisPhe	420							
QY	1008	AGTGTGACCCGATCCAGCTGCAGTTCATCAATCTTGGCCAGCTCCAGACCTCCACACCTCC	106							
Db	421	AspArgLysIleGlyLeuGlnGlnGlnPheArgLysLeuThrHisValAlaGlyIleMetLysGlu	440							
QY	1068	CGCTTCATCAGCGCCACCTCCCTCCGACAAAGTTCAAGAACCGCGCTGTGAACATCATG	112							
Db	441	AsnMetArgThrGlnAsnIlePheProAlaMetLeuLysAlaArgValIleGlnIleIle	460							
QY	1128	CCCTTCAGAAATTGACCCGCTGTGTCTGTGCAGGCCATCCGCTGGTGTGAGGGCTGTACTAC	118							
Db	461	ProTyrAspPheAsnArgValAlaLeuSerMetLysArgGlyGlnGlnPheThrAspTyr	480							
QY	1188	ATCATATGCCAGCTTCCTGGATGTATATGACACAGACAGAGGCTCATAGCTACACAGGG	124							
Db	481	IleAsnAlaSerPheIleAspGlyTyrArgGlnLysAspTyrPheMetAlaThrGlnGly	500							
QY	1248	CCCTGGCAGAGACGACCGGACGACTTGTGGCATGCTATGGAGACCAATTCCACCATC	130							
Db	501	ProLeuAlaHisThrValGlnIleAspPheThrArgMetValIleArgLysSerHisThr	520							
QY	1308	ATCCGATGCTGCACCAACTCCGGGAATGGGACGGAGAAATGCCACACATCTAGTGGCCA	136							
Db	521	IleValMetLeuThrGlnValGlnGlnArgGlnGlnAspLysCysTyrGlnTyrTyrPro	540							
QY	1368	GCAGACCCCTGCTGCCTGCTACCACTACTTTGTTTACCCGAGGCTGAGTGAACAATG	142							
Db	541	ThrGlnLysSerValThrHisGlyAspIleThrIleGluIleLysSerAspThrLeuSer	560							
QY	1428	CCCCAGTATATCTGCTGCTGATCCAAAGTCCAG------GATGCCCGGAGT	147							
Db	561	GlnAlaIleSerValArgAspPheLeuValThrPheLysGlnProLeuAlaIleArgGlnGlu	580							
QY	1473	GGGCGATAGAGACAAATCCGCGACTTCCAGTTTCACAAATCGCCACAGACGGCGGTGCC	153							
Db	581	GlnGlnValArgMetValArgGlnPheHisIlePheHisIleGlyTyrProGlnValGlyIlePro	600							
QY	1533	AAGACACGCGAGGATTTATGACTTATCCGCGAGGTCATGAACACCAAGGACGAGCTTT	159							
Db	601	AlaGlnGlyLysGlyMetIleAspLeuIleAlaValAlaGlnLysGlnGlnGlnGlnThr	620							
QY	1593	GGACAGAGTGGGCGCTATCCAGGTGCACATCGTGCCTGGCGGCGCCACCGGAGTTC	165							
Db	621	Gly--AsnHisProIleThrValHisCysSerAlaGlyAlaGlyThrGlyThrPhe	639							
QY	1653	ATCACTGTGACATCTGCTCTGGAGGCGATCGGCTATAGAGGCGCTGGTGCACATGTTTCA	171							
Db	640	IleAlaLeuSerAsnIleLeuGlnIleArgValLysAlaGlnGlyLeuLeuAspValPheGln	659							
QY	1713	ACCGTGAAGACCCGTGCATACACAGTCTCCATCTGGTGGCAGACAGAGCCAGTATCCAG	177							
Db	660	AlaValLysSerLeuArgLeuGlnIleArgProHisMetValGlnThrLeuGlnGlnGlnGln	679							
QY	1773	CTGTGCTACCTGTGGCGCTGGATACCTCGGACGCTTGTACACCATATGCA	1823							
Db	680	PheCysTyrGlnValAlaGlnAspPheIleAspIlePheSerAspTyrAla	696							

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OY 495 TGCCAGCCCGTCGACCCGAGACCTGTGGCTTATTGAGGTGACCCGTGTGACACAGTG 554
    |||||||
Db 101 TTPRQALARGGLYTHRGTHRCYSGLYLEUILLLEUVALTHRLEUENASPRHVAL 120
OY 555 GAGCTGGCCACATACACTGTGGCCACTTTCGCACTCCACAAAGAGTGCTTCAGTGAGAA 614
    |||||||
Db 121 GLULEUALATHRTYRTHRVAL-----PHEALALEUHLISYSSERGLYSERSEGLULYS 138
OY 615 CGTAGACTGCGTGAAGTTTCAGTTTCATGAGCTGGCCGACAGACCAGAGTGAAGTACCA 674
    |||||||
Db 139 ARGGLULEUARGLINPHEGLINPHEMETALATRPDASPHISGLYVALPROGLUTYRPRO 158
OY 675 ACTCCCATCTCGCTCTTCTACAGACGGGTCAAGGCTGCAACCCCTAGACGAGGGCC 734
    |||||||
Db 159 THRPROILLEUVALPHELEUARGVALLYSALACYSASNPROLEUASPALAGLYPRO 178
OY 735 ATGGTGTCACATGACCGCGCGGTGGCCGACCGGCTTCATGCGATTGATGGCC 794
    |||||||
Db 179 METVALVALHISYSSERRAAGLYVALGLYARGTHRGLYCYSPELLEVALILEASPA 198
OY 795 ATGTTGAGCGGATGAAGACGAGAAAGCGTGACATCTATGGCCAGCTGACCTGCATG 854
    |||||||
Db 199 METLEUGLUARGMETLYSHISGLULYSTHRVALASPILETYRGLYHISVALTHRCYSMET 218
OY 855 CGATCACAGAGACTACATGCTGTCAGACGAGGAGGACCATGACTGTTCATCCATGAGCG 914
    |||||||
Db 219 ARGSEGLARGASNTRYMETVALGLINTHGLUASPGINTYRVALPHEILEHISGLUALA 238
OY 915 CTGCTGAGAGCTCCACGTCGCGCCACACAGAGGTG 950
    |||||||
Db 239 LEULEUGLUALAATHRCYSGLYHISTHGLUVAL 250

```

```

RESULT 15
US-09-144-925-7
: Sequence 7, Application US/09144925
: Patent No. 5951979
: GENERAL INFORMATION:
: APPLICANT: Tonks, Nicholas
: APPLICANT: Flint, Andrew J.
: TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
: TITLE OF INVENTION: TYROSINE PHOSPHATASES
: NUMBER OF SEQUENCES: 36
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P. C.
: STREET: Two Mallitia Drive
: CITY: Lexington
: STATE: MA
: COUNTRY: USA
: ZIP: 02421-4799
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: OPERATING SYSTEM: Windows 95
: SOFTWARE: FastSeq for Windows Version 2.0b
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/144,925
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/685,992
: FILING DATE: July 25, 1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Granahan, Patricia
: REGISTRATION NUMBER: 32,227
: REFERENCE/DOCKET NUMBER: CSHL96-032
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 781-861-6240
: TELEFAX: 781-861-9540
: TELEX:
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 250 amino acids

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: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
US-09-144-925-7

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Alignment Scores:

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Pred. No.: 6,14e-107 Length: 250
Score: 1334.00 Matches: 250
Percent Similarity: 99.21% Conservative: 0
Best Local Similarity: 99.21% Mismatches: 0
Query Match: 20.70% Indels: 2
DB: 2 Gaps: 1

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US-09-743-492-1 (1-3467) x US-09-144-925-7 (1-250)

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OY 195 CAGTTCACGTCGGAGAGATTCAACCTGGAGGTGACAAAGCCCAAGAACCGCTATGGCAAT 254
    |||||||
Db 1 GlnPheThrTrpPoluSnSerAsnLeuGluValAsnLysProLysAsnArgIYrAlaAsn 20
OY 255 GTCATGCGCTACGACACATCTCGAGTCATCCCTTACCTATGATGAGCGCTCCCGGAGT 314
    |||||||
Db 21 ValIleAlaTyraSPHSSERRARGVALILEUETHRSERILEASPGLYVALPROGLYSER 40
OY 315 GACTACATCAATGCCAATACATCATGATGGCTACCCGACAGAGATGCTTACATCGCCAGC 374
    |||||||
Db 41 AspTYRILEASNALEASNTRYILEASPGIYTYRARGLYSGILEASNALEATYRILEALATHR 60
OY 375 CAGGGCCCCCTGCCCCGAGACCATGGCGATTTCGGGAATGGTGGGAACAGCCGACG 434
    |||||||
Db 61 GlnGlyProLeuProGluThrMetGlyAspPheTrpArgMetValITRPGluGlnArgThr 80
OY 435 GCCACTGTGTGTCATGATGACACGCGTGAAGAGAACTCCCGGCTAAATGTATCAGTAC 494
    |||||||
Db 81 AlaThrValValMetMetThrArgLeuGluGluLysSerArgValLysCysAspGlnTYR 100
OY 495 TGCCAGCCCGTGGACACCGAGACCTGTGGCTTATTCAGGTGACCTGTGGACACAGTG 554
    |||||||
Db 101 TTPRQALARGGLYTHRGTHRCYSGLYLEUILLLEUVALTHRLEUENASPRHVAL 120
OY 555 GAGCTGGCCACATACACTGTGGCCACTTTCGCACTCCACAAAGAGTGCTTCAGTGAGAA 614
    |||||||
Db 121 GLULEUALATHRTYRTHRVAL-----PHEALALEUHLISYSSERGLYSERSEGLULYS 138
OY 615 CGTAGACTGCGTGAAGTTTCAGTTTCATGAGCTGGCCGACAGACCAGAGTGAAGTACCA 674
    |||||||
Db 139 ARGGLULEUARGLINPHEGLINPHEMETALATRPDASPHISGLYVALPROGLUTYRPRO 158
OY 675 ACTCCCATCTCGCTCTTCTACAGACGGGTCAAGGCTGCAACCCCTAGACGAGGGCC 734
    |||||||
Db 159 THRPROILLEUVALPHELEUARGVALLYSALACYSASNPROLEUASPALAGLYPRO 178
OY 735 ATGGTGTCACATGACCGCGCGGTGGCCGACCGGCTTCATGCGATTGATGGCC 794
    |||||||
Db 179 METVALVALHISYSSERRAAGLYVALGLYARGTHRGLYCYSPELLEVALILEASPA 198
OY 795 ATGTTGAGCGGATGAAGACGAGAAAGCGTGACATCTATGGCCAGCTGACCTGCATG 854
    |||||||
Db 199 METLEUGLUARGMETLYSHISGLULYSTHRVALASPILETYRGLYHISVALTHRCYSMET 218
OY 855 CGATCACAGAGACTACATGCTGTCAGACGAGGAGGACCATGACTGTTCATCCATGAGCG 914
    |||||||
Db 219 ARGSEGLARGASNTRYMETVALGLINTHGLUASPGINTYRVALPHEILEHISGLUALA 238
OY 915 CTGCTGAGAGCTCCACGTCGCGCCACACAGAGGTG 950
    |||||||
Db 239 LEULEUGLUALAATHRCYSGLYHISTHGLUVAL 250

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Search completed: January 17, 2003, 10:16:44
Job time : 90.5 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 09:11:01 : Search time 16 Seconds
(without alignments)
72.101 Million cell updates/sec

Title: US-09-743-492-4
Perfect score: 65
Sequence: 1 VVHCSAGVGRG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR-73:*
1: pirl:*
2: pirl:*
3: pirl:*
4: pirl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	100.0	198	2 T27722	hypothetical prote
2	65	100.0	236	2 A40169	protein-tyrosine-p
3	65	100.0	398	2 I56540	protein-tyrosine-p
4	65	100.0	483	2 T25992	hypothetical prote
5	65	100.0	582	2 A57068	protein-tyrosine-p
6	65	100.0	583	2 S17671	protein-tyrosine-p
7	65	100.0	699	2 JC6132	protein-tyrosine-p
8	65	100.0	700	2 SI2053	protein-tyrosine-p
9	65	100.0	796	1 JC1285	protein-tyrosine-p
10	65	100.0	802	1 A36065	protein-tyrosine-p
11	65	100.0	829	1 A47373	protein-tyrosine-p
12	65	100.0	1187	1 JC4155	protein-tyrosine-p
13	65	100.0	1189	1 JC2366	protein-tyrosine-p
14	65	100.0	1200	2 T43148	probable protein-t
15	65	100.0	1237	2 A54080	protein-tyrosine-p
16	65	100.0	1262	1 B48758	protein-tyrosine-p
17	65	100.0	1273	1 TDFRIT	leukocyte common a
18	65	100.0	1290	2 A56493	leukocyte common a
19	65	100.0	1291	1 A28334	protein-tyrosine-p
20	65	100.0	1301	1 A41622	protein-tyrosine-p
21	65	100.0	1304	1 A46546	leukocyte common a
22	65	100.0	1422	2 T42636	protein-tyrosine-p
23	65	100.0	1437	2 T31093	probable protein-t
24	65	100.0	1496	1 A48758	protein-tyrosine-p
25	65	100.0	1499	2 I50212	protein-tyrosine-p
26	65	100.0	1501	2 I58148	protein-tyrosine-p
27	65	100.0	1691	2 D54689	protein-tyrosine-p
28	65	100.0	1863	2 S46217	protein-tyrosine-p
29	65	100.0	1894	2 C54689	protein-tyrosine-p

30	65	100.0	1897	1 TDHULK	leukocyte antigen-
31	65	100.0	1898	2 S46216	leukocyte antigen-
32	65	100.0	1907	2 S50893	protein-tyrosine-p
33	65	100.0	1912	2 A56178	protein-tyrosine-p
34	65	100.0	1997	1 S12050	protein-tyrosine-p
35	65	100.0	2051	2 T30938	receptor tyrosine
36	65	100.0	2302	2 T14328	protein-tyrosine-p
37	65	100.0	2314	1 A46151	protein-tyrosine-p
38	64	98.5	135	2 H88683	protein-tyrosine-p
39	64	98.5	332	2 T06536	protein C2B10.6 l
40	64	98.5	335	1 A39862	protein-tyrosine-p
41	64	98.5	344	2 T32869	hypothetical prote
42	64	98.5	352	2 T20729	hypothetical prote
43	64	98.5	360	1 JH0692	protein-tyrosine-p
44	64	98.5	365	2 T25917	hypothetical prote
45	64	98.5	374	2 F88712	protein C17H12.3 l

ALIGNMENTS

RESULT 1

T27722

hypothetical protein ZK1251.5 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T27722

R:McMurray, A. submitted to the EMBL Data Library, December 1995

A:Reference number: Z20411

A:Accession: T27722

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-198 <MIL>

A:Cross-references: EMBL:Z68222; PIDN:CAA92501.1; GSPDB:GN00022; CESP:ZK1251.5

A:Experimental source: clone ZK1251

C:Genetics:

A:Gene: CESP:ZK1251.5

A:Map position: 4

A:Introns: 46/3; 101/2; 185/3

Query Match 100.0% Score 65; DB 2; Length 198;
Best Local Similarity 100.0%; Pred. NO. 0.00063;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVHCSAGVGRG 12

Db 105 VVHCSAGVGRG 116

RESULT 2

A40169

protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type zeta - rat (fragment)

N:Alternate names: protein-tyrosine-phosphatase beta; protein-tyrosine-phosphatase PT

C:Species: Rattus norvegicus (Norway rat)

C>Date: 05-Jun-1992 #sequence #sequence_revision 05-Jun-1992 #text_change 24-Apr-1998

C:Accession: A40169

R:Guan, K.; Dixon, J.E. Science 249, 553-556, 1990

A>Title: Protein tyrosine phosphatase activity of an essential virulence determinant

A:Reference number: A40169; MUID:90341778; PMID:2166336

A:Accession: A40169

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-256 <GVA>

C:Function:

A:Description: may be involved in the regulation of specific developmental processes
C:Superfamily: protein-tyrosine-phosphatase, receptor type zeta; carbonic anhydrase h
C:Keywords: brain; glycoprotein; phosphoprotein; phosphoric monoester hydrolase; rece
F:6-237/Domain: protein-tyrosine-phosphatase homology <PTP1>
F:189/Active site: Cys (phosphocysteine intermediate) #status predicted
F:195/Binding site: substrate phosphate (Arg) #status predicted

Query Match 100.0%; Score 65; DB 2; Length 256;
 Best Local Similarity 100.0%; Pred. No. 0.00079;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVHCSAGVGRGTG 12
 |||||
 Db 186 VVHCSAGVGRGTG 197

RESULT 3
 I56540
 protein-tyrosine-phosphatase (EC 3.1.3.48) cphpl - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 23-Jul-1999
 C:Accession: I56540
 R:Sahin, M.; Hockfield, S.
 J. Neurosci. 13, 4968-4978, 1993
 A:Title: Protein tyrosine phosphatases expressed in the developing rat brain.
 A:Reference number: I56540; MID:94043925; PMID:8229209
 A:Accession: I56540
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-398 <RES>
 C:Cross-references: EMBL:003273; NID:9414996; PIDN:AAC52124.1; PID:9414997
 C:Genetics:
 A:Gene: cphpl
 C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
 ogy
 C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase
 F:1-157/Domain: protein-tyrosine-phosphatase homology (fragment) <PRP1>
 F:1225-398/Domain: protein-tyrosine-phosphatase homology (fragment) <PRP>
 F:109/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:115/Binding site: substrate phosphate (Arg) #status predicted

Query Match 100.0%; Score 65; DB 2; Length 398;
 Best Local Similarity 100.0%; Pred. No. 0.0012;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVHCSAGVGRGTG 12
 |||||
 Db 106 VVHCSAGVGRGTG 117

RESULT 4
 T25992
 hypothetical protein ZK354.8 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T25992
 R:Johnson, D.; Wamsley, P.; Bradshaw, H.
 submitted to the EMBL Data Library, February 1997
 A:Description: The sequence of C. elegans cosmid ZK354.
 A:Reference number: Z20120
 A:Accession: T25992
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-483 <JON>
 A:Cross-references: EMBL:U88172; PIDN:AAB42260.1; GSPDB:GN00022; CESP:ZK354.8
 A:Experimental source: strain Bristol N2; clone ZK354
 C:Genetics:
 A:Gene: CESP:ZK354.8
 A:Map position: 4
 A:Intons: 7/1; 70/3; 180/2; 256/2; 331/3; 386/2; 470/3

Query Match 100.0%; Score 65; DB 2; Length 483;
 Best Local Similarity 100.0%; Pred. No. 0.0014;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVHCSAGVGRGTG 12
 |||||
 Db 390 VVHCSAGVGRGTG 401

RESULT 5
 A57068
 protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type f - mouse (fragment)
 N:Alternate names: Leukocyte antigen-related protein LAR
 C:Species: Mus musculus (house mouse)
 C:Date: 03-Oct-1995 #sequence_revision 09-Mar-1996 #text_change 23-Jul-1999
 C:Accession: A57068; S40280
 R:Schaapveld, R.Q.J.; van den Maagdenberg, A.M.J.M.; Schepens, J.T.G.; Olde Weghuis,
 Genomics 27, 124-130, 1995
 A:Title: The mouse gene Ppfrf encoding the leukocyte common antigen-related molecule
 A:Reference number: A57068; MID:95394448; PMID:7665159
 A:Accession: A57068
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-582 <SCH>
 A:Cross-references: GB:Z37988; NID:9993005; PIDN:CAA6070.1; PID:9993006
 R:Hendriks, W.; Brugman, C.; Zeuwen, P.; Schepens, J.; Wieringa, B.
 submitted to the EMBL Data Library, June 1993
 A:Description: Assessment of the expression levels of murine protein-tyrosine phosphatase
 A:Reference number: S40280
 A:Accession: S40280
 A:Molecule type: mRNA
 A:Residues: 116-221 <HEN>
 A:Cross-references: EMBL:Z23049; NID:9438135; PIDN:CAA80584.1; PID:9438136
 C:Genetics:
 A:Gene: Ppfrf
 C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology
 ogy
 C:Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembr
 F:1-582/Domain: leukocyte common antigen cytosolic domain homology (fragment) <LAC>
 F:50-271/Domain: protein-tyrosine-phosphatase homology <PRP1>
 F:339-562/Domain: protein-tyrosine-phosphatase homology <PRP2>
 F:223/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:229/Binding site: substrate phosphate (Arg) #status predicted
 F:514/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:520/Binding site: substrate phosphate (Arg) #status predicted

Query Match 100.0%; Score 65; DB 2; Length 582;
 Best Local Similarity 100.0%; Pred. No. 0.0017;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVHCSAGVGRGTG 12
 |||||
 Db 220 VVHCSAGVGRGTG 231

RESULT 6
 S17671
 protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type beta - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 22-Nov-1993 #sequence_revision 15-Mar-1996 #text_change 23-Jul-1999
 C:Accession: S17671; S40287
 R:Gebpink, M.F.B.G.; van Etten, I.; Hatober, G.; Suijkerbuijk, R.; Beljersbergen, R.
 FEBS Lett. 290, 123-130, 1991
 A:Title: Cloning, expression and chromosomal localization of a new putative receptor-
 A:Reference number: S17671
 A:Accession: S17671
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-583 <GEB>
 A:Cross-references: EMBL:X58289
 R:Hendriks, W.; Brugman, C.; Zeuwen, P.; Schepens, J.; Wieringa, B.
 submitted to the EMBL Data Library, June 1993
 A:Description: Assessment of the expression levels of murine protein-tyrosine phosphatase
 A:Reference number: S40280
 A:Accession: S40287
 A:Molecule type: mRNA
 A:Residues: 377-483, 'T', 485-486 <HEN>
 A:Cross-references: EMBL:Z23056; NID:9438149; PIDN:CAA80591.1; PID:9438150
 C:Superfamily: protein-tyrosine-phosphatase, receptor type beta; fibronectin type III
 C:Keywords: phosphoprotein; phosphoric monoester hydrolase; receptor; transmembrane p
 F:311-536/Domain: protein-tyrosine-phosphatase homology <PRP>
 F:488/Active site: Cys (phosphocysteine intermediate) #status predicted

F:494/Binding site: substrate phosphate (Arg) #status predicted

Query Match 100.0%; Score 65; DB 2; Length 583;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVHCSAGVGRG 12
DB 485 VVHCSAGVGRG 496

RESULT 7

JC6132

protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type epsilon precursor - mouse
N:Alternate names: phosphotyrosine phosphatase; protein-tyrosine-phosphate phosphotyrol
C:Species: Mus musculus (house mouse)
C>Date: 16-Apr-1997 #sequence_revision 09-May-1997 #text_change 21-Jun-2002

C:Accession: JC6132

R:Schmidt, A.; Rutledge, S.J.; Endo, N.; Opas, E.E.; Tanaka, H.; Wesolowski, G.; Leu, C.
Proc. Natl. Acad. Sci. U.S.A. 93, 3068-3073, 1996

A:Title: Protein-tyrosine phosphatase activity regulates osteoclast formation and functi
A:Reference number: JC6132; MUID:96181534; PMID:8610169

A:Contents: Bone marrow cell

A:Accession: JC6132

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-699 <SCCH>

A:Cross-references: GB:040280; NID:q1373052; PIDN:AAB02190.1; PID:q1373053

C:Comment: This enzyme plays an important role in osteoclast formation and function in t
hosphonate action.

C:Genetics:

A:Gene: ptp

C:Superfamily: protein-tyrosine-phosphatase, receptor type alpha; leukocyte common anti
C:Keywords: phosphoprotein; phosphoric monoster hydrolase; transmembrane protein; tyros
F:77-697/Domain: leukocyte common antigen cytosolic domain homology <LAC>

F:158-382/Domain: protein-tyrosine-phosphatase homology <PTP1>

F:334/Active site: Cys (phosphocysteine intermediate) #status predicted

F:340/Binding site: substrate phosphate (Arg) #status predicted

F:632/Active site: Cys (phosphocysteine intermediate) #status predicted

F:635/Binding site: substrate phosphate (Arg) #status predicted

Query Match 100.0%; Score 65; DB 2; Length 699;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVHCSAGVGRG 12
DB 331 VVHCSAGVGRG 342

RESULT 8

S12053

protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type epsilon precursor - human
C:Species: Homo sapiens (man)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: S12053

R:Kueger, N.X.; Streuli, M.; Saito, H.
EMBO J. 9, 3241-3252, 1990

A:Title: Structural diversity and evolution of human receptor-like protein tyrosine phos
A:Reference number: S12049; MUID:91006018; PMID:2170109

A:Accession: S12053

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-700 <RNU>

A:Cross-references: GB:X54134; NID:g35791; PIDN:CAA38069.1; PID:g35792

C:Genetics:

A:Gene: GDB:PTPRE

A:Cross-references: GDB:131385; OMIM:600926

A:Map position: 10q26-10q26

C:Function:

A:Description: catalyzes the hydrolysis of peptidyl-phosphotyrosine to release phosphate
C:Superfamily: protein-tyrosine-phosphatase, receptor type alpha; leukocyte common anti
C:Keywords: phosphoprotein; phosphoric monoster hydrolase; receptor; transmembrane prot

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-700/Product: protein-tyrosine-phosphatase, receptor type epsilon #status predict

F:47-63/Domain: transmembrane #status predicted <TM>

F:78-696/Domain: leukocyte common antigen cytosolic domain homology <LAC>

F:159-383/Domain: protein-tyrosine-phosphatase homology <PTP1>

F:335/Active site: Cys (phosphocysteine intermediate) #status predicted

F:341/Binding site: substrate phosphate (Arg) #status predicted

F:630/Active site: Cys (phosphocysteine intermediate) #status predicted

F:636/Binding site: substrate phosphate (Arg) #status predicted

Query Match 100.0%; Score 65; DB 1; Length 700;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVHCSAGVGRG 12
DB 332 VVHCSAGVGRG 343

RESULT 9

JC1285

protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type alpha precursor - rat
N:Alternate names: protein-tyrosine-phosphatase LRP
C:Species: Rattus norvegicus (Norway rat)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: JC1285; S23253; JH0450

R:Moriyama, T.; Fujiwara, Y.; Imai, E.; Takenaka, M.; Kawanishi, S.; Inoue, T.; Noguc
Biochem. Biophys. Res. Commun. 188, 34-39, 1992

A:Title: cDNA cloning of rat LRP, a receptor like protein tyrosine phosphatase, and e
A:Reference number: JC1285; MUID:93038682; PMID:1417854

A:Accession: JC1285

A:Molecule type: mRNA

A:Residues: 1-796 <MOR>

A:Experimental source: kidney

A:Note: the authors translated the codon TCC for residue 788 as Ala

R:Hashimoto, N.; Zhang, W.R.; Goldstein, B.J.
Biochem. J. 284, 569-576, 1992

A:Title: Insulin receptor and epidermal growth factor receptor dephosphorylation by t
A:Reference number: S23126; MUID:92287069; PMID:1599438

A:Accession: S23253

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 254-267, 'I', 269-354, 'T', 356-501 <HAS>

R:Zhang, W.R.; Goldstein, B.J. Commun. 178, 1291-1297, 1991

A:Title: Identification of skeletal muscle protein-tyrosine phosphatases by amplifica
A:Reference number: JH0450; MUID:91337074; PMID:1651716

A:Accession: JH0450

A:Molecule type: mRNA

A:Residues: 324-354, 'T', 356-434 <HAS>

A:Experimental source: skeletal muscle, strain Sprague-Dawley

C:Function:

A:Description: catalyzes the hydrolysis of peptidyl-phosphotyrosine to release phosph
A:Note: allows recovery from insulin stimulation by dephosphorylating insulin recepto
C:Superfamily: protein-tyrosine-phosphatase, receptor type alpha; leukocyte common an
C:Keywords: phosphoprotein; phosphoric monoster hydrolase; receptor; transmembrane p
F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-706/Product: protein-tyrosine-phosphatase, receptor type alpha #status predicted

F:149-165/Domain: extracellular #status predicted <EXT>

F:166-796/Domain: transmembrane #status predicted <TM>

F:178-794/Domain: leukocyte common antigen cytosolic domain homology <LAC>

F:259-484/Domain: protein-tyrosine-phosphatase homology <PTP1>

F:552-774/Domain: protein-tyrosine-phosphatase homology <PTP2>

F:436/Active site: Cys (phosphocysteine intermediate) #status predicted

F:442/Binding site: substrate phosphate (Arg) #status predicted

F:726/Active site: Cys (phosphocysteine intermediate) #status predicted

F:732/Binding site: substrate phosphate (Arg) #status predicted

Query Match 100.0%; Score 65; DB 1; Length 796;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCASAGVGRGTG 12
 |||
 Db 433 VHCASAGVGRGTG 444

RESULT 10
 A36065

protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type alpha precursor - human

C:Species: Homo sapiens (man)

C>Date: 10-Sep-1999 #sequence, revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: A36065; S12049; S12905; S13085

R:Kaplan, R.; Morse, B.; Huebner, K.; Croce, C.; Howk, R.; Ravera, M.; Ricca, G.; Jaye, Proc. Natl. Acad. Sci. U.S.A. 87, 7000-7004, 1990

A>Title: Cloning of three human tyrosine phosphatases reveals a multigene family of receptors

A:Reference number: A36065; MUID:90384936; PMID:2169617

A:Accession: A36065

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-802 <NAP>

A:Cross-references: GB:M34668; NID:q190738; PIDN:AAA36528.1; PID:q190739

R:Kruiger, N.X.; Streuli, M.; Saito, H.

EMBO J. 9, 3241-3252, 1990

A>Title: Structural diversity and evolution of human receptor-like protein tyrosine phosphatases

A:Reference number: S12049; MUID:91006018; PMID:2170109

A:Accession: S12049

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-138,148-802 <KR0>

A:Cross-references: GB:X54130; NID:q35785; PIDN:CAA38065.1; PID:q35786

R:Jirik, F.R.; Janzen, N.M.; Melhado, I.G.; Harder, K.W.; Leslie, K.B.

submitted to the EMBL Data Library, June 1990

A>Description: Isolation of a cDNA encoding a novel protein-tyrosine phosphatase from thymocytes

A:Reference number: S17371

A:Accession: S17371

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-121, 'P', 123-138, 148-199, 'G', 201-203, 'C', 205-802 <JIR>

A:Cross-references: EMBL:X53364

R:Jirik, F.R.; Janzen, N.M.; Melhado, I.G.; Harder, K.W.

FEBS Lett. 273, 239-242, 1990

A>Title: Cloning and chromosomal assignment of a widely expressed human receptor-like protein

A:Reference number: S12905; MUID:91032191; PMID:2172030

A:Accession: S12905

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-61, 'V', 62-82, 84-121, 'P', 123-138, 148-199, 'G', 201-203, 'C', 205-802 <JIR>

R:Obagi, S.; Nishii, M.; Steiner, D.F.

Nucleic Acids Res. 18, 7159, 1990

A>Title: Sequence of a cDNA encoding human LRP (leukocyte common antigen-related peptide)

A:Reference number: S13085; MUID:91088320; PMID:2175890

A:Accession: S13085

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-113, 'W', 115-138, 148-288, 'E', 290-366, 'A', 368-492, 'S', 494-785, 'E', 787-802 <C>

A:Cross-references: EMBL:X54890; NID:q32312; PIDN:CAA38662.1; PID:q32313

C:Genetics:

A:Gene: GDB:PTPPA; PTPA

A:Cross-references: GDB:126732; OMIM:176884

A:Map position: 20p13-20p13

C:Function:

A>Description: catalyzes the hydrolysis of peptidyl-phosphotyrosine to release phosphate

A>Note: allows recovery from insulin stimulation by dephosphorylating insulin receptor

A:Superfamily: protein-tyrosine-phosphatase, receptor type alpha; leukocyte common antigen

C:Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; receptor

F:1-19/Domain: signal sequence #status predicted <SIS>

F:20-802/Product: protein-tyrosine-phosphatase, receptor type alpha #status predicted <W>

F:20-154/Domain: extracellular #status predicted <EXN>

F:155-171/Domain: transmembrane #status predicted <TMN>

F:172-802/Domain: intracellular #status predicted <INT>

F:184-800/Domain: leukocyte common antigen cytosolic domain homology <LAC>

F:265-490/Domain: protein-tyrosine-phosphatase homology <PTP1>

F:558-780/Domain: protein-tyrosine-phosphatase homology <PTP2>

F:442/Active site: Cys (phosphocysteine intermediate) #status predicted

F:448/Binding site: substrate phosphate (Arg) #status predicted

F:732/Active site: Cys (phosphocysteine intermediate) #status predicted

F:738/Binding site: substrate phosphate (Arg) #status predicted

QY 1 VHCASAGVGRGTG 12
 |||
 Db 439 VHCASAGVGRGTG 450

RESULT 11
 A47373

protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type alpha precursor - mouse

N:Alternate names: leukocyte common antigen-related protein LRP; PTPY28; receptor pr

C:Species: Mus musculus (house mouse)

C>Date: 10-Sep-1999 #sequence, revision 10-Sep-1999 #text_change 21-Jan-2000

C:Accession: A47373; B35501; A35501; P50367; S40285; S40286; A36004; D61180

R:Mong, E.C.; Mullersman, J.E.; Thomas, M.L.

Genomics 17, 33-38, 1993

A>Title: Leukocyte common antigen-related phosphatase (LRP) gene structure: conservat

A:Reference number: A47373; MUID:94010906; PMID:8406469

A:Accession: A47373

A:Molecule type: DNA

A:Residues: 1-829 <MON>

A:Cross-references: GB:L13607

R:Matthews, R.J.; Cahill, E.D.; Thomas, M.L.

Proc. Natl. Acad. Sci. U.S.A. 87, 4444-4448, 1990

A>Title: Identification of a novel murine non-receptor protein tyrosine phosphatase f

A:Reference number: A35501; MUID:90280391; PMID:2162042

A:Accession: B35501

A:Molecule type: mRNA

A:Residues: 1-829 <MA1>

A:Cross-references: GB:M36033; NID:q198876; PIDN:AAA39448.1; PID:q198877; GB:M3671

A>Note: the authors translated the codon GAT for residue 30 as Tyr

A:Accession: A35501

A:Molecule type: mRNA

A:Residues: 1-267, 'Y', 305-829 <MA2>

A:Cross-references: GB:M36033; GB:M3671

R:den Hertog, J.; Pals, C.E.G.M.; Jonk, L.J.C.; Kruiter, W.

Biochem. Biophys. Res. Commun. 184, 1241-1249, 1992

A>Title: Differential expression of a novel murine non-receptor protein tyrosine phos

A:Reference number: JH0609; MUID:92272714; PMID:1590786

A:Accession: P50367

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 322-325, 'G', 327-356 <DEN>

A:Experimental source: embryonal carcinoma cell, p19 cell

R:Hendriks, W.; Brugman, C.; Zeewen, P.; Schepens, J.; Wieringa, B.

submitted to the EMBL Data Library, June 1993

A>Description: Assessment of the expression levels of murine protein-tyrosine phosphat

A:Reference number: S40280

A:Accession: S40280

A:Molecule type: mRNA

A:Residues: 358-467 <HEN>

A:Cross-references: EMBL:Z23054; NID:q438145; PIDN:CAA80589.1; PID:q438146

A:Accession: S40286

A:Molecule type: mRNA

A:Residues: 651-756 <HB2>

A:Cross-references: EMBL:Z23055; NID:q438147; PIDN:CAA80590.1; PID:q438148

R:Rap, J.; D'Eustachio, P.; Givol, D.; Schlessinger, J.

Proc. Natl. Acad. Sci. U.S.A. 87, 6112-6116, 1990

A>Title: Cloning and expression of a widely expressed receptor tyrosine phosphatase.

A:Reference number: A36004; MUID:90349565; PMID:2166945

A:Accession: A36004

A:Molecule type: mRNA

A:Residues: 1-230, 'L', 232-267, 'Y', 305-410, 'S', 412-829 <NAP>

A:Cross-references: GB:M34668

R:Yi, T.; Cleveland, J.L.; Ihle, J.N.

Blood 78, 2222-2228, 1991

A:Title: Identification of novel protein tyrosine phosphatases of hematopoietic cells by
 A:Reference number: A61180; MUID:92032882; PMID:193742
 A:Accession: D61180
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 358-467 <YIA>
 C:Genetics:
 A:Map position: 2
 C:Function:
 A:Description: catalyzes the hydrolysis of peptidyl phosphotyrosine to release phosphate
 A:Note: allows recovery from insulin stimulation by dephosphorylating insulin receptor
 C:Superfamily: protein-tyrosine-phosphatase, receptor type alpha; leukocyte common antigen
 C:Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hyd
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-829/Product: protein-tyrosine-phosphatase, receptor type alpha #status predicted <W
 F:20-14/Domain: extracellular #status predicted <EXT>
 F:143-166/Domain: transmembrane #status predicted <TM>
 F:167-829/Domain: intracellular #status predicted <INT>
 F:175-827/Domain: leukocyte common antigen cytosolic domain homology <LAC>
 F:585-807/Domain: protein-tyrosine-phosphatase homology <PP>
 F:21-47,51,68,80,86,104,124/Binding site: carbohydrate (Aan) (covalent) #status predicte
 F:469/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:475/Binding site: substrate phosphate (Arg) #status predicted
 F:759/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:765/Binding site: substrate phosphate (Arg) #status predicted

Query Match 100.0%; Score 65; DB 1; Length 829;
 Best Local Similarity 100.0%; Pred. No. 0.0024;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VVHCSAGVGRG 12
 Db 466 VVHCSAGVGRG 477

RESULT 12
 JC4155
 N:protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 14 - human
 N:Alternate names: PZ protein; protein-tyrosine-phosphatase/ezrin-like protein
 C:Species: Homo sapiens (man)
 C:Date: 27-Aug-1995 #sequence_revision 23-Feb-1996 #text_change 21-Jul-2000
 C:Accession: JC4155
 R:Smith, A.L.; Mitchell, P.J.; Shipley, J.; Gusterson, B.A.; Rogers, M.V.; Crompton, M.F.
 Biochem. Biophys. Res. Commun. 209: 959-965, 1995
 A:Title: PZ: a novel human cDNA encoding protein tyrosine phosphatase-and ezrin-like dom
 A:Reference number: JC4155; MUID:95251727; PMID:7733990
 A:Accession: JC4155
 A:Molecule type: mRNA
 A:Residues: 1-1187 <SMID>
 A:Cross-references: EMBL:X82676; NID:93929753; PIDN:CA57993.1; PID:9809029
 A:Experimental source: Breast
 C:Genetics:
 A:Gene: GDB:PTPN14
 A:Cross-references: GDB:454485
 A:Map position: 1q32.2-1q32.2
 C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 14; protein 4.1 membrane-t
 C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatas
 F:23-302/Domain: protein 4.1 membrane-binding domain homology <B41>
 F:566-575/Region: proline-rich
 F:709-716/Region: acidic
 F:933-1169/Domain: protein-tyrosine-phosphatase homology <PP2>
 F:1121/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:1127/Binding site: substrate phosphate (Arg) #status predicted

Query Match 100.0%; Score 65; DB 1; Length 1187;
 Best Local Similarity 100.0%; Pred. No. 0.0033;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VVHCSAGVGRG 12
 Db 1118 VVHCSAGVGRG 1129

RESULT 13
 JC2366
 N:protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 14 - mouse
 N:Alternate names: PZ protein; protein-tyrosine-phosphatase PTP36; protein-tyrosine-
 C:Species: Mus musculus (house mouse)
 C:Date: 24-Feb-1995 #sequence_revision 23-Feb-1996 #text_change 21-Jul-2000
 C:Accession: JC2366
 R:Sawada, M.; Ogata, M.; Fujino, Y.; Hamoka, T.
 Biochem. Biophys. Res. Commun. 203: 479-484, 1994
 A:Title: cDNA cloning of a novel protein tyrosine phosphatase with homology to cytosk
 A:Reference number: JC2366; MUID:94354845; PMID:8074693
 A:Accession: JC2366
 A:Molecule type: mRNA
 A:Residues: 1-1189 <SNM>
 A:Cross-references: GB:D51842; NID:9507330; PIDN:BA06628.1; PID:9507331
 A:Experimental source: thymus
 C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 14; protein 4.1 membran
 C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosph
 F:23-302/Domain: protein 4.1 membrane-binding domain homology <B41>
 F:566-575/Region: proline-rich
 F:712-718/Region: acidic
 F:933-1171/Domain: protein-tyrosine-phosphatase homology <PP2>
 F:1123/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:1129/Binding site: substrate phosphate (Arg) #status predicted

Query Match 100.0%; Score 65; DB 1; Length 1189;
 Best Local Similarity 100.0%; Pred. No. 0.0033;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VVHCSAGVGRG 12
 Db 1120 VVHCSAGVGRG 1131

RESULT 14
 T43148
 N:probable protein-tyrosine-phosphatase (EC 3.1.3.48) - horn shark
 N:Alternate names: CD45 homolog
 C:Species: Heterodontus francisci (horn shark)
 C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
 C:Accession: T43148
 R:Okumura, M.; Matthews, R.J.; Robb, B.; Bork, P.; Thomas, M.L.
 submitted to the EMBL Data Library, August 1995
 A:Reference number: Z22317
 A:Accession: T43148
 A:Status: Preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1200 <ORU>
 A:Cross-references: EMBL:U34750; NID:91304393; PID:91335805; PIDN:AA01087.1
 C:Superfamily: leukocyte common antigen; leukocyte common antigen cytosolic domain ho
 C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphat

Query Match 100.0%; Score 65; DB 2; Length 1200;
 Best Local Similarity 100.0%; Pred. No. 0.0033;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VVHCSAGVGRG 12
 Db 748 VVHCSAGVGRG 759

RESULT 15
 A54080
 N:protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta precursor - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 02-Aug-1994 #sequence_revision 02-Aug-1994 #text_change 21-Jan-2000
 C:Accession: A54080; I50592
 R:Fang, K.S.; Barker, K.; Sudol, M.; Hanafusa, H.
 J. Biol. Chem. 269: 14056-14063, 1994
 A:Title: A transmembrane protein-tyrosine phosphatase contains spectrin-like repeats
 A:Reference number: A54080; MUID:94245724; PMID:8188686
 A:Accession: A54080
 A:Status: Preliminary

A:Molecule type: mRNA
 A:Residues: 1-1237 <PAN>
 A:Cross-references: EMBL:Z21960; NID:9510510; PID:CAA79972.1; PID:9510511; GB:L13285
 C:Superfamily: leukocyte common antigen; leukocyte common antigen cytosolic domain homol
 C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatas
 F:528-1170/Domain: leukocyte common antigen cytosolic domain homology <LAC>
 F:610-834/Domain: protein-tyrosine-phosphatase homology <PTP>
 F:786/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:792/Binding site: substrate phosphate (Arg) #status predicted

Query Match 100.0%; Score 65; DB 2; Length 1237;
 Best Local Similarity 100.0%; Pred. No. 0.0034;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVHCSAGVGRGTG 12
 |||||
 Db 783 VVHCSAGVGRGTG 794

Search completed: January 17, 2003, 09:12:21
 Job time : 17 secs

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OM protein - protein search, using sw model

Run on: January 17, 2003, 09:10:56 ; Search time 10 Seconds
(without alignments)
49.772 Million cell updates/sec

Title: US-09-743-492-4
Perfect score: 65
Sequence: 1 VVHCSAGVGRGTG 12

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40 :
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	65	100.0	PTPE_MOUSE	P49446 mus musculu
2	65	100.0	PTPE_HUMAN	P23469 homo sapien
3	65	100.0	PTRA_RAT	Q03348 rattus norv
4	65	100.0	PTRA_HUMAN	P18433 homo sapien
5	65	100.0	PTRA_MOUSE	P18052 mus musculu
6	65	100.0	CD45_MOUSE	P06800 mus musculu
7	65	100.0	PTNE_MOUSE	Q15678 homo sapien
8	65	100.0	PTNE_HUMAN	Q62130 mus musculu
9	65	100.0	CD45_MOUSE	P04157 rattus norv
10	65	100.0	CD45_RAT	P35832 dtrosophila
11	65	100.0	PTP9_DROME	P08575 homo sapien
12	65	100.0	CD45_HUMAN	Q08936 gallus gall
13	65	100.0	PTPG_CHICK	P10566 homo sapien
14	65	100.0	PTPD_HUMAN	P23468 homo sapien
15	65	100.0	PTPD_MOUSE	P23467 homo sapien
16	65	100.0	PTPB_HUMAN	P23471 homo sapien
17	65	100.0	PTPB_MOUSE	Q02636 rattus norv
18	65	100.0	PTP2_RAT	P25044 saccharomyc
19	65	98.5	PTP1_YEAST	P49445 rattus norv
20	64	98.5	PTN7_RAT	P35236 homo sapien
21	64	98.5	PTN7_HUMAN	P41337 dictyostell
22	64	98.5	PTN1_DICDI	P27524 schizosacch
23	64	98.5	PTN1_SCHPO	P35235 mus musculu
24	64	98.5	PTN2_MOUSE	P43338 mus musculu
25	64	98.5	PTN3_MOUSE	Q06124 homo sapien
26	64	98.5	PTN3_HUMAN	P29074 rattus norv
27	64	98.5	PTN4_HUMAN	P28191 caenorhabdi
28	64	98.5	PTN4_MOUSE	P16621 dtrosophila
29	64	98.5	PTN5_HUMAN	P35234 rattus norv
30	63	96.9	PTN5_MOUSE	P44829 homo sapien
31	63	96.9	PTN5_RAT	P24830 mus musculu
32	63	96.9	PTN5_HUMAN	P29350 homo sapien
33	63	96.9	PTN5_MOUSE	

34	63	96.9	595	1	PTN6_MOUSE	P29351 mus musculu
35	62	95.4	1174	1	PTNL_HUMAN	Q16825 homo sapien
36	62	95.4	1175	1	PTNL_RAT	Q62728 rattus norv
37	62	95.4	1176	1	PTNL_MOUSE	Q62136 mus musculu
38	62	95.4	1238	1	PTPJ_MOUSE	Q64455 mus musculu
39	62	95.4	1337	1	PTPJ_HUMAN	Q12913 homo sapien
40	62	95.4	1442	1	PTPG_MOUSE	Q05909 mus musculu
41	62	95.4	1445	1	PTPG_HUMAN	P23470 homo sapien
42	62	95.4	1462	1	PTP6_DROME	P16620 dtrosophila
43	62	95.4	1705	1	PTP6_MOUSE	P70289 mus musculu
44	62	95.4	1711	1	PTP6_RAT	Q64612 rattus norv
45	61	93.8	711	1	PYP2_SCHPO	P32586 schizosacch

ALIGNMENTS

```

RESULT 1
PTPE_MOUSE
ID PTPE_MOUSE STANDARD: PRT: 699 AA.
AC P49446; Q62134; Q62444; Q64496;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Protein-tyrosine phosphatase epsilon precursor (EC 3.1.3.48) (R-PTP-
epsilon).
GN PTPE OR PTPE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
STRAIN=FVB/N;
MEDLINE=96064677; PubMed=7592814;
RA Elson A., Leder P.;
RT "Protein-tyrosine phosphatase epsilon. An isoform specifically
expressed in mouse mammary tumors initiated by v-Ha-ras OR neu.";
RL J. Biol. Chem. 270:26116-26122(1995).
[2]
SEQUENCE FROM N.A.
STRAIN=DBA/2;
Mukoyama Y.;
Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
[3]
SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain, and lung;
Hou E.W., Li S.L.;
Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
[4]
SEQUENCE OF 224-332 FROM N.A.
STRAIN=BALB/c; TISSUE=Brain;
MEDLINE=93086603; PubMed=1454056;
Schepens J., Zeeuwen P., Wieringa B.;
RT "Identification and typing of members of the protein-tyrosine
phosphatase gene family expressed in mouse brain.";
Mol. Biol. Rep. 16:241-248(1992).
[5]
SEQUENCE OF 224-332 FROM N.A.
STRAIN=BALB/c; TISSUE=Brain;
MEDLINE=95134232; PubMed=7832766;
Hendriks W., Schepens J., Brugman C., Zeeuwen P., Wieringa B.;
RT "A novel receptor-type protein tyrosine phosphatase with a single
catalytic domain is specifically expressed in mouse brain.";
Biochem. J. 305:499-504(1995).
-1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
tyrosine + phosphate.
-1- SUBCELLULAR LOCATION: Type I membrane protein.
-1- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.
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CC -----
DR EMBL: U35368; AAC52281.1; -
DR EMBL: D83484; BAA11927.1; -
DR EMBL: U62387; AAB04553.1; -
DR EMBL: Z23052; CAA80587.1; -
DR EMBL: Z23053; CAA80588.1; -
DR HSSP: P18052; 1YFO.
DR MGD: MGI:97813; PTPRE.
DR InterPro: IPR000387; TYR_phosphatase.
DR Pfam: PF00102; Y_phosphatase; 2.
DR SMART: SM00194; PTPC; 2.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 2.
DR Glycoprotein: Transmembrane; Hydrolase; Phosphorylation; Repeat;
KW Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 699 PROTEIN-TYROSINE PHOSPHATASE EPSILON.
FT TRANSMEM 20 45 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 46 68 POTENTIAL.
FT DOMAIN 69 699 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 153 392 PROTEIN-TYROSINE PHOSPHATASE 1.
FT DOMAIN 393 699 PROTEIN-TYROSINE PHOSPHATASE 2.
FT ACT_SITE 334 334 BY SIMILARITY.
FT ACT_SITE 629 629 BY SIMILARITY.
FT CARBOHYD 23 23 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 31 31 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 500 500 G -> A (IN REF. 2).
FT CONFLICT 506 506 G -> V (IN REF. 2).
FT CONFLICT 521 522 IV -> ML (IN REF. 1).
FT CONFLICT 606 606 IV -> I (IN REF. 1).
SQ SEQUENCE 699 AA; 80645 MW; 4D04467438017FEB CRC64;

Query Match 100.0%; Score 65; DB 1; Length 699;
Best Local Similarity 100.0%; Pred. No. 0.00063;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVHCSAGVGRGT 12
   |||||||
Db 331 VVHCSAGVGRGT 342

RESULT 2
PTPE_HUMAN
ID PTPE_HUMAN STANDARD; PRT; 700 AA.
AC P23469;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Protein-tyrosine phosphatase epsilon precursor (EC 3.1.3.48) (R-PTP-
DE epsilon).
GN PTPRE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=91006018; PubMed=2170109;
RA Krueger N.X., Streuli M., Saito H.;
RA "Structural diversity and evolution of human receptor-like protein
RT tyrosine phosphatases.";
RL EMBL J. 9:3241-3252(1990).
CC -I- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
```

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CC -I- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X54134; CAA38069.1; -
DR PIR: S12053; S12053.
DR HSSP: P18052; 1YFO.
DR Genew: HGNC:9669; PTPRE.
DR MIM: 600926; -
DR InterPro: IPR000387; TYR_phosphatase.
DR InterPro: IPR000242; TYR_PP.
DR Pfam: PF00102; Y_phosphatase; 2.
DR PRINTS: PR00700; PRTYPHTASE.
DR SMART: SM00194; PTPC; 2.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 2.
DR Glycoprotein: Transmembrane; Hydrolase; Phosphorylation; Repeat;
KW Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 700 PROTEIN-TYROSINE PHOSPHATASE EPSILON.
FT TRANSMEM 20 46 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 47 69 POTENTIAL.
FT DOMAIN 70 700 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 154 393 PROTEIN-TYROSINE PHOSPHATASE 1.
FT DOMAIN 394 700 PROTEIN-TYROSINE PHOSPHATASE 2.
FT ACT_SITE 335 335 BY SIMILARITY.
FT ACT_SITE 630 630 BY SIMILARITY.
FT CARBOHYD 23 23 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 30 30 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 700 AA; 80641 MW; D096BCADCEA65708 CRC64;

Query Match 100.0%; Score 65; DB 1; Length 700;
Best Local Similarity 100.0%; Pred. No. 0.00063;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVHCSAGVGRGT 12
   |||||||
Db 332 VVHCSAGVGRGT 343

RESULT 3
PTPE_RAT
ID PTPE_RAT STANDARD; PRT; 796 AA.
AC O03348;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Protein-tyrosine phosphatase alpha precursor (EC 3.1.3.48) (R-PTP-
DE alpha).
GN pTPRA OR LRP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=93038682; PubMed=1417854;
RA Moriyama T., Fujiwara Y., Imai E., Takenaka M., Kawanishi S.,
RA "DNA cloning of rat LRP, a receptor like protein tyrosine
RT phosphatase, and evidence for its gene regulation in cultured rat
RT mesangial cells.";
RL Biochem. Biophys. Res. Commun. 188:34-39(1992).
CC -I- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
```

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.
 CC -----
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 CC -----
 DR EMBL: L01702; AAA1983.1; -
 DR HSSP: P18052; 1YFO.
 DR InterPro: IPR000387; TYR_phosphatase.
 DR InterPro: IPR000242; TYR_PP.
 DR Pfam: PF00102; Y_phosphatase; 2.
 DR PRINTS: PR00700; PRTYPHPTASE.
 DR SMART: SM00194; PTPc; 2.
 DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 2.
 DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 2.
 DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 2.
 KW Glycoprotein; Transmembrane; Hydrolase; Phosphorylation; Repeat;
 KW Signal.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 796 PROTEIN-TYROSINE PHOSPHATASE ALPHA.
 FT DOMAIN 20 145 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 146 169 POTENTIAL.
 FT DOMAIN 170 796 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 234 494 PROTEIN-TYROSINE PHOSPHATASE 1.
 FT DOMAIN 495 796 PROTEIN-TYROSINE PHOSPHATASE 2.
 FT ACT_SITE 436 436 BY SIMILARITY.
 FT ACT_SITE 726 726 BY SIMILARITY.
 FT CARBOHYD 20 20 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 21 21 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 47 47 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 51 51 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 80 80 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 104 104 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 127 127 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 796 AA; 90260 MW; 4793796191056920 CRC64;
 Query Match 100.0%; Score 65; DB 1; Length 796;
 Best Local Similarity 100.0%; Pred. NO. 0.00071;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VVHCSAGVGRGTG 12
 DB 433 VVHCSAGVGRGTG 444
 RESULT 4
 PTRA_HUMAN STANDARD; PRT; 802 AA.
 ID PTRA_HUMAN
 AC P18433; O14513;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Protein-tyrosine phosphatase alpha precursor (EC 3.1.3.48) (R-PTP-
 DE alpha).
 GN PTPRA OR PTPA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90349565; PubMed=2166945;
 RA Sap J., D'Eustachio P., Givol D., Schlessinger J.,
 RT "Cloning and expression of a widely expressed receptor tyrosine
 RT phosphatase.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:6112-6116(1990).

RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90384936; PubMed=2169617;
 RA Kaplan R., Morse B., Huebner K., Croce C., Howk R., Ravera M.,
 RA Ricca G., Jaye M., Schlessinger J.,
 RT "Cloning of three human tyrosine phosphatases reveals a multigene
 RT family of receptor-linked protein-tyrosine-phosphatases expressed in
 RT brain.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:7000-7004(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91006018; PubMed=2170109;
 RA Krueger N.X., Streuli M., Saito H.,
 RT "Structural diversity and evolution of human receptor-like protein
 RT tyrosine phosphatases.";
 RL EMBO J. 9:3241-3252(1990).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=91088320; PubMed=2175890;
 RA Ohagi S., Nishi M., Steiner D.F.,
 RT "Sequence of a cDNA encoding human LRP (leukocyte common antigen-
 RT related peptide).";
 RL Nucleic Acids Res. 18:7159-7159(1990).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91032191; PubMed=2172030;
 RA Jirik F.R., Janzen N.M., Melhado I.G., Harder K.W.,
 RT "Cloning and chromosomal assignment of a widely expressed human
 RT receptor-like protein-tyrosine phosphatase.";
 RL FEBS Lett. 273:239-242(1990).
 RN [6]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21638749; PubMed=11780052;
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavriles G., Almeida J.P., Babbage A.K., Bagquley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Bead L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Cordy N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Hunt E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights K., Laird G.K., Lawlor S.,
 RA Leharvasialho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConachie L.J., McLeay K., McMurray A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.,
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871(2001).
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
 CC tyrosine + phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.
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DR EMBL: M34668; AAA36528.1; -
DR EMBL: X54130; CAA38065.1; -
DR EMBL: X54890; CAA38662.1; -
DR EMBL: X53364; CAA37447.1; -
DR EMBL: AL121905; CAC10337.1; -
DR PIR: A36065; A36065.
DR PIR: S12049; S12049.
DR HSSP: P18052; 1YFO.
DR Genew: HGNC:9664; PTPRA.
DR MIM: 176884; -
DR InterPro: IPR000387; TYR_phosphatase.
DR InterPro: IPR000242; TYR_PP.
DR Pfam: PF00102; Y_phosphatase_2.
DR PRINTS: PR00700; PRYPPHTASE.
DR SMART: SM00194; PTPC; 2.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 2.
DR Glycoprotein: Transmembrane; Hydrolyase; Phosphorylation; Signal;
KW Repeat; Alternative splicing.
FT SIGNAL 1 19
FT CHAIN 20 802
FT DOMAIN 20 142
FT TRANSMEM 143 165
FT DOMAIN 166 802
FT DOMAIN 241 500
FT DOMAIN 501 802
FT ACT_SITE 442 442
FT ACT_SITE 732 732
FT CARBOHYD 21 21
FT CARBOHYD 36 36
FT CARBOHYD 68 68
FT CARBOHYD 80 80
FT CARBOHYD 86 86
FT CARBOHYD 104 104
FT CARBOHYD 124 124
FT VARSPIC 139 147
FT CONFLICT 114 114
FT CONFLICT 122 122
FT CONFLICT 138 138
FT CONFLICT 179 187
FT CONFLICT 289 289
FT CONFLICT 367 367
FT CONFLICT 493 493
FT CONFLICT 786 786
SQ SEQUENCE 802 AA; 90599 MW; 8E964C3B56B32 CRC64;

Query Match 100.0%; Score 65; DB 1; Length 802;
Best Local Similarity 100.0%; Pred. No. 0.00072;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVHCSAGVGRG 12
Db 439 VVHCSAGVGRG 450

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RESULT 5
PTRA.MOUSE STANDARD; PRT; 829 AA.
AC P18052; 061808;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Protein-tyrosine phosphatase alpha precursor (EC 3.1.3.48) (R-PTP-
DE alpha) (LCA-related phosphatase).
GN PTPRA OR LRP OR PTPA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.

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RC STRAIN-G57BL/6 X DBA/2;
RA MEDLINE=90280391; PubMed=2162042;
RX Matthews R.J., Cahir E.D., Thomas M.L.;
RT "Identification of an additional member of the protein-tyrosine-
RT phosphatase family: evidence for alternative splicing in the tyrosine
RT phosphatase domain."
RT Proc. Natl. Acad. Sci. U.S.A. 87:4444-4448(1990).
RN [2]
RP SEQUENCE OF 358-467 FROM N.A.
RC STRAIN-BALB/c; TISSUE=Brain;
RX MEDLINE=95134232; PubMed=7837266;
RA Hendriks W., Schepens J., Brugman C., Zeeuwen P., Wieringa B.;
RT "A novel receptor-type protein tyrosine phosphatase with a single
RT catalytic domain is specifically expressed in mouse brain."
RT Biochem. J. 305:499-504(1995).
RN [3]
RP SEQUENCE OF 651-756 FROM N.A.
RC STRAIN-BALB/c; TISSUE=Brain;
RX MEDLINE=93086603; PubMed=1454056;
RA Schepens J., Zeeuwen P., Wieringa B., Hendriks W.;
RT "Identification and typing of members of the protein-tyrosine
RT phosphatase gene family expressed in mouse brain."
RT Mol. Biol. Rep. 16:241-248(1992).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 202-503.
RX MEDLINE=96320562; PubMed=8700232;
RA Bilwes A.M., den Hertog J., Hunter T., Noel J.P.;
RT "Structural basis for inhibition of receptor protein-tyrosine
RT phosphatase-alpha by dimerization."
RT Nature 382:555-559(1996).
RL -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
RL tyrosine + phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM (SHOWN HERE) AND
CC A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED.
CC -1- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.
CC -----
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CC -----
DR EMBL: M36033; AAA39448.1; -
DR EMBL: M36034; AAA39449.2; -
DR EMBL: Z23054; CAA80589.1; -
DR EMBL: Z23055; CAA80590.1; -
DR PIR: A35501; A35501.
DR PIR: B35501; B35501.
DR PDB: 1YFO; 01-APR-97.
DR MGD; MGI:97808; Ptptra.
DR InterPro: IPR000387; TYR_phosphatase.
DR InterPro: IPR000242; TYR_PP.
DR Pfam: PF00102; Y_phosphatase_2.
DR PRINTS: PR00700; PRYPPHTASE.
DR SMART: SM00194; PTPC; 2.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 2.
KW Glycoprotein; Transmembrane; Hydrolyase; Phosphorylation; Signal;
KW Repeat; Alternative splicing; 3D-structure.
FT SIGNAL 1 19
FT CHAIN 20 829
FT DOMAIN 20 142
FT TRANSMEM 143 166
FT DOMAIN 167 829
FT DOMAIN 232 527
FT DOMAIN 528 829
FT ACT_SITE 469 469
FT ACT_SITE 759 759

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CC FT CARBOHYD 21 21 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 47 47 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 51 51 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 80 80 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 104 104 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 124 124 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT VASAPLIC 268 303 MISSING (IN SHORT ISOFORM).
CC SQ SEQUENCE 829 AA; 93697 MW; 7B1E335D4CCEB09B CRC64;

Query Match 100.0%; Score 65; DB 1; Length 829;
Best Local Similarity 100.0%; Pred. No. 0.00074;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VVHCSAGVGRG 12
Db 466 VVHCSAGVGRG 477

RESULT 6
CD45_MOUSE STANDARD; PRT; 1152 AA.
ID CD45_MOUSE
AC P06800;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Leukocyte common antigen precursor (EC 3.1.3.48) (L-CA) (Lymphocyte
DE common antigen Ly-5) (CD45) (T200).
DE PTPRC OR LY-5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
OX [1]
RX SEQUENCE FROM N.A.
RX MEDLINE=66313686; PubMed=2944116;
RA Saga Y., Tung J.-S., Shen F.-W., Boyse E.A.;
RT "Sequences of Ly-5 cDNA: Isoform-related diversity of Ly-5 mRNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:6940-6944(1986).
RN [2]
RP REVISIONS.
RA Saga Y., Tung J.-S., Shen F.-W., Boyse E.A.;
RL Proc. Natl. Acad. Sci. U.S.A. 84:1991-1991(1987).
RN [3]
RP SEQUENCE OF 10-124 FROM N.A.
RC TISSUE=T-cell;
RX MEDLINE=66042665; PubMed=3864163;
RA Shen F.-W., Saga Y., Litman G., Freeman G., Tung J.-S., Cantor H.,
RA Boyse E.A.;
RT "Cloning of Ly-5 cDNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:7360-7363(1985).
RN [4]
RP SEQUENCE OF 822-1152 FROM N.A.
RX MEDLINE=67092355; PubMed=2948186;
RA Raschke W.C.;
RT "Cloned murine T200 (Ly-5) cDNA reveals multiple transcripts within
RT B- and T-lymphocyte lineages.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:161-165(1987).
CC -1- FUNCTION: REQUIRED FOR T-CELLS ACTIVATION THROUGH THE ANTIGEN
CC RECEPTOR. THE FIRST PTPASE DOMAIN HAS ENZYMTIC ACTIVITY, WHILE
CC THE SECOND ONE SEEMS TO AFFECT THE SUBSTRATE SPECIFICITY OF THE
CC FIRST ONE.
CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
CC tyrosine + phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: A NUMBER OF ISOFORMS ARE PRODUCED BY
CC ALTERNATIVE SPLICING.
CC -1- DEVELOPMENTAL STAGE: EXPRESSION IS RESTRICTED TO THE HEMATOPOIETIC
CC COMPARTMENT OF DEVELOPMENT.
CC -1- PIM: HEAVILY N- AND O-GLYCOSYLATED.
CC -1- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.

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CC -----
CC DR EMBL; M14342; AAA39458.1; -
CC DR EMBL; M11934; AAA39461.1; -
CC DR EMBL; M15174; AAA40161.1; -
CC DR PIR; A29381; A29381.
CC DR HSSP; P18052; LYPO.
CC DR MGD; MGI:97810; Ptpc.
CC DR InterPro; IPR003961; FM_III.
CC DR InterPro; IPR000387; TYR_PHSphatase.
CC DR InterPro; IPR000242; Tyr_pp.
CC DR Pfam; PF00041; fn3; 3.
CC DR Pfam; PF00102; Y_phosphatase; 2.
CC DR PRINTS; PR00700; PRTYPHSASE.
CC DR SMART; SM00194; PTPc; 2.
CC DR PROSITE; PS00383; TYR_PHSPHATASE_1; 2.
CC DR PROSITE; PS50056; TYR_PHSPHATASE_2; 2.
CC DR PROSITE; PS50055; TYR_PHSPHATASE_PTP; 2.
CC KW Glycoprotein; Transmembrane; Phosphorylation; B-cell; T-cell; Repeat;
CC Alternative splicing; Hydrolase; Signal.
CC FT SIGNAL 1 23
CC FT CHAIN 24 1152 LEUCOCYTE COMMON ANTIGEN.
CC FT DOMAIN 24 425 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 426 447 POTENTIAL.
CC FT DOMAIN 448 1152 CYTOPLASMIC (POTENTIAL).
CC FT DOMAIN 233 329 FIBRONECTIN TYPE-III 1.
CC FT DOMAIN 330 421 FIBRONECTIN TYPE-III 2.
CC FT DOMAIN 520 769 PROTEIN-TYROSINE PHOSPHATASE 1.
CC FT DOMAIN 811 1084 PROTEIN-TYROSINE PHOSPHATASE 2.
CC FT ACT_SITE 701 701 BY SIMILARITY.
CC FT ACT_SITE 1016 1016 BY SIMILARITY.
CC FT CARBOHYD 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 79 79 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 208 208 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 288 288 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 318 318 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 379 379 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SQ SEQUENCE 1152 AA; 130421 MW; BAD956B4E32EA812 CRC64;

Query Match 100.0%; Score 65; DB 1; Length 1152;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VVHCSAGVGRG 12
Db 698 VVHCSAGVGRG 709

RESULT 7
PTNE_HUMAN STANDARD; PRT; 1187 AA.
ID PTNE_HUMAN
AC Q15678;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein tyrosine phosphatase, non-receptor type 14 (EC 3.1.3.48)
DE (Protein-tyrosine phosphatase pez).
CC GN PTN14 OR PEZ.

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Breast carcinoma;
RX MEDLINE=95251727; Pubmed=7733990;
RA Smith A.L., Mitchell P.J., Shipley J., Gusterson B.A., Rogers M.V.,
RT Crompton M.R.;
RT "Pez: a novel human cDNA encoding protein tyrosine phosphatase- and
RT ezrin-like domains.";
RU Biochem. Biophys. Res. Commun. 209:959-965(1995).
CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
CC tyrosine + phosphate.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF HUMAN TISSUES
CC INCLUDING KIDNEY, SKELETAL MUSCLE, LUNG AND PLACENTA.
CC -1- SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC TYROSINE PHOSPHATASE FAMILY.
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DR EMBL: X82676; CAA57993.1;
DR HSSP: P28350; 1GMZ.
DR Genew: HGNC:9647; PTPN14.
DR DR MIM: 603155;
DR DR InterPro: IPR000299; Band_4.1.
DR DR InterPro: IPR000387; TYR_P.
DR DR InterPro: IPR000242; TYR_PP.
DR DR Pfam: PF00102; Y-phosphatase; 1.
DR DR Pfam: PF00373; Band_4.1; 1.
DR DR PRINTS: PR00935; BAND4.1.
DR DR PRINTS: PR00700; PRTYPHPTASE.
DR DR SMART: SM00295; B41; 1.
DR DR SMART: SM00194; PTPC; 1.
DR DR PROSITE: PS00660; BAND_4.1; 1.
DR DR PROSITE: PS00661; BAND_4.1; 1.
DR DR PROSITE: PS50057; BAND_4.1; 1.
DR DR PROSITE: PS50057; TYR_PHOSPHATASE_1; 1.
DR DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 1.
DR DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
DR DR Structural protein; Cytoskeleton; Hydrolyase.
KW Structural protein; Cytoskeleton; Hydrolyase.
FT DOMAIN 75 239 BAND 4.1-LIKE.
FT DOMAIN 933 1187 PROTEIN-TYROSINE PHOSPHATASE.
FT ACT_SITE 1121 1121 BY SIMILARITY.
FT DOMAIN 566 573 POLY-PRO.
FT DOMAIN 709 716 POLY-GLU.
FT DOMAIN 712 718 POLY-GLU.
SQ SEQUENCE 1187 AA; 135239 MW; 015760B75E3574E3 CRC64;

Query Match 100.0%; Score 65; DB 1; Length 1187;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVHCSAGVGRG 12
Db 1118 VVHCSAGVGRG 1129

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DE (Protein-tyrosine phosphatase ptp36).
GN PTPN14.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CB-17-SCID; TISSUE=Thymus;
RX MEDLINE=94354845; Pubmed=8074693;
RA Sawada M., Ogata M., Fujino Y., Hamaoka T.;
RT "cDNA cloning of a novel protein tyrosine phosphatase with homology
RT to cytoskeletal protein 4.1 and its expression in T-lineage cells.";
RU Biochem. Biophys. Res. Commun. 203:479-484(1994).
CC -1- FUNCTION: MAY BE INVOLVED IN THE REGULATION OF T CELL DEVELOPMENT.
CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
CC tyrosine + phosphate.
CC -1- TISSUE SPECIFICITY: THYMUS; IN CELLS OF BOTH HEMATOPOIETIC AND
CC NON-HEMATOPOIETIC ORIGINS.
CC -1- SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC TYROSINE PHOSPHATASE FAMILY.
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DR EMBL: D31842; BAA06628.1;
DR HSSP: O06124; ZSHP.
DR DR MGD: MGI:102467; Ptpn14.
DR DR InterPro: IPR000299; Band_4.1.
DR DR InterPro: IPR000387; TYR_P.
DR DR InterPro: IPR000242; TYR_PP.
DR DR Pfam: PF00102; Y-phosphatase; 1.
DR DR Pfam: PF00373; Band_4.1; 1.
DR DR PRINTS: PR00935; BAND4.1.
DR DR PRINTS: PR00700; PRTYPHPTASE.
DR DR SMART: SM00295; B41; 1.
DR DR SMART: SM00194; PTPC; 1.
DR DR PROSITE: PS00660; BAND_4.1; 1.
DR DR PROSITE: PS00661; BAND_4.1; 1.
DR DR PROSITE: PS50057; BAND_4.1; 1.
DR DR PROSITE: PS50057; TYR_PHOSPHATASE_1; 1.
DR DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 1.
DR DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
DR DR Structural protein; Cytoskeleton; Hydrolyase.
KW Structural protein; Cytoskeleton; Hydrolyase.
FT DOMAIN 75 239 BAND 4.1-LIKE.
FT DOMAIN 935 1189 PROTEIN-TYROSINE PHOSPHATASE.
FT ACT_SITE 1123 1123 BY SIMILARITY.
FT DOMAIN 566 573 POLY-PRO.
FT DOMAIN 635 639 POLY-GLY.
FT DOMAIN 712 718 POLY-GLU.
SQ SEQUENCE 1189 AA; 135030 MW; 2B85BE5F9C723303 CRC64;

Query Match 100.0%; Score 65; DB 1; Length 1189;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVHCSAGVGRG 12
Db 1120 VVHCSAGVGRG 1131

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RESULT 8
ID PTNE_MOUSE STANDARD; PRT; 1189 AA.
AC 062130;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein tyrosine phosphatase, non-receptor type 14 (EC 3.1.3.48)

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RESULT 9
ID CD45_RAT STANDARD; PRT; 1255 AA.
AC P04157;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1988 (Rel. 08, Last sequence update)

```

DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Leukocyte common antigen variant 4 precursor (EC 3.1.3.48) (L-CA)
 DE (CD45) (Fragment).
 GN PPRC.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Barclay A.N., Jackson D.I., Willis A.C., Williams A.F.;
 RL Submitted (May-1987) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE OF 190-1255 FROM N.A.
 RA MEDLINE=85201691; PubMed=3158393;
 RA Thomas M.L., Barclay A.N., Gagnon J., Williams A.F.;
 RT "Evidence from cDNA clones that the rat leukocyte-common antigen
 RT (T200) spans the lipid bilayer and contains a cytoplasmic domain of
 RT 80,000 Mr.";
 RL Cell 41:83-93(1985).
 RN [3]
 RP ALTERNATIVE SPLICING.
 RX MEDLINE=87275817; PubMed=2440674;
 RA Barclay A.N., Jackson D.I., Willis A.C., Williams A.F.;
 RT "Lymphocyte specific heterogeneity in the rat leukocyte common
 RT antigen (T200) is due to differences in polypeptide sequences near
 RT the NH2-terminus".
 RL EMBL J. 6:1259-1264(1987).
 CC -1- FUNCTION: REQUIRED FOR T-CELLS ACTIVATION THROUGH THE ANTIGEN
 CC RECEPTOR. THE FIRST PTASE DOMAIN HAS ENZYMAIC ACTIVITY, WHILE
 CC THE SECOND ONE SEEMS TO AFFECT THE SUBSTRATE SPECIFICITY OF THE
 CC FIRST ONE.
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
 CC tyrosine + phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: A number of isoforms are produced by
 CC alternative splicing.
 CC -1- TISSUE SPECIFICITY: VARIANTS 4 AND 3 ARE FOUND IN THE LYMPH NODE,
 CC VARIANTS 1 AND 2 ARE FOUND IN THYMOCYTE AND LYMPH NODE.
 CC -1- PTM: HEAVILY N- AND O-GLYCOSYLATED.
 CC -1- PTM: THE CYTOPLASMIC DOMAIN CONTAINS POTENTIAL PHOSPHORYLATION
 CC SITES.
 CC -1- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
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 CC
 CC EMBL: Y00065; CA68272.1; -
 CC EMBL: Y00065; CA68273.1; -
 CC EMBL: Y00065; CA68274.1; -
 CC EMBL: Y00065; CA68275.1; -
 CC EMBL: M25820; AAA41518.1; -
 CC EMBL: M25821; AAA41519.1; -
 CC EMBL: M25822; AAA41520.1; -
 CC EMBL: M25823; AAA41521.1; -
 CC PIR: A60241; TDRTLT.
 CC HSSP: P18052; TYRO.
 CC InterPro: IPR003961; FN_III.
 CC InterPro: IPR000387; Tyr_P Kinase.
 CC InterPro: IPR000242; Tyr_PP.
 CC Pfam: PF00041; fn3; 2.
 CC Pfam: PF00102; Y_phosphatase; 2.
 CC SMART: SM00060; FN3; 2.
 CC SMART: SM00194; PTPc; 2.
 CC PROSITE: PS00383; TYR_PHOSPHATASE_1; 2.
 CC PROSITE: PS50056; TYR_PHOSPHATASE_2; 2.
 CC PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 2.

KW glycoprotein; Transmembrane; Phosphorylation; B-cell; T-cell; Repeat;
 KW Alternative splicing; Hydrolase; Signal.
 FT STGNAL 1 1
 FT NON_TER 1 5
 FT CHAIN 1 1255
 FT DOMAIN 6 528
 FT TRANSMEM 529 550
 FT DOMAIN 551 1255
 FT DOMAIN 341 432
 FT DOMAIN 433 524
 FT DOMAIN 623 872
 FT ACT_SITE 914 1187
 FT ACT_SITE 804 804
 FT CARBOHYD 1119 1119
 FT CARBOHYD 44 44
 FT CARBOHYD 124 124
 FT CARBOHYD 135 135
 FT CARBOHYD 146 146
 FT CARBOHYD 160 160
 FT CARBOHYD 182 182
 FT CARBOHYD 227 227
 FT CARBOHYD 232 232
 FT CARBOHYD 253 253
 FT CARBOHYD 264 264
 FT CARBOHYD 309 309
 FT CARBOHYD 315 315
 FT CARBOHYD 353 353
 FT CARBOHYD 356 356
 FT CARBOHYD 453 453
 FT CARBOHYD 484 484
 FT VARSPPLIC 12 53
 FT VARSPPLIC 12 102
 FT VARSPPLIC 53 143
 FT VARSPPLIC 103 143
 FT CONFLICT 38 38
 SQ SEQUENCE 1255 AA; 141208 MW; C257CBD2A355BCEA CRC64;
 Query Match 100.0%; Score 65; DB 1; Length 1255;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VVHCSAGVGRTG 12
 DB 801 VVHCSAGVGRTG 812
 RESULT 10
 ID PTP9_DROME STANDARD; PRT; 1301 AA.
 AC P35832;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Protein-tyrosine phosphatase 99A precursor (EC 3.1.3.48) (Receptor-
 DE linked protein-tyrosine phosphatase 99A).
 GN PTP99A.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 NC NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A. (LONG ISOFORM).
 RC TISSUE=Eye Imaginal disk;
 RX MEDLINE=92107930; PubMed=1662390;
 RA Hartharain I.K., Chuang P.-T., Rubin G.M.;
 RT "Cloning and characterization of a receptor-class phosphotyrosine
 RT phosphatase gene expressed on central nervous system axons in
 RT Drosophila melanogaster".
 RL Proc. Natl. Acad. Sci. U.S.A. 88:11266-11270(1991).
 RN [2]
 RP SEQUENCE FROM N.A. (SHORT ISOFORM).
 RC TISSUE=Embryo;

RA MEDLINE-92034989; PubMed-1657402;
 RA Tian S.-S., Tsoulfas P., Zinn K.;
 RT "Three receptor-linked protein-tyrosine phosphatases are selectively
 RT expressed on central nervous system axons in the Drosophila embryo.";
 RL Cell 67:675-685(1991).
 RN [3]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE-Embryo;
 RX MEDLINE-92034988; PubMed-1657401;
 RA Yang X., Seow K.T., Bahri S.M., Oon S.H., Chia W.;
 RT "Two Drosophila receptor-like tyrosine phosphatase genes are
 RT expressed in a subset of developing axons and pioneer neurons in the
 RT embryonic CNS.";
 RL Cell 67:661-673(1991).
 CC -1- FUNCTION: MAY PLAY A KEY ROLE IN SIGNAL TRANSDUCTION AND GROWTH
 CC CONTROL.
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
 CC tyrosine + phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; a long form (shown here) and a
 CC short form; are produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: SELECTIVELY EXPRESSED IN A SUBSET OF AXONS AND
 CC PIONEER NEURONS IN THE EMBRYO.
 CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.
 CC -----
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 DR EMBL: M81795; AAA28483.1; -
 DR EMBL: M80539; AAA28485.1; -
 DR EMBL: M80464; AAA28486.1; -
 DR PIR: A41622; A41622.
 DR PIR: A41214; A41214.
 DR PIR: B41214; B41214.
 DR PIR: B41215; B41215.
 DR HSP: P18052; IYFO.
 DR FlyBase: FBgn0004369; Ptp99A.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003962; FNIII_repeat.
 DR InterPro: IPR000387; Tyr_phosphatase.
 DR InterPro: IPR000242; Tyr_PP.
 DR Pfam: PF00041; f03; 2.
 DR Pfam: PF00102; Y-phosphatase; 2.
 DR PRINTS: PR00014; ENTPHITI.
 DR PRINTS: PR00700; PRTPHPTASE.
 DR SMART: SM00060; FN3; 2.
 DR SMART: SM00194; PTPc; 2.
 DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
 DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 2.
 DR Trnasembirane; Hydrolase; Repeat; Signal; Alternative splicing.
 KW SIGNAL
 FT CHAIN 1 29
 FT DOMAIN 30 1301
 FT TRANSMEM 30 394
 FT DOMAIN 395 415
 FT DOMAIN 416 1301
 FT DOMAIN 169 268
 FT DOMAIN 269 368
 FT DOMAIN 467 747
 FT DOMAIN 748 975
 FT ACT_SITE 682
 FT DOMAIN 1076 1091
 FT CARBOHYD 33 33
 FT CARBOHYD 176 176
 FT CARBOHYD 212 212
 FT CARBOHYD 278 278

FT CARBOHYD 322 322 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPPLIC 1050 1119 MISSING (IN SHORT ISOFORM).
 FT CONFLICT 586 586 P -> R (IN REF. 2 AND 3).
 FT CONFLICT 1205 1205 N -> H (IN REF. 3).
 SQ SEQUENCE 1301 AA: 145336 MW: 82413E19A4CA5BD CRC64;
 Query Match 100.0%; Score 65; DB 1; Length 1301;
 Best local Similarity 100.0%; Pred. No. 0.0011;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VVHCSAGVGRGTG 12
 Db 679 VVHCSAGVGRGTG 690
 RESULT 11
 CD45_HUMAN
 ID CD45_HUMAN STANDARD; PRT; 1304 AA.
 AC P08575;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Leukocyte common antigen precursor (EC 3.1.1.3.48) (L-CA) (CD45 antigen)
 DE (T200).
 GN PTPRC OR CD45.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI:Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Lymphocytes;
 RX MEDLINE-88061067; PubMed-2824653;
 RA Streuli M., Hall L.R., Saga Y., Schlossman S.F., Saito H.;
 RT "Differential usage of three exons generates at least five different
 RT mRNAs encoding human leukocyte common antigens.";
 RL J. Exp. Med. 166:1548-1566(1987).
 RN [2]
 RP FUNCTION.
 RX MEDLINE-89017162; PubMed-2845400;
 RA Charbonneau H., Tonks N.K., Walsh K.A., Fischer E.H.;
 RT "The leukocyte common antigen (CD45): a putative receptor-linked
 RT protein tyrosine phosphatase.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:7182-7186(1988).
 RN [3]
 RP MUTAGENESIS.
 RX MEDLINE-90316093; PubMed-1695146;
 RA Streuli M., Krueger N.X., Thal T., Tang M., Saito H.;
 RT "Distinct functional roles of the two intracellular phosphatase like
 RT domains of the receptor-linked protein tyrosine phosphatases LCA and
 RT LAR.";
 RL EMBO J. 9:2399-2407(1990).
 CC -1- FUNCTION: REQUIRED FOR T-CELLS ACTIVATION THROUGH THE ANTIGEN
 CC RECEPTOR. THE FIRST PTPASE DOMAIN HAS ENZYMAIC ACTIVITY, WHILE
 CC THE SECOND ONE SEEMS TO AFFECT THE SUBSTRATE SPECIFICITY OF THE
 CC FIRST ONE.
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
 CC tyrosine + phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 8 ISOFORMS ARE PRODUCED BY
 CC ALTERNATIVE SPLICING.
 CC -1- PTM: HEAVILY N- AND O-GLYCOSYLATED.
 CC -1- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD45 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd45.htm".
 CC -----
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CC -----

DR EMBL: Y00638; CA66669.1; -.

DR HSSP: P18052; 1YFO.

DR GlycoSuiteDB: P08575; -.

DR Genew: HGNC:9666; PTPRC.

DR MIM: 151460; -.

DR InterPro: IPR003961; FN_III.

DR InterPro: IPR000387; TYR_PP.

DR InterPro: IPR000242; TYR_PP.

DR Pfam: PF00041; fn3; 2.

DR Pfam: PF00102; Y-phosphatase; 2.

DR PRINTS: PR00700; PRTYPHPTASE.

DR SMART: SM00060; FN3; 2.

DR SMART: SM00194; PTPC; 2.

DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 2.

DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 2.

DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 2.

DR GlycoProtein: Transmembrane: Phosphorylation; B-cell; T-cell; Repeat; Alternative splicing; Hydrolase; Signal.

KM SIGNL 1 23

FT CHAIN 24 1304

FT DOMAIN 24 575

FT TRANSMEM 576 597

FT DOMAIN 598 1304

FT DOMAIN 387 479

FT DOMAIN 480 571

FT DOMAIN 670 919

FT DOMAIN 961 1235

FT ACT_SITE 851 851

FT ACT_SITE 1167 1167

FT CARBOHYD 78 78

FT CARBOHYD 90 90

FT CARBOHYD 95 95

FT CARBOHYD 184 184

FT CARBOHYD 190 190

FT CARBOHYD 197 197

FT CARBOHYD 232 232

FT CARBOHYD 260 260

FT CARBOHYD 270 270

FT CARBOHYD 276 276

FT CARBOHYD 335 335

FT CARBOHYD 378 378

FT CARBOHYD 419 419

FT CARBOHYD 468 468

FT CARBOHYD 488 488

FT CARBOHYD 529 529

FT MUTAGEN 851 851

SEQ 1304 AA; 147253 MW; 1F357BC5632618B2 CRC64;

Query Match 100.0%; Score 65; DB 1; Length 1304;

Best Local Similarity 100.0%; Pred. No. 0.0011;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVHCSAGVGRG 12

DB 848 VVHCSAGVGRG 859

RESULT 12

PTPG:CHICK

AC 098936;

DT 15-JUL-1999 (Rel. 38, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Protein-tyrosine phosphatase gamma precursor (EC 3.1.3.48) (R-PTP-gamma).

GN PTPRC.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

CC Gallus.

OX NCBI_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Kidney, and Brain;

RA Qinghua X., Xiaojun G., Cong S., Zong S.M., Jong Y.J., Chan J., Wang L.-H.;

RA Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.

RL -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase H(2)O = protein tyrosine + phosphate.

CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Probable).

CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE EUKARYOTIC-TYPE CARBONIC ANHYDRASE FAMILY.

CC -1- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.

CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.

CC -----

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CC -----

DR EMBL: U38349; AAB16910.1; -.

DR HSSP: P18052; 1YFO.

DR InterPro: IPR001148; Euk_COanhd.

DR InterPro: IPR003961; FN_III.

DR InterPro: IPR000387; TYR_phosphatase.

DR InterPro: IPR000242; TYR_PP.

DR Pfam: PF00041; fn3; 1.

DR Pfam: PF00102; Y-phosphatase; 2.

DR Pfam: PF00194; Carb_anhdase; 1.

DR PRINTS: PR00700; PRTYPHPTASE.

DR PRODOM: PD000865; Euk_COanhd; 1.

DR SMART: SM00060; FN3; 2.

DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.

DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 2.

DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 2.

DR GlycoProtein: Transmembrane; Hydrolase; Repeat; Signal.

FT CHAIN 1 19

FT DOMAIN 20 1422

FT TRANSMEM 20 742

FT DOMAIN 743 768

FT DOMAIN 769 1422

FT DOMAIN 56 322

FT DOMAIN 347 441

FT DOMAIN 846 1102

FT DOMAIN 1103 1422

FT ACT_SITE 1037 1037

FT SITE 1328 1328

FT CARBOHYD 109 109

FT CARBOHYD 113 113

FT CARBOHYD 156 156

FT CARBOHYD 359 359

FT CARBOHYD 444 444

FT CARBOHYD 620 620

FT CARBOHYD 632 632

FT CARBOHYD 640 640

FT CARBOHYD 728 728

SEQ 1422 AA; 159766 MW; DD48405593DA74F CRC64;

Query Match 100.0%; Score 65; DB 1; Length 1422;

Best Local Similarity 100.0%; Pred. No. 0.0012;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVHCSAGVGRG 12

DB 1034 VVHCSAGVGRG 1045

RESULT 13

PTPF_HUMAN STANDARD; PRT; 1897 AA.
 ID P10586;
 AC 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE LAR protein precursor (Leukocyte antigen related) (EC 3.1.3.48).
 GN PTPRF OR LAR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Tonsil;
 RA MEDLINE=89035978; PubMed=2972792;
 RA Streuli M., Krueger N.X., Hall L.R., Schlossman S.F., Saito H.;
 RT "A new member of the immunoglobulin superfamily that has a
 RT cytoplasmic region homologous to the leukocyte common antigen.";
 RL J. Exp. Med. 168:1523-1530(1988).
 RN [2]
 RP MUTAGENESIS.
 RA MEDLINE=90046860; PubMed=2554325;
 RA Streuli M., Krueger N.X., Tsai A.Y.M., Saito H.;
 RT "A family of receptor-linked protein tyrosine phosphatases in humans
 RT and Drosophila.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:8698-8702(1989).
 RN [3]
 RP MUTAGENESIS.
 RA MEDLINE=90316093; PubMed=1695146;
 RA Streuli M., Krueger N.X., Thai T., Tang M., Saito H.;
 RT "Distinct functional roles of the two intracellular phosphatase like
 RT domains of the receptor-linked protein tyrosine phosphatases LCA and
 RT LAR.";
 RL EMBO J. 9:2399-2407(1990).
 CC -1- FUNCTION: IT IS POSSIBLE THAT LAR IS A CELL ADHESION RECEPTOR.
 CC IT POSSESSES AN INTRINSIC PROTEIN TYROSINE PHOSPHATASE ACTIVITY
 CC (PTPASE).
 CC -1- FUNCTION: THE FIRST PTPASE DOMAIN HAS ENZYMAIC ACTIVITY, WHILE
 CC THE SECOND ONE SEEMS TO AFFECT THE SUBSTRATE SPECIFICITY OF THE
 CC FIRST ONE.
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
 CC tyrosine + phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 8 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: Y00815; CAA68754.1; -
 CC PIR: S03841; TDHULK.
 CC HSSP: P18052; IYPO.
 CC GeneW: HGNC:9670; PTPRF.
 CC MIM: 179590; -
 CC InterPro: IPR003961; FN_III.
 CC InterPro: IPR003962; FNIII_repeat.
 CC InterPro: IPR003006; Ig_MHC.
 CC InterPro: IPR003598; Ig_C2.
 CC InterPro: IPR000387; TYR_phosphatase.
 CC InterPro: IPR000242; Tyr_Pp.
 CC Pfam: PF00041; fn3; 7.
 CC Pfam: PF00047; Ig; 3.
 CC Pfam: PF00102; Y_phosphatase; 2.
 CC PRINTS: PR00014; FNTPYPTIII.
 CC PRINTS: PR00700; PTPYPTPHASE.
 CC SMART: SM00060; FN3; 5.

DR SMART: SM00408; IGC2; 3.
 DR SMART: SM00194; PTPC; 2.
 DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 2.
 DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 2.
 DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 2.
 KW Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane;
 KW Cell adhesion; Immunoglobulin domain; Repeat.
 FT SIGNAL 1
 FT CHAIN 16
 FT DOMAIN 17 1897
 FT TRANSMEM 17 1250
 FT TRANSMEM 1251 1274
 FT DOMAIN 1275 1897
 FT DOMAIN 1360 1606
 FT DOMAIN 1649 1897
 FT ACT_SITE 1538 1538
 FT ACT_SITE 1829 1829
 FT CARBOHYD 107 107
 FT CARBOHYD 240 240
 FT CARBOHYD 285 285
 FT CARBOHYD 711 711
 FT CARBOHYD 956 956
 FT MUTAGEN 1538 1538
 SQ SEQUENCE 1897 AA; 211844 MW; 439850F1D50C31EF CRC64;
 Query Match 100.0%; Score 65; DB 1; Length 1897;
 Best Local Similarity 100.0%; Pred. No. 0.0017;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VVHCSAGVGRGTG 12
 DB 1535 VVHCSAGVGRGTG 1546
 RESULT 14
 ID PTPD_HUMAN STANDARD; PRT; 1912 AA.
 AC P23468;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Protein-tyrosine phosphatase delta precursor (EC 3.1.3.48) (R-PTP-
 DE delta).
 GN PTPRD.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND MUTAGENESIS OF ARG-1178.
 RA MEDLINE=95204468; PubMed=7896816;
 RA Pulido R., Krueger N.X., Serra-Pages C., Saito H., Streuli M.;
 RT "Molecular characterization of the human transmembrane protein-
 RT tyrosine phosphatase delta. Evidence for tissue-specific expression of
 RT alternative human transmembrane protein-tyrosine phosphatase delta
 RT isoforms.";
 RL J. Biol. Chem. 270:6722-6728(1995).
 RN [2]
 RP SEQUENCE OF 390-1912 FROM N.A.
 RC TISSUE=Placenta;
 RA MEDLINE=91006018; PubMed=2170109;
 RA Krueger N.X., Streuli M., Saito H.;
 RT "Structural diversity and evolution of human receptor-like protein
 RT tyrosine phosphatases.";
 RL EMBO J. 9:3241-3252(1990).
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
 CC tyrosine + phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: A number of isoforms are produced by
 CC alternative splicing.
 CC -1- PTM: A CLEAVAGE OCCURS THAT SEPARATES THE EXTRACELLULAR DOMAIN
 CC FROM THE TRANSMEMBRANE SEGMENT.
 CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 8 FIBRONECTIN TYPE III-LIKE DOMAINS.

```

CC -1-SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L38929; AAC41749.1; -.
DR EMBL: X54133; CAA38068.1; -.
DR PIR: S12052; S12052.
DR HSSP: P18052; 1YFO.
DR Genew: HGNC:9665; PTPRD.
DR MIM: 601598; -.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003962; FNIII_repeat.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003598; Ig_C2.
DR InterPro: IPR000387; TYR_PP.
DR InterPro: IPR000242; TYR_PP.
DR Pfam: PF00047; fn3; 8.
DR Pfam: PF00102; Y_phosphatase; 2.
DR PRINTS: PR00014; ENTPEIII.
DR PRINTS: PR00700; PRTYPHPTASE.
DR SMART: SM00060; FN3; 8.
DR SMART: SM00194; IGC2; 3.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE: PS00383; TYR_PHOSPHATASE_2; 2.
DR PROSITE: PS50056; TYR_PHOSPHATASE_PP; 2.
DR PROSITE: PS50055; TYR_PHOSPHATASE_PP; 2.
DR Hydrolase: Receptor; Glycoprotein; Signal; Transmembrane; Repeat;
KW Immunoglobulin domain; Alternative splicing.
FT SIGNAL 1 20
FT CHAIN 21 1912
FT DOMAIN 21 1265
FT TRANSMEM 1266 1290
FT DOMAIN 1291 1912
FT DOMAIN 23 115
FT DOMAIN 118 225
FT DOMAIN 232 318
FT DOMAIN 320 414
FT DOMAIN 417 513
FT DOMAIN 516 606
FT DOMAIN 609 708
FT DOMAIN 711 822
FT DOMAIN 825 916
FT DOMAIN 918 1017
FT DOMAIN 1020 1137
FT DOMAIN 1375 1618
FT DOMAIN 1619 1912
FT ACT_SITE 1553 1553
FT ACT_SITE 1844 1844
FT SITE 1175 1178
FT CARBOHYD 254 254
FT CARBOHYD 299 299
FT CARBOHYD 724 724
FT CARBOHYD 832 832
FT CARBOHYD 832 832
FT VARSPIC 181 189
FT VARSPIC 226 229
FT VARSPIC 775 783
FT VARSPIC 609 1137
FT VARSPIC 1178 1178
SQ SEQUENCE 1912 AA; 214759 MW; 3AE8CBDD32182E26 CRC64;

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DB 1550 VVHCSAGVGRG 1561
RESULT 15
ID PTPR_HUMAN STANDARD; PRT; 1997 AA.
AC P23467;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Protein-tyrosine phosphatase beta precursor (PC 3.1.3.48) (R-PTP-
DE beta).
GN PTPR OR PTPR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=91006018; PubMed=2170109;
RA Krueger N.X., Streuli M., Saito H.;
RT "Structural diversity and evolution of human receptor-like protein
RT tyrosine phosphatases.";
RL EMBL J. 9:3241-3252(1990).
CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: CONTAINS 1 PROTEIN-TYROSINE PHOSPHATASE DOMAIN.
CC -1- SIMILARITY: CONTAINS 16 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
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CC -----
DR EMBL: X54131; CAA38066.1; -.
DR PIR: S12050; S12050.
DR HSSP: P18052; 1YFO.
DR Genew: HGNC:9665; PTPRB.
DR MIM: 176882; -.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR000387; TYR_phosphatase.
DR InterPro: IPR000242; TYR_PP.
DR Pfam: PF00041; fn3; 16.
DR Pfam: PF00102; Y_phosphatase; 1.
DR PRINTS: PR00700; PRTYPHPTASE.
DR SMART: SM00060; FN3; 15.
DR SMART: SM00194; PTPC; 1.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
DR PROSITE: PS50055; TYR_PHOSPHATASE_PP; 1.
KW Glycoprotein; Transmembrane; Hydrolase; Phosphorylation; Repeat;
KW Signal.
FT SIGNAL 1 22
FT CHAIN 23 1997
FT DOMAIN 23 1621
FT TRANSMEM 1622 1642
FT TRANSMEM 1643 1997
FT DOMAIN 23 110
FT DOMAIN 111 200
FT DOMAIN 201 286
FT DOMAIN 287 374
FT DOMAIN 375 464
FT DOMAIN 465 551
FT DOMAIN 552 640
FT DOMAIN 641 728
FT DOMAIN 729 816
FT DOMAIN 817 904
FT DOMAIN 905 992

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Query Match 100.0%; Score 65; DB 1; Length 1912;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 VVHCSAGVGRG 12
|||||

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FT DOMAIN 993 1082 FIBRONECTIN TYPE-III 12.
FT DOMAIN 1083 1170 FIBRONECTIN TYPE-III 13.
FT DOMAIN 1171 1268 FIBRONECTIN TYPE-III 14.
FT DOMAIN 1269 1352 FIBRONECTIN TYPE-III 15.
FT DOMAIN 1353 1442 FIBRONECTIN TYPE-III 16.
FT DOMAIN 1722 1997 PROTEIN-TYROSINE PHOSPHATASE.
FT ACT_SITE 1904 1904 BY SIMILARITY.
FT CARBOHYD 28 28 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 267 267 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 321 321 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 414 414 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 421 421 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 479 479 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 544 544 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 574 574 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 598 598 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 652 652 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 721 721 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 829 829 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1040 1040 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1096 1096 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1163 1163 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1185 1185 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1212 1212 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1274 1274 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1367 1367 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1470 1470 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1474 1474 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1518 1518 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1997 AA: 224267 MW: 691E99BA7A1515DD CRC64;
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Query Match 100.0%; Score 65; DB 1; Length 1997;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 VVHCSAGVGRTG 12
   |||
DB 1901 VVHCSAGVGRTG 1912
```

Search completed: January 17, 2003, 09:11:59
Job time : 11 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 09:36:13 : Search time 29 Seconds

(Without alignments)
85.261 Million cell updates/sec

Title: US-09-743-492-4

Sequence: 1 VVHCSAGVGRGTG 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 45 summaries

SPREMBL_21:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.podent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*
15: sp.virus:*
16: sp.bacteriaph:*
17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	100.0	24	11 088570	088570 mus musculus
2	65	100.0	24	11 088571	088571 mus musculus
3	65	100.0	112	11 091J6	091J6 mus musculus
4	65	100.0	198	5 023433	023433 caenorhabditis
5	65	100.0	253	13 09N100	09N100 eptatretus
6	65	100.0	358	11 062604	062604 rattus norvegicus
7	65	100.0	460	11 062917	062917 rattus norvegicus
8	65	100.0	468	13 09N106	09N106 eptatretus
9	65	100.0	468	13 091BA5	091BA5 potamogeton
10	65	100.0	468	13 091BA2	091BA2 potamogeton
11	65	100.0	468	13 091BA0	091BA0 potamogeton
12	65	100.0	469	5 09N114	09N114 branchiostoma
13	65	100.0	470	5 09N108	09N108 eptatretus
14	65	100.0	471	5 09N115	09N115 branchiostoma
15	65	100.0	471	5 09Y1X6	09Y1X6 ephyra
16	65	100.0	471	13 091BA3	091BA3 potamogeton

17	65	100.0	473	13 09N105	09N105 eptatretus
18	65	100.0	473	13 091B97	091B97 potamogeton
19	65	100.0	483	5 091568	091568 caenorhabditis
20	65	100.0	487	5 09N113	09N113 branchiostoma
21	65	100.0	488	5 09N112	09N112 branchiostoma
22	65	100.0	497	13 091B98	091B98 potamogeton
23	65	100.0	505	13 091B96	091B96 potamogeton
24	65	100.0	508	13 090YJ5	090YJ5 brachydanio
25	65	100.0	511	13 09N107	09N107 eptatretus
26	65	100.0	536	4 08TE48	08TE48 homo sapien
27	65	100.0	579	11 09J307	09J307 mus musculus
28	65	100.0	582	11 064696	064696 mus musculus
29	65	100.0	615	13 091A18	091A18 xenopus laevis
30	65	100.0	642	4 096K06	096K06 homo sapien
31	65	100.0	642	11 060986	060986 mus musculus
32	65	100.0	659	11 063477	063477 rattus norvegicus
33	65	100.0	699	11 061042	061042 mus musculus
34	65	100.0	749	11 08R169	08R169 mus musculus
35	65	100.0	793	11 091Y35	091Y35 mus musculus
36	65	100.0	802	4 096TD9	096TD9 homo sapien
37	65	100.0	807	13 091B69	091B69 gallus galli
38	65	100.0	822	13 091556	091556 xenopus laevis
39	65	100.0	832	13 090947	090947 gallus galli
40	65	100.0	833	13 090B57	090B57 brachydanio
41	65	100.0	849	11 091J18	091J18 mus musculus
42	65	100.0	1114	4 09H0Y6	09H0Y6 homo sapien
43	65	100.0	1143	4 016614	016614 homo sapien
44	65	100.0	1200	13 091054	091054 heterodontu
45	65	100.0	1214	5 09VAL3	09VAL3 drosophila

ALIGNMENTS

RESULT 1	088570	PRELIMINARY:	PRT:	24 AA.
ID	088570			
AC	088570			
DT	01-NOV-1998 (TREMBLrel. 08, Created)			
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	Protein tyrosine phosphatase, rPTP-GMCI (Fragment).			
CN	PTPRQ.			
OC	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
NCBI	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J;			
RC	MEDLINE=98395110; PubMed=9727007;			
RA	Wright M.B., Hugo C., Seifert R., Distche C.M., Bowen-Pope D.F.;			
RT	"Proliferating and migrating mesangial cells responding to injury			
RT	express a novel receptor protein-tyrosine phosphatase in experimental			
RT	mesangial proliferative glomerulonephritis.";			
RL	J. Biol. Chem. 273:23929-23937(1998).			
DR	EMBL: AF073998; AAC34822.1; -.			
DR	MGI: 1096349; Pprip.			
DR	InterPro: IPR000387; TYR.phosphatase.			
DR	PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.			
DR	PROSITE: PS00356; TYR_PHOSPHATASE_2; 1.			
KW	Hydrolyase.			
FT	NON_TER			
FT	NON_TER			
FT	NON_TER			
SO	SEQUENCE	24 AA;	2483 MW;	7E81A5FBF2BC2E2B CRC64;
QY	1 VVHCSAGVGRGTG 12			
DB	9 VVHCSAGVGRGTG 20			
Query Match	100.0%;	Score 65;	DB 11;	Length 24;
Best Local Similarity	100.0%;	Pred. No. 7.2e-05;		
Matches 12;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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RESULT 2
ID 088571 PRELIMINARY: PRT: 24 AA.
AC 088571:
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Protein tyrosine phosphatase PTP-GMC1 (Fragment).
GN PTPRO.
OS Mus spretus (Western wild mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10096;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98395110; PubMed=9727007;
RT Wright M.B., Hugo C., Selfert R., Distecche C.M., Bowen-Pope D.F.;
RT "Proliferating and migrating mesangial cells responding to injury
RT express a novel receptor protein-tyrosine phosphatase in experimental
RT mesangial proliferative glomerulonephritis.";
RL J. Biol. Chem. 273:23929-23937(1998).
DR EMBL: AF073999; AAC34823.1; -.
DR MGD: MGI:1096349; Pcpq.
DR InterPro: IPR000387; TYR_phosphatase.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
KW Hydrolase.
FT NON_TER 1 1
FT NON_TER 24 24
SQ SEQUENCE 24 AA: 2483 MW: 7881A5FBE2BC2E2B CRC64;

Query Match 100.0%; Score 65; DB 11; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVHCSAGVGRGTG 12
Db 9 VVHCSAGVGRGTG 20

RESULT 3
ID 09JLJ6 PRELIMINARY: PRT: 112 AA.
AC 09JLJ6:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE PTP36-D isoform.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-DDY;
RX MEDLINE=20068798; PubMed=10600535;
RA Aoyama K., Matsuda T., Aoki N.;
RT "Characterization of newly identified four isoforms for a putative
RT cytosolic protein tyrosine phosphatase PTP36.";
RL Biochem. Biophys. Res. Commun. 266:523-531(1999);
DR EMBL: AF170905; AAF27551.1; -.
DR HSSP: P18052; IYFO.
DR InterPro: IPR003595; PTPc_motif.
DR InterPro: IPR000387; TYR_phosphatase.
DR InterPro: IPR000242; TYR_PP.
DR Pfam: PF00102; Y_phosphatase_1.
DR PRINTS: PR00700; PRTYPPHTASE.
DR SMART: SM00404; PTPc_motif.1.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 1.

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KW Hydrolase. 112 AA: 13195 MW: BD4656A8512B3466 CRC64;
SQ SEQUENCE 112 AA: 13195 MW: BD4656A8512B3466 CRC64;

Query Match 100.0%; Score 65; DB 11; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.00038;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVHCSAGVGRGTG 12
Db 43 VVHCSAGVGRGTG 54

RESULT 4
ID Q23433 PRELIMINARY: PRT: 198 AA.
AC Q23433:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE ZK1251.5 protein.
GN ZK1251.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA McMurray A.A.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RX SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C. elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2010(1998).
DR EMBL: Z68222; CAAG2501.1; -.
DR HSSP: P18052; IYFO.
DR InterPro: IPR000387; TYR_phosphatase.
DR Pfam: PF00102; Y_phosphatase_1.
DR SMART: SM00194; FTRC; 1.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 1.
KW Hydrolase.
SQ SEQUENCE 198 AA: 22551 MW: CB586BF32D06375D CRC64;

Query Match 100.0%; Score 65; DB 5; Length 198;
Best Local Similarity 100.0%; Pred. No. 0.00069;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVHCSAGVGRGTG 12
Db 105 VVHCSAGVGRGTG 116

RESULT 5
ID 09NLU0 PRELIMINARY: PRT: 253 AA.
AC 09NLU0:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE HGPRP5B protein (Fragment).
GN HGPRP5B.
OS Epplatretus burgeri (Inshore hagfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Hyperotretli; Myxiniiformes;
OC Myxiniidae; Epplatretinae; Epplatretus.
OX NCBI_TaxID=7764;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20219325; PubMed=10754074;

```

RA Ono-Koyanagi K., Suga H., Katoh K., Miyata T.;
 RT "Protein tyrosine phosphatases from amphioxus, hagfish, and ray:
 RT divergence of tissue-specific isoform genes in the early evolution of
 RT vertebrates.";
 RL J. Mol. Evol. 50:302-311(2000).
 DR EMBL: AB033577; BAA95184.1; -.
 DR HSSP: P28827; IRPM.
 DR InterPro: IPR000387; TYR_phosphatase.
 DR InterPro: IPR000242; Tyr_PP.
 DR Pfam: PF00102; Y_phosphatase; 1.
 DR PRINTS: PR00700; PRTYPHPTASE.
 DR SMART: SM00194; PTPc; 1.
 DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
 DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 1.
 KM Hydrolyase.
 FT NON_TER
 SQ SEQUENCE 253 AA; 28315 MW; 27845DD6FC154C96 CRC64;

Query Match 100.0%; Score 65; DB 13; Length 253;
 Best Local Similarity 100.0%; Pred. No. 0.0009;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVHCSAGVGRG 12
 Db 143 VVHCSAGVGRG 154
 |||

RESULT 6
 ID 062604 PRELIMINARY; PRT; 398 AA.
 AC 062604;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
 DE Hypothetical 45.6 kDa protein (Fragment).
 GN CPPL.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE DAWLEY; TISSUE=OCCIPITAL CORTEX;
 RX MEDLINE=94045925; PubMed=8229209;
 RA Sahin M., Hookfield S.;
 RT "Protein tyrosine phosphatases expressed in the developing rat
 RT brain.";
 RL J. Neurosci. 13:4968-4978(1993).
 DR EMBL: U03273; AAC52124.1; -.
 DR HSSP: P18052; IYFO.
 DR InterPro: IPR000387; TYR_phosphatase.
 DR InterPro: IPR000242; Tyr_PP.
 DR Pfam: PF00102; Y_phosphatase; 2.
 DR PRINTS: PR00700; PRTYPHPTASE.
 DR SMART: SM00194; PTPc; 2.
 DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
 DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 2.
 KM Hydrolyase; Hypothetical protein.
 FT NON_TER
 SQ SEQUENCE 398 AA; 45618 MW; A7CAB3AE6D589E17 CRC64;

Query Match 100.0%; Score 65; DB 11; Length 398;
 Best Local Similarity 100.0%; Pred. No. 0.0015;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVHCSAGVGRG 12
 Db 106 VVHCSAGVGRG 117
 |||

RESULT 7
 ID 062917 PRELIMINARY; PRT; 460 AA.
 AC 062917;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
 DE LAR receptor-linked tyrosine phosphatase.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE DAWLEY; TISSUE=BRAIN;
 RX MEDLINE=94075340; PubMed=8253779;
 RA Longo F.M., Martignetti J.A., Le Beau J.M., Zhang J.S., Barnes J.P.,
 RA Brosius J.;
 RT "Leukocyte common antigen-related receptor-linked tyrosine
 RT phosphatase. Regulation of mRNA expression.";
 RL J. Biol. Chem. 268:26503-26511(1993).
 DR EMBL: U00477; AAC04306.1; -.
 DR HSSP: P18052; IYFO.
 DR InterPro: IPR000387; TYR_phosphatase.
 DR InterPro: IPR000242; Tyr_PP.
 DR Pfam: PF00102; Y_phosphatase; 2.
 DR PRINTS: PR00700; PRTYPHPTASE.
 DR SMART: SM00194; PTPc; 2.
 DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 2.
 DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 2.
 DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 2.
 KM Hydrolyase; Receptor.
 SQ SEQUENCE 460 AA; 52989 MW; B78C8E504F1260FA CRC64;

Query Match 100.0%; Score 65; DB 11; Length 460;
 Best Local Similarity 100.0%; Pred. No. 0.0017;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVHCSAGVGRG 12
 Db 98 VVHCSAGVGRG 109
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RESULT 8
 ID 09N106 PRELIMINARY; PRT; 468 AA.
 AC 09N106;
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
 DE HgPpR2AB protein (Fragment).
 GN HgPpR2AB.
 OS Epiplatelus burgeri (Inshore hagfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniiformes;
 OC Myxiniidae; Epiplatretidae; Epiplatretus.
 OX NCBI_TaxID=7764;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=20219325; PubMed=10754074;
 RX Ono-Koyanagi K., Suga H., Katoh K., Miyata T.;
 RT "Protein tyrosine phosphatases from amphioxus, hagfish, and ray:
 RT divergence of tissue-specific isoform genes in the early evolution of
 RT vertebrates.";
 RL J. Mol. Evol. 50:302-311(2000).
 DR EMBL: AB033571; BAA95178.1; -.
 DR HSSP: P18052; IYFO.
 DR InterPro: IPR000387; TYR_phosphatase.
 DR InterPro: IPR000242; Tyr_PP.
 DR Pfam: PF00102; Y_phosphatase; 2.
 DR PRINTS: PR00700; PRTYPHPTASE.
 DR SMART: SM00194; PTPc; 2.
 DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 2.
 DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 2.

DR PROSITE; PSS0055; TYR_PHOSPHATASE_PTP; 2.
KW Hydrolase.
FT NON_TER
SQ SEQUENCE 468 AA; 53952 MW; 7E123B7D3EAD69D CRC64;
Query Match 100.0%; Score 65; DB 13; Length 468;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VVHCSAGVGRG 12
DB 106 VVHCSAGVGRG 117
RESULT 9
Q91BA5 PRELIMINARY; PRT; 468 AA.
AC Q91BA5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE RYPRR2Aa protein (Fragment).
GN RYPRR2Aa.
OS Potamoxygon motoro (South American freshwater stingray).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squala; Hypnosquala; Pristiogryae; Batoidae;
OC Myliobatiformes; Myliobatoidei; Potamoxygonidae; Potamoxygon.
OX NCBI_TaxID=86373;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20219325; PubMed=10754074;
RX Ono-Koyanagi K., Suga H., Katoh K., Miyata T.;
RT "Protein tyrosine phosphatases from amphioxus, hagfish, and ray;
RT divergence of tissue-specific isoform genes in the early evolution of
RT vertebrates.";
RL J. Mol. Evol. 50:302-311(2000).
DR EMBL; AB033581; BAA95188.1; -.
DR HSSP; P18052; 1YFO.
DR InterPro; IPR000387; TYR-phosphatase.
DR InterPro; IPR000242; TYR_PP.
DR Pfam; PF00102; Y-phosphatase; 2.
DR RYPRR2Ac protein (Fragment).
GN RYPRR2Ac.
OS Potamoxygon motoro (South American freshwater stingray).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squala; Hypnosquala; Pristiogryae; Batoidae;
OC Myliobatiformes; Myliobatoidei; Potamoxygonidae; Potamoxygon.
OX NCBI_TaxID=86373;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20219325; PubMed=10754074;
RX Ono-Koyanagi K., Suga H., Katoh K., Miyata T.;
RT "Protein tyrosine phosphatases from amphioxus, hagfish, and ray;
RT divergence of tissue-specific isoform genes in the early evolution of
RT vertebrates.";
RL J. Mol. Evol. 50:302-311(2000).
DR EMBL; AB033581; BAA95188.1; -.
DR HSSP; P18052; 1YFO.
DR InterPro; IPR000387; TYR-phosphatase.
DR InterPro; IPR000242; TYR_PP.
DR Pfam; PF00102; Y-phosphatase; 2.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00194; PTPC; 2.
DR PROSITE; PSS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PSS0056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PSS0055; TYR_PHOSPHATASE_PTP; 2.
KW Hydrolase.
FT NON_TER
SQ SEQUENCE 468 AA; 53862 MW; 0051F5E0EDD7A580 CRC64;
Query Match 100.0%; Score 65; DB 13; Length 468;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VVHCSAGVGRG 12
DB 106 VVHCSAGVGRG 117
RESULT 10
Q91BA2 PRELIMINARY; PRT; 468 AA.
AC Q91BA2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE RYPRR2Ab protein (Fragment).
GN RYPRR2Ab.
OS Potamoxygon motoro (South American freshwater stingray).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squala; Hypnosquala; Pristiogryae; Batoidae;
OC Myliobatiformes; Myliobatoidei; Potamoxygonidae; Potamoxygon.
OX NCBI_TaxID=86373;

RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20219325; PubMed=10754074;
RX Ono-Koyanagi K., Suga H., Katoh K., Miyata T.;
RT "Protein tyrosine phosphatases from amphioxus, hagfish, and ray;
RT divergence of tissue-specific isoform genes in the early evolution of
RT vertebrates.";
RL J. Mol. Evol. 50:302-311(2000).
DR EMBL; AB033584; BAA95191.1; -.
DR HSSP; P18052; 1YFO.
DR InterPro; IPR000387; TYR-phosphatase.
DR InterPro; IPR000242; TYR_PP.
DR Pfam; PF00102; Y-phosphatase; 2.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00194; PTPC; 2.
DR PROSITE; PSS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PSS0056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PSS0055; TYR_PHOSPHATASE_PTP; 2.
KW Hydrolase.
FT NON_TER
SQ SEQUENCE 468 AA; 53885 MW; 8B1CABE0E9692E4 CRC64;
Query Match 100.0%; Score 65; DB 13; Length 468;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VVHCSAGVGRG 12
DB 106 VVHCSAGVGRG 117
RESULT 11
Q91BA0 PRELIMINARY; PRT; 468 AA.
AC Q91BA0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE RYPRR2Ac protein (Fragment).
GN RYPRR2Ac.
OS Potamoxygon motoro (South American freshwater stingray).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squala; Hypnosquala; Pristiogryae; Batoidae;
OC Myliobatiformes; Myliobatoidei; Potamoxygonidae; Potamoxygon.
OX NCBI_TaxID=86373;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20219325; PubMed=10754074;
RX Ono-Koyanagi K., Suga H., Katoh K., Miyata T.;
RT "Protein tyrosine phosphatases from amphioxus, hagfish, and ray;
RT divergence of tissue-specific isoform genes in the early evolution of
RT vertebrates.";
RL J. Mol. Evol. 50:302-311(2000).
DR EMBL; AB033586; BAA95193.1; -.
DR HSSP; P18052; 1YFO.
DR InterPro; IPR000387; TYR-phosphatase.
DR InterPro; IPR000242; TYR_PP.
DR Pfam; PF00102; Y-phosphatase; 2.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00194; PTPC; 2.
DR PROSITE; PSS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PSS0056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PSS0055; TYR_PHOSPHATASE_PTP; 2.
KW Hydrolase.
FT NON_TER
SQ SEQUENCE 468 AA; 53976 MW; 76C975D92D437A86 CRC64;
Query Match 100.0%; Score 65; DB 13; Length 468;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VVHCSAGVGRG 12
DB 106 VVHCSAGVGRG 117

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Db 106 VVHCSAGVGRG 117

RESULT 12
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ID Q9NL14
AC Q9NL14;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DE 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE AMPPR4b protein (Fragment).
GN AMPPR4b.
OS Branchiostoma belcheri (Amphioxus).
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC Branchiostoma.
OX NCBI_TaxID=7741;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20219325; PubMed=10754074;
RA Oho-Koyanagi K., Suga H., Katoh K., Miyata T.;
RT "Protein tyrosine phosphatases from amphioxus, hagfish, and ray:
RT divergence of tissue-specific isoform genes in the early evolution of
RT vertebrates."
RL J. Mol. Evol. 50:302-311(2000).
DR EMBL; AB033563; BAA95170.1; -.
DR HSSP; PI8052; IYEO.
DR InterPro; IPR001664; IF.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; TYR_PP.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PR00700; PRYPPHPTASE.
DR SMART; SM00194; PTPC; 2.
DR PROSITE; PS00383; IF; UNKNOWN.1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
DR Hydroxylase.
KW NON_TER
SQ SEQUENCE 469 AA; 53631 MW; C2CBED629815317 CRC64;

Query Match 100.0%; Score 65; DB 5; Length 469;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVHCSAGVGRG 12
Db 105 VVHCSAGVGRG 116

RESULT 13
Q9NL08 PRELIMINARY; PRT; 469 AA.
ID Q9NL08
AC Q9NL08;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DE 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE HgPpR2Aa protein (Fragment).
GN HgPpR2Aa.
OS Eptatretus burgeri (Inshore hagfish).
OC Eukaryota; Metazoa; Chordata; Granata; Hyperotretti; Myxiniiformes;
OC Myxiniidae; Eptatretinae; Eptatretus.
OX NCBI_TaxID=7764;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20219325; PubMed=10754074;
RA Oho-Koyanagi K., Suga H., Katoh K., Miyata T.;
RT "Protein tyrosine phosphatases from amphioxus, hagfish, and ray:
RT divergence of tissue-specific isoform genes in the early evolution of
RT vertebrates."
RL J. Mol. Evol. 50:302-311(2000).
DR EMBL; AB033569; BAA95176.1; -.
DR HSSP; PI8052; IYEO.
DR InterPro; IPR000387; TYR_phosphatase.

Db 106 VVHCSAGVGRG 117

RESULT 14
Q9NL15 PRELIMINARY; PRT; 470 AA.
ID Q9NL15
AC Q9NL15;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DE 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE AMPPR4a protein (Fragment).
GN AMPPR4a.
OS Branchiostoma belcheri (Amphioxus).
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC Branchiostoma.
OX NCBI_TaxID=7741;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20219325; PubMed=10754074;
RA Oho-Koyanagi K., Suga H., Katoh K., Miyata T.;
RT "Protein tyrosine phosphatases from amphioxus, hagfish, and ray:
RT divergence of tissue-specific isoform genes in the early evolution of
RT vertebrates."
RL J. Mol. Evol. 50:302-311(2000).
DR EMBL; AB033562; BAA95169.1; -.
DR HSSP; PI8052; IYEO.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; TYR_PP.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PR00700; PRYPPHPTASE.
DR SMART; SM00194; PTPC; 2.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
DR Hydroxylase.
KW NON_TER
SQ SEQUENCE 470 AA; 53329 MW; CDA72BCF423B75D4 CRC64;

Query Match 100.0%; Score 65; DB 5; Length 470;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVHCSAGVGRG 12
Db 107 VVHCSAGVGRG 118

RESULT 15
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ID Q9Y1X6
AC Q9Y1X6;
DT 01-NOV-1999 (TREMblrel. 12, Created)
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
DE 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE SPMPR4 (Fragment).
OS Ephydatia fluviatilis.

```

```

OC Eukaryota; Metazoa; Porifera; Demospongiae; Ceractinomorpha;
OC Haplosclerida; Spongillidae; Ephydalia.
OX NCBI_TaxID=31330;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99246376; PubMed=10229569;
RA Ono K., Suga H., Iwabe N., Kuma K., Miyata T.;
RT "Multiple protein tyrosine phosphatases in sponges and explosive gene
RT duplication in the early evolution of animals before the parazoan-
RT eumetazoan split.";
RL J. Mol. Evol. 48:654-662(1999).
DR EMBL: AB019125; BAA82558.1; -.
DR HSSP; P18052; 1YFO.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; TYR_PP.
DR Pfam: PF00102; Y_phosphatase; 2.
DR PRINTS: PR00700; PRYDPHPTASE.
DR SMART; SM00194; PTPC; 2.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 2.
KW Hydrolase.
FT NON_TER 1 1
SQ SEQUENCE 471 AA; 54509 MM; 7DA62456154A6A56 CRC64;

Query Match 100.0%; Score 65; DB 5; Length 471;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVHCSAGVGRTG 12
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DB 106 VVHCSAGVGRTG 117

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Search completed: January 17, 2003, 09:38:30
 Job time : 30 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 09:10:56 : Search time 36 seconds
(without alignments)
44.417 Million cell updates/sec

Title: US-09-743-492-4

Perfect score: 65

Sequence: 1 VVHCAGYGRFG 12

Scoring table:
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Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by change to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	100.0	12	21	AA181786
2	65	100.0	236	20	AA104707
3	65	100.0	236	20	AA104700
4	65	100.0	240	13	AA120745
5	65	100.0	250	22	AA159370
6	65	100.0	253	22	AA159373
7	65	100.0	253	22	AA159374
8	65	100.0	254	22	AA159372
9	65	100.0	254	22	AA159377
10	65	100.0	257	22	AA159369

11	65	100.0	260	22	AA159367	Human protein tyro
12	65	100.0	260	22	AA159388	Human protein tyro
13	65	100.0	261	22	AA159366	Human protein tyro
14	65	100.0	306	22	AA159368	Human DCA-D1. Hom
15	65	100.0	309	22	AA159371	Human PTP-epsilon-
16	65	100.0	309	22	AA159372	Mouse Cda5-D1. Mu
17	65	100.0	310	22	AA159373	Human PTP-alpha-D1
18	65	100.0	310	22	AA159375	Human PTP-bola. H
19	65	100.0	313	22	AA159367	Drosophila PTP99A-
20	65	100.0	316	22	AA159365	Human PTP-zeta-D1.
21	65	100.0	317	22	AA159366	Human PTP-xi-D1.
22	65	100.0	442	21	AA159372	Human prostate can
23	65	100.0	579	21	AA159373	Mouse vascular-end
24	65	100.0	607	21	AA159373	Human protein tyro
25	65	100.0	607	21	AA159373	Human protein tyro
26	65	100.0	607	21	AA159373	LAR tyrosine phosph
27	65	100.0	647	22	AA159374	Human ESR encoded
28	65	100.0	647	22	AA159375	Human novel protei
29	65	100.0	659	20	AA159376	Mouse protein tyro
30	65	100.0	659	20	AA159377	Mouse protein tyro
31	65	100.0	699	22	AA159378	Mouse protein tyro
32	65	100.0	699	22	AA159379	Mouse protein tyro
33	65	100.0	700	22	AA159380	Mouse ischaemic co
34	65	100.0	700	22	AA159381	Human ESR encoded
35	65	100.0	717	22	AA159382	Human polypeptide
36	65	100.0	793	13	AA159383	Human polypeptide
37	65	100.0	793	17	AA159384	Murine receptor-ty
38	65	100.0	793	20	AA159385	Murine receptor-ty
39	65	100.0	802	13	AA159386	Mouse receptor-ty
40	65	100.0	802	17	AA159387	Human receptor-ty
41	65	100.0	802	20	AA159388	Human receptor-ty
42	65	100.0	807	23	AA159389	Human receptor-ty
43	65	100.0	807	23	AA159390	Human ovarian anti
44	65	100.0	1214	22	AA159391	Human polypeptide
45	65	100.0	1237	19	AA159392	Drosophila melanog
					AA159393	Chicken protein ty

ALIGNMENTS

RESULT 1	AA181786	standard; peptide; 12 AA.
ID	AA181786	
XX	AA181786	
AC	AA181786	
XX		
DT	07-JUN-2000	(first entry)
XX		
DE	Protein tyrosine phosphatase motif #1.	
XX		
KW	Human; protein tyrosine phosphatase; antibody; intracellular domain; LAR;	
KW	CD45; PTP; diagnosis; insulin resistance related disease; syndrome X;	
KW	non-insulin dependent diabetes mellitus; arteriosclerosis; therapy;	
KW	heart disorder; signature motif.	
XX		
OS	Unidentified.	
XX		
PN	WO200002922-A1.	
PD	20-JAN-2000.	
XX		
PF	06-JUL-1999; 99WO-JP03656.	
XX		
PR	10-JUL-1998; 98WO-JP03120.	
XX		
PA	(FUSO) FUSO PHARM IND LTD.	
XX		
PI	Yamamoto H, Tsujikawa K, Uchino Y;	
XX		
DR	WPI, 2000-182215/16.	
XX		
PT	Antibody for diagnosis and treatment of insulin resistance disorders	
	and syndrome X recognises the intracellular domains of tyrosine	

PT phosphatase -
XX
PS Example 3; Page 32; 83pp; Japanese.
XX
CC This sequence represents a motif of a protein tyrosine
phosphatases. The invention relates to an antibody of the invention that
CC has sites specifically recognising the intracellular domain
CC of two or more protein tyrosine phosphatases (PTPs). The antibody is
CC useful for the detection and assay of PTP including novel phosphatases
CC generated by cloning; and diagnosis, treatment and prevention of insulin
CC resistance related diseases and non-insulin dependent diabetes mellitus,
CC syndrome x and arteriosclerosis and heart disorders.
XX
SQ Sequence 12 AA;
Query Match 100.0%; Score 65; DB 21; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VVHCSAGVGRTG 12
Db 1 VVHCSAGVGRTG 12
IIIIIIIIIIII
RESULT 2
AA04707
ID AA04707 standard; Protein: 236 AA.
XX
AC AA04707;
XX
DT 22-JUN-1999 (first entry)
XX
DE Mouse RPTPa amino acids 265-500.
XX
KM Receptor-type protein tyrosine phosphatase; RPTP; mouse; enzyme; cancer;
cellular metabolism; regulation; insulin; diabetes; oncoprotein;
negative growth regulator.
XX
OS Mus sp.
XX
PN US5888794-A.
PD 30-MAR-1999.
XX
PF 23-MAY-1995; 95US-0448288.
XX
PR 10-FEB-1993; 93US-0015985.
PR 11-JUL-1990; 90US-0551270.
PR 26-FEB-1991; 91US-0654188.
PR 23-MAY-1995; 95US-0448288.
XX
PA (UYNV) UNIV NEW YORK STATE.
XX
PI Sap JM, Schlessinger J;
XX
DR WPI: 1999-253232/21.
PT Receptor-type protein tyrosine phosphatase from mouse and human
XX
PS Claim 6; Page -: 50pp; English.
XX
CC This sequence represents a claimed peptide comprising amino acids
265-500 of the receptor-type protein tyrosine phosphatase alpha (RPTPa)
CC present in mice (AA04695). The protein, optionally immobilized or
CC present in cells, is used to screen for specific binding agents or agents
CC that stimulate/inhibit its enzymatic activity. These agents may be used
CC to regulate major pathways of cellular metabolism. Activation of RPTPa
CC may be an endogenous regulatory mechanism against cancer and may counter
CC the effects of insulin (possibly causing insulin-resistant diabetes),
CC i.e. RPTPa may be a recessive oncoprotein and negative growth regulator.
CC (Note: this sequence is not given in the specification but is generated
CC from information disclosed in the specification by the inventors).
XX

SQ Sequence 236 AA;
Query Match 100.0%; Score 65; DB 20; Length 236;
Best Local Similarity 100.0%; Pred. No. 0.004;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VVHCSAGVGRTG 12
Db 166 VVHCSAGVGRTG 177
IIIIIIIIIIII
RESULT 3
AA04700
ID AA04700 standard; Protein: 236 AA.
XX
AC AA04700;
XX
DT 22-JUN-1999 (first entry)
XX
DE Human RPTPa amino acids 265-500.
XX
KM Receptor-type protein tyrosine phosphatase; RPTP; human; enzyme; cancer;
cellular metabolism; regulation; insulin; diabetes; oncoprotein;
negative growth regulator.
XX
OS Homo sapiens.
XX
PN US5888794-A.
PD 30-MAR-1999.
XX
PF 23-MAY-1995; 95US-0448288.
XX
PR 10-FEB-1993; 93US-0015985.
PR 11-JUL-1990; 90US-0551270.
PR 26-FEB-1991; 91US-0654188.
PR 23-MAY-1995; 95US-0448288.
XX
PA (UYNV) UNIV NEW YORK STATE.
XX
PI Sap JM, Schlessinger J;
XX
DR WPI: 1999-253232/21.
PT Receptor-type protein tyrosine phosphatase from mouse and human
XX
PS Claim 2; Page -: 50pp; English.
XX
CC This sequence represents a claimed peptide comprising amino acids
265-500 of the receptor-type protein tyrosine phosphatase alpha (RPTPa)
CC present in humans (AA04694). The protein, optionally immobilized or
CC present in cells, is used to screen for specific binding agents or agents
CC that stimulate/inhibit its enzymatic activity. These agents may be used
CC to regulate major pathways of cellular metabolism. Activation of RPTPa
CC may be an endogenous regulatory mechanism against cancer and may counter
CC the effects of insulin (possibly causing insulin-resistant diabetes),
CC i.e. RPTPa may be a recessive oncoprotein and negative growth regulator.
CC (Note: this sequence is not given in the specification but is generated
CC from information disclosed in the specification by the inventors).
XX
SQ Sequence 236 AA;
Query Match 100.0%; Score 65; DB 20; Length 236;
Best Local Similarity 100.0%; Pred. No. 0.004;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VVHCSAGVGRTG 12
Db 175 VVHCSAGVGRTG 186
IIIIIIIIIIII
RESULT 4
AAR20745

ID AAK20745 standard; Protein; 240 AA.
 XX
 AC AAR20745;
 XX
 DT 28-MAY-1992 (first entry)
 XX
 DE Human R-PTPase beta first conserved phosphatase.
 XX
 KM Receptor-type protein tyrosine phosphatase; cellular metabolism;
 cancer; diabetes.
 XX
 OS Homo sapiens.
 XX
 PN WO9201050-A.
 XX
 PD 23-JUN-1992.
 XX
 PF 11-JUL-1991; 91WO-US04892.
 XX
 PR 26-FEB-1991; 91US-065418.
 PR 11-JUL-1990; 90US-0551270.
 XX
 PA (UYNY-) NEW YORK UNIV.
 XX
 PI Schlessinger J;
 XX
 DR WPI; 1992-056865/07.
 XX
 PT Human receptor-type protein tyrosine phosphatase - has DNA
 encoding it and antibodies specific for it, useful for screening
 PT drugs affecting R-PTPase activity, and detection of mutant genes
 XX
 PS Claim 5; Fig 5A; 77pp; English.
 XX
 CC The amino acid sequence is that of human receptor-type protein
 CC tyrosine phosphatase (R-PTPase) beta first conserved phosphatase. It
 CC is useful in methods for screening drugs and other agents which are
 CC capable of activating or inhibiting the R-PTPase activity and thereby
 CC affecting major pathways of cellular metabolism. Activation of
 CC R-PTPases, leading to dephosphorylation would serve as a counter-
 CC regulatory mechanism to prevent or inhibit growth, and may serve as
 CC an endogenous regulatory mechanism against cancer. Mutation or
 CC dysregulation of this receptor/enzyme system may promote susceptibility
 CC to cancer, diabetes, or other diseases associated with alterations in
 CC cellular phosphotyrosine metabolism. It can be used to raise antibodies
 CC which can be used in immunoassays to determine the presence and amt.
 CC of R-PTPases, or in immunoelectron microscopy for in situ detection of
 CC R-PTPase. See also AAR20743-R20748.
 CC
 SQ Sequence 240 AA;
 QY
 Db 1 VVHCSAGVGRTG 12
 179 VVHCSAGVGRTG 190

Query Match 100.0%; Score 65; DB 13; Length 240;
 Best Local Similarity 100.0%; Pred. No. 0.0041;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
 AAB59370
 ID AAB59370 standard; Protein; 250 AA.
 XX
 AC AAB59370;
 XX
 DT 21-MAR-2001 (first entry)
 XX
 DE Human protein tyrosine phosphatase #6.
 XX
 KM Protein tyrosine phosphatase; human; mouse; fruit fly; PTP;
 substrate trapping.
 XX

OS Homo sapiens.
 XX
 PN WO200075339-A1.
 XX
 PD 14-DEC-2000.
 XX
 PF 24-MAY-2000; 2000WO-US14211.
 XX
 PR 03-JUN-1999; 99US-0137319.
 PR 16-JUN-1999; 99US-0334575.
 XX
 PA (COLD-) COLD SPRING HARBOR LAB.
 XX
 PI Tonks NK, Zhang S;
 XX
 DR WPI; 2001-080598/09.
 XX
 PT New substrate trapping mutant protein tyrosine phosphatases (PTP) in
 PT which the wild type PTP catalytic domain invariant aspartate is
 PT replaced with an unphosphorylated amino acid, useful in gene therapy
 XX
 PS Disclosure; Fig 1; 109pp; English.
 XX
 CC The present invention provides substrate trapping mutant protein tyrosine
 CC phosphatases (PTPs). They can be used to reduce the activity of tyrosine
 CC phosphorylated proteins and to screen for modulators capable of altering
 CC the binding of protein tyrosine phosphatases to their substrate. These
 CC may be used in disease diagnosis and treatment.
 XX
 SQ Sequence 250 AA;
 QY
 Db 1 VVHCSAGVGRTG 12
 180 VVHCSAGVGRTG 191

Query Match 100.0%; Score 65; DB 22; Length 250;
 Best Local Similarity 100.0%; Pred. No. 0.0043;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6
 AAB59373
 ID AAB59373 standard; Protein; 253 AA.
 XX
 AC AAB59373;
 XX
 DT 21-MAR-2001 (first entry)
 XX
 DE Human protein tyrosine phosphatase #9.
 XX
 KM Protein tyrosine phosphatase; human; mouse; fruit fly; PTP;
 substrate trapping.
 XX
 OS Homo sapiens.
 XX
 PN WO200075339-A1.
 XX
 PD 14-DEC-2000.
 XX
 PF 24-MAY-2000; 2000WO-US14211.
 XX
 PR 03-JUN-1999; 99US-0137319.
 PR 16-JUN-1999; 99US-0334575.
 XX
 PA (COLD-) COLD SPRING HARBOR LAB.
 XX
 PI Tonks NK, Zhang S;
 XX
 DR WPI; 2001-080598/09.
 XX
 PT New substrate trapping mutant protein tyrosine phosphatases (PTP) in
 PT which the wild type PTP catalytic domain invariant aspartate is
 PT replaced with an unphosphorylated amino acid, useful in gene therapy

XX Disclosure; Fig 1; 109pp; English.
PS
XX
XX The present invention provides substrate trapping mutant protein tyrosine
CC phosphatases (PTPs). They can be used to reduce the activity of tyrosine
CC phosphorylated proteins and to screen for modulators capable of altering
CC the binding of protein tyrosine phosphatases to their substrate. These
CC may be used in disease diagnosis and treatment.
XX
SQ Sequence 253 AA;
Query Match 100.0%; Score 65; DB 22; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 VVHCSAGVGRGTG 12
DB 183 VVHCSAGVGRGTG 194
RESULT 7
AAB59374
ID AAB59374 standard; Protein; 253 AA.
XX
AC AAB59374;
XX
DT 21-MAR-2001 (first entry)
XX
DE Murine protein tyrosine phosphatase #1.
XX
KM Protein tyrosine phosphatase; human; mouse; fruit fly; PTP;
KW substrate trapping.
XX
OS Mus sp.
XX
PN WO200075339-A1.
XX
PD 14-DEC-2000.
XX
PF 24-MAY-2000; 2000WO-US14211.
XX
PR 03-JUN-1999; 99US-0137319.
PR 16-JUN-1999; 99US-0334575.
XX
PA (COLD-) COLD SPRING HARBOR LAB.
XX
PI Tonks NK, Zhang S;
XX
DR WPI; 2001-080598/09.
XX
PT New substrate trapping mutant protein tyrosine phosphatases (PTP) in
PT which the wild type PTP catalytic domain invariant aspartate is
PT replaced with an unphosphorylated amino acid, useful in gene therapy
XX
PS Disclosure; Fig 1; 109pp; English.
XX
CC The present invention provides substrate trapping mutant protein tyrosine
CC phosphatases (PTPs). They can be used to reduce the activity of tyrosine
CC phosphorylated proteins and to screen for modulators capable of altering
CC the binding of protein tyrosine phosphatases to their substrate. These
CC may be used in disease diagnosis and treatment.
XX
SQ Sequence 253 AA;
Query Match 100.0%; Score 65; DB 22; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 VVHCSAGVGRGTG 12
DB 183 VVHCSAGVGRGTG 194

RESULT 8
AAB59372
ID AAB59372 standard; Protein; 254 AA.
XX
AC AAB59372;
XX
DT 21-MAR-2001 (first entry)
XX
DE Human protein tyrosine phosphatase #8.
XX
KM Protein tyrosine phosphatase; human; mouse; fruit fly; PTP;
KW substrate trapping.
XX
OS Homo sapiens.
XX
PN WO200075339-A1.
XX
PD 14-DEC-2000.
XX
PF 24-MAY-2000; 2000WO-US14211.
XX
PR 03-JUN-1999; 99US-0137319.
PR 16-JUN-1999; 99US-0334575.
XX
PA (COLD-) COLD SPRING HARBOR LAB.
XX
PI Tonks NK, Zhang S;
XX
DR WPI; 2001-080598/09.
XX
PT New substrate trapping mutant protein tyrosine phosphatases (PTP) in
PT which the wild type PTP catalytic domain invariant aspartate is
PT replaced with an unphosphorylated amino acid, useful in gene therapy
XX
PS Disclosure; Fig 1; 109pp; English.
XX
CC The present invention provides substrate trapping mutant protein tyrosine
CC phosphatases (PTPs). They can be used to reduce the activity of tyrosine
CC phosphorylated proteins and to screen for modulators capable of altering
CC the binding of protein tyrosine phosphatases to their substrate. These
CC may be used in disease diagnosis and treatment.
XX
SQ Sequence 254 AA;
Query Match 100.0%; Score 65; DB 22; Length 254;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 VVHCSAGVGRGTG 12
DB 184 VVHCSAGVGRGTG 195
RESULT 9
AAB59377
ID AAB59377 standard; Protein; 254 AA.
XX
AC AAB59377;
XX
DT 21-MAR-2001 (first entry)
XX
DE Human protein tyrosine phosphatase #12.
XX
KM Protein tyrosine phosphatase; human; mouse; fruit fly; PTP;
KW substrate trapping.
XX
OS Homo sapiens.
XX
PN WO200075339-A1.
XX
PD 14-DEC-2000.
XX
PF 24-MAY-2000; 2000WO-US14211.

XX 03-JUN-1999; 99US-0137319.
PR 16-JUN-1999; 99US-0334575.
XX
XX (COLD-) COLD SPRING HARBOR LAB.
PI Tonks NK, Zhang S;
XX
DR WPI: 2001-080598/09.
XX
PT New substrate trapping mutant protein tyrosine phosphatases (PTP) in
PT which the wild type PTP catalytic domain invariant aspartate is
PT replaced with an unphosphorylated amino acid, useful in gene therapy
XX
PS Disclosure; Fig 1; 109pp; English.
XX
CC The present invention provides substrate trapping mutant protein tyrosine
CC phosphatases (PTPs). They can be used to reduce the activity of tyrosine
CC phosphorylated proteins and to screen for modulators capable of altering
CC the binding of protein tyrosine phosphatases to their substrate. These
CC may be used in disease diagnosis and treatment.
XX
SQ Sequence 254 AA;

Query Match 100.0%; Score 65; DB 22; Length 254;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVHCSAGVGRGTG 12
DB 184 VVHCSAGVGRGTG 195
IIIIIIIIII

RESULT 10
AAB59369
ID AAB59369 standard; Protein; 257 AA.
XX
AC AAB59369;
XX
DT 21-MAR-2001 (first entry)
XX
DE Drosophila protein tyrosine phosphatase #1.
XX
KM Protein tyrosine phosphatase; human; mouse; fruit fly; PTP;
KM substrate trapping.
XX
OS Drosophila sp.
XX
PN WO200075339-A1.
XX
PD 14-DEC-2000.
XX
PF 24-MAY-2000; 2000WO-US14211.
XX
PR 03-JUN-1999; 99US-0137319.
PR 16-JUN-1999; 99US-0334575.
XX
PA (COLD-) COLD SPRING HARBOR LAB.
XX
PI Tonks NK, Zhang S;
XX
DR WPI: 2001-080598/09.
XX
XX
PT New substrate trapping mutant protein tyrosine phosphatases (PTP) in
PT which the wild type PTP catalytic domain invariant aspartate is
PT replaced with an unphosphorylated amino acid, useful in gene therapy
XX
PS Disclosure; Fig 1; 109pp; English.
XX
CC The present invention provides substrate trapping mutant protein tyrosine
CC phosphatases (PTPs). They can be used to reduce the activity of tyrosine
CC phosphorylated proteins and to screen for modulators capable of altering
CC the binding of protein tyrosine phosphatases to their substrate. These

CC may be used in disease diagnosis and treatment.
XX
SQ Sequence 257 AA;

Query Match 100.0%; Score 65; DB 22; Length 257;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVHCSAGVGRGTG 12
DB 187 VVHCSAGVGRGTG 198
IIIIIIIIII

RESULT 11
AAB59367
ID AAB59367 standard; Protein; 260 AA.
XX
AC AAB59367;
XX
DT 21-MAR-2001 (first entry)
XX
DE Human protein tyrosine phosphatase #4.
XX
KM Protein tyrosine phosphatase; human; mouse; fruit fly; PTP;
KM substrate trapping.
XX
OS Homo sapiens.
XX
PN WO200075339-A1.
XX
PD 14-DEC-2000.
XX
PF 24-MAY-2000; 2000WO-US14211.
XX
PR 03-JUN-1999; 99US-0137319.
PR 16-JUN-1999; 99US-0334575.
XX
PA (COLD-) COLD SPRING HARBOR LAB.
XX
PI Tonks NK, Zhang S;
XX
DR WPI: 2001-080598/09.
XX
XX
PT New substrate trapping mutant protein tyrosine phosphatases (PTP) in
PT which the wild type PTP catalytic domain invariant aspartate is
PT replaced with an unphosphorylated amino acid, useful in gene therapy
XX
PS Disclosure; Fig 1; 109pp; English.
XX
CC The present invention provides substrate trapping mutant protein tyrosine
CC phosphatases (PTPs). They can be used to reduce the activity of tyrosine
CC phosphorylated proteins and to screen for modulators capable of altering
CC the binding of protein tyrosine phosphatases to their substrate. These
CC may be used in disease diagnosis and treatment.
XX
SQ Sequence 260 AA;

Query Match 100.0%; Score 65; DB 22; Length 260;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVHCSAGVGRGTG 12
DB 190 VVHCSAGVGRGTG 201
IIIIIIIIII

RESULT 12
AAB59388
ID AAB59388 standard; Protein; 260 AA.
XX
AC AAB59388;
XX
DT 21-MAR-2001 (first entry)

XX Human protein tyrosine phosphatase #16.
DE Protein tyrosine phosphatase; human; mouse; fruit fly; PTP;
XX substrate trapping.
KW Homo sapiens.
XX WO200075339-A1.
XX 14-DEC-2000.
XX 24-MAY-2000; 2000WO-US14211.
XX 03-JUN-1999; 99US-0137319.
XX 16-JUN-1999; 99US-0334575.
XX (COLD-) COLD SPRING HARBOR LAB.
PA Tonks NK, Zhang S;
XX WPI; 2001-080598/09.
XX New substrate trapping mutant protein tyrosine phosphatases (PTP) in
PT which the wild type PTP catalytic domain invariant aspartate is
XX replaced with an unphosphorylated amino acid, useful in gene therapy
XX
XX Disclosure; Fig 1; 109pp; English.
XX
XX The present invention provides substrate trapping mutant protein tyrosine
CC phosphatases (PTPs). They can be used to reduce the activity of tyrosine
CC phosphorylated proteins and to screen for modulators capable of altering
CC the binding of protein tyrosine phosphatases to their substrate. These
CC may be used in disease diagnosis and treatment.
XX
XX Sequence 260 AA:
SQ
Query Match 100.0%; Score 65; DB 22; Length 260;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 VVHCSAGVGRGTG 12
DB 190 VVHCSAGVGRGTG 201
RESULT 13
AAB59366
ID AAB59366 standard; Protein; 261 AA.
XX AAB59366;
XX AAB59366;
XX 21-MAR-2001 (first entry)
XX Human protein tyrosine phosphatase #3.
DE Protein tyrosine phosphatase; human; mouse; fruit fly; PTP;
KW substrate trapping.
XX Homo sapiens.
XX WO200075339-A1.
XX 14-DEC-2000.
XX 24-MAY-2000; 2000WO-US14211.
XX 03-JUN-1999; 99US-0137319.
XX 16-JUN-1999; 99US-0334575.
XX (COLD-) COLD SPRING HARBOR LAB.
PA Tonks NK, Zhang S;
XX

XX WPI; 2001-080598/09.
XX New substrate trapping mutant protein tyrosine phosphatases (PTP) in
PT which the wild type PTP catalytic domain invariant aspartate is
XX replaced with an unphosphorylated amino acid, useful in gene therapy
XX
XX Disclosure; Fig 1; 109pp; English.
XX
XX The present invention provides substrate trapping mutant protein tyrosine
CC phosphatases (PTPs). They can be used to reduce the activity of tyrosine
CC phosphorylated proteins and to screen for modulators capable of altering
CC the binding of protein tyrosine phosphatases to their substrate. These
CC may be used in disease diagnosis and treatment.
XX
XX Sequence 261 AA:
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Query Match 100.0%; Score 65; DB 22; Length 261;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 VVHCSAGVGRGTG 12
DB 191 VVHCSAGVGRGTG 202
RESULT 14
AAG78268
ID AAG78268 standard; Protein; 306 AA.
XX AAG78268;
XX AAG78268;
XX 19-DEC-2001 (first entry)
XX Human DCA-D1.
XX PTP; protein tyrosine phosphatase; tyrosine phosphorylated polypeptide;
KW dephosphorylation; phosphotyrosine; human; PTPB; mouse; fruit fly;
KW yeast.
XX Homo sapiens.
XX WO200161031-A2.
XX 23-AUG-2001.
XX 13-FEB-2001; 2001WO-US05180.
XX 14-FEB-2000; 2000US-0181769.
XX (CEPT-) CEPTYR INC.
XX Flint AJ, Cool DE;
XX WPI; 2001-570570/64.
XX Screening assays to identify agents that alter protein tyrosine
PT phosphatase (PTP) binding to, and PTP-mediated catalytic
PT dephosphorylation of phosphotyrosine peptide substrates
XX
XX Disclosure; Fig 1; 79pp; English.
XX
XX The invention relates to identifying agents which alter the interaction
CC between a protein tyrosine phosphatase (PTP) and a tyrosine
CC phosphorylated polypeptide using fluorescence energy signals. The methods
CC are useful for performing screening assay to identify agents that alter
CC PTP binding to and PTP-mediated catalytic dephosphorylation of
CC phosphotyrosine peptide substrates. The present sequence is that of a
CC catalytic domain of a PTP for comparison with human PTPB (AAG78262).
XX
XX Sequence 306 AA:
SQ
Query Match 100.0%; Score 65; DB 22; Length 306;

Best Local Similarity 100.0%; Pred. No. 0.0052;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVHCSAGVGRGTG 12
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DB 180 VVHCSAGVGRGTG 191

RESULT 15

AAG78271
ID AAG78271 standard; Protein; 309 AA.

AC AAG78271;

DT 19-DEC-2001 (first entry)

DE Human PTP-epsilon-DL.

KM PTP; protein tyrosine phosphatase; tyrosine phosphorylated polypeptide;
KW dephosphorylation; phosphotyrosine; human; PTP1B; mouse; fruit fly;
yeast.

OS Homo sapiens.

PN W0200161031-A2.

PD 23-AUG-2001.

PF 13-FEB-2001; 2001WO-US05180.

PR 14-FEB-2000; 2000US-0181769.

PA (CEPT-) CEPTYR INC.

PI Flint AJ, COOL DE;

DR WPI; 2001-570570/64.

PT Screening assays to identify agents that alter protein tyrosine
phosphatase (PTP) binding to, and PTP-mediated catalytic
dephosphorylation of phosphotyrosine peptide substrates -

PS Disclosure; Fig 1; 79pp; English.

CC The invention relates to identifying agents which alter the interaction
between a protein tyrosine phosphatase (PTP) and a tyrosine
phosphorylated polypeptide using fluorescence energy signals. The methods
are useful for performing screening assay to identify agents that alter
PTP binding to and PTP-mediated catalytic dephosphorylation of
phosphotyrosine peptide substrates. The present sequence is that of a
catalytic domain of a PTP for comparison with human PTP1B (AAG78262).

SQ Sequence 309 AA;

Query Match

100.0%; Score 65; DB 22; Length 309;

Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVHCSAGVGRGTG 12
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DB 183 VVHCSAGVGRGTG 194

Search completed: January 17, 2003, 09:11:41
Job time : 37 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 09:12:06 : Search time 11 Seconds
(without alignments)
21.686 Million cell updates/sec

Title: US-09-743-492-4

Perfect score: 65
Sequence: 1 VVHCSAGVGRIG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 120991 seqs, 19878514 residues

Total number of hits satisfying chosen parameters: 120991

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications AA:*

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- 2: /cgn2_6/ptodata/1/pubppa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep.*
- 5: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep.*
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- 9: /cgn2_6/ptodata/1/pubppa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep.*
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- 12: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	65	100.0	248	10	US-09-848-294-10
2	65	100.0	306	10	US-09-788-626-8
3	65	100.0	309	10	US-09-788-626-11
4	65	100.0	309	10	US-09-788-626-12
5	65	100.0	310	10	US-09-788-626-10
6	65	100.0	310	10	US-09-788-626-15
7	65	100.0	313	10	US-09-788-626-7
8	65	100.0	316	10	US-09-788-626-5
9	65	100.0	316	10	US-09-788-626-26
10	65	100.0	317	10	US-09-788-626-4
11	65	100.0	442	10	US-09-925-300-950
12	65	100.0	1502	9	US-09-808-602-54
13	65	100.0	1948	9	US-09-808-602-55
14	65	100.0	2308	12	US-10-000-954-2
15	64	98.5	307	10	US-09-788-626-20
16	64	98.5	312	10	US-09-788-626-24
17	64	98.5	313	10	US-09-788-626-17
18	64	98.5	325	10	US-09-788-626-13
19	64	98.5	341	10	US-09-788-626-23

20	64	98.5	360	12	US-10-028-748-2	Sequence 2, Appl1
21	64	98.5	593	10	US-09-820-021A-3	Sequence 3, Appl1
22	63	96.9	291	10	US-09-788-626-18	Sequence 18, Appl1
23	63	96.9	322	10	US-09-788-626-14	Sequence 14, Appl1
24	63	96.9	595	10	US-09-920-021A-1	Sequence 1, Appl1
25	62	95.4	313	10	US-09-788-626-19	Sequence 19, Appl1
26	62	95.4	319	10	US-09-788-626-6	Sequence 6, Appl1
27	61	93.8	244	10	US-09-848-294-7	Sequence 7, Appl1
28	61	93.8	291	10	US-09-788-626-22	Sequence 22, Appl1
29	61	93.8	294	10	US-09-788-626-27	Sequence 27, Appl1
30	61	93.8	305	10	US-09-788-626-9	Sequence 9, Appl1
31	61	93.8	307	10	US-09-788-626-25	Sequence 25, Appl1
32	61	93.8	309	10	US-09-788-626-16	Sequence 16, Appl1
33	61	93.8	523	10	US-09-799-777-76	Sequence 76, Appl1
34	61	93.8	603	10	US-09-906-779-4	Sequence 4, Appl1
35	61	93.8	913	10	US-09-848-294-2	Sequence 2, Appl1
36	61	93.8	1274	9	US-10-020-215-2	Sequence 2, Appl1
37	60	92.3	250	10	US-09-848-294-8	Sequence 8, Appl1
38	60	92.3	254	10	US-09-788-626-2	Sequence 2, Appl1
39	60	92.3	435	10	US-09-986-240-1	Sequence 1, Appl1
40	59	90.8	246	10	US-09-848-294-9	Sequence 9, Appl1
41	59	90.8	251	10	US-09-788-626-3	Sequence 3, Appl1
42	58	89.2	13	10	US-09-906-779-6	Sequence 6, Appl1
43	57	87.7	281	10	US-09-788-626-28	Sequence 28, Appl1
44	57	87.7	298	10	US-09-788-626-29	Sequence 29, Appl1
45	57	87.7	750	10	US-09-801-368-280	Sequence 280, Appl1

ALIGNMENTS

RESULT 1
US-09-848-294-10
Sequence 10, Application US/09848294
Patent No. US20020049179A1
GENERAL INFORMATION:
APPLICANT: Tonks, Nicholas K.
TITLE OF INVENTION: Isolation of A cDNA Encoding A No. US20020049179A1el
TITLE OF INVENTION: Protein Tyrosine Phosphatase Which Localizes to Focal
FILE REFERENCE: CSHL90-04F2A
CURRENT APPLICATION NUMBER: US/09/848,294
CURRENT FILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: 09/235,251
PRIOR FILING DATE: 1999-01-22
PRIOR APPLICATION NUMBER: 08/759,536
PRIOR FILING DATE: 1996-12-04
PRIOR APPLICATION NUMBER: 08/107,420
PRIOR FILING DATE: 1993-08-16
PRIOR APPLICATION NUMBER: 07/663,579
PRIOR FILING DATE: 1991-03-01
PRIOR APPLICATION NUMBER: 07/494,036
PRIOR FILING DATE: 1990-03-14
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 10
LENGTH: 248
TYPE: PRT
ORGANISM: Homosapiens
US-09-848-294-10
Query Match 100.0%; Score 65; DB 10; Length 248;
Best Local Similarity 100.0%; Pred. No. 0.00085;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VVHCSAGVGRIG 12
DB 174 VVHCSAGVGRIG 185
RESULT 2
US-09-788-626-8
Sequence 8, Application US/09788626

```
; Patent No. US20020009762A1
; GENERAL INFORMATION:
; APPLICANT: Flint, Andrew J.
; APPLICANT: Cool, Deborah E.
; TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATES
; FILE REFERENCE: 200125.401
; CURRENT APPLICATION NUMBER: US/09/788,626
; CURRENT FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-788-626-8

Query Match
Best Local Similarity 100.0%; Score 65; DB 10; Length 306;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVHCSAGVGRGTG 12
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Db 180 VVHCSAGVGRGTG 191

RESULT 3
; US-09-788-626-11
; Sequence 11, Application US/09788626
; Patent No. US20020009762A1
; GENERAL INFORMATION:
; APPLICANT: Flint, Andrew J.
; APPLICANT: Cool, Deborah E.
; TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATES
; FILE REFERENCE: 200125.401
; CURRENT APPLICATION NUMBER: US/09/788,626
; CURRENT FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-788-626-11

Query Match
Best Local Similarity 100.0%; Score 65; DB 10; Length 309;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVHCSAGVGRGTG 12
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Db 183 VVHCSAGVGRGTG 194

RESULT 4
; US-09-788-626-12
; Sequence 12, Application US/09788626
; Patent No. US20020009762A1
; GENERAL INFORMATION:
; APPLICANT: Flint, Andrew J.
; APPLICANT: Cool, Deborah E.
; TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATES
; FILE REFERENCE: 200125.401
; CURRENT APPLICATION NUMBER: US/09/788,626
; CURRENT FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Mus musculus
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US-09-788-626-12

Query Match
Best Local Similarity 100.0%; Score 65; DB 10; Length 309;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 183 VVHCSAGVGRGTG 194

RESULT 5
; US-09-788-626-10
; Sequence 10, Application US/09788626
; Patent No. US20020009762A1
; GENERAL INFORMATION:
; APPLICANT: Flint, Andrew J.
; APPLICANT: Cool, Deborah E.
; TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATES
; FILE REFERENCE: 200125.401
; CURRENT APPLICATION NUMBER: US/09/788,626
; CURRENT FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-788-626-10

Query Match
Best Local Similarity 100.0%; Score 65; DB 10; Length 310;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVHCSAGVGRGTG 12
    |||||
Db 184 VVHCSAGVGRGTG 195

RESULT 6
; US-09-788-626-15
; Sequence 15, Application US/09788626
; Patent No. US20020009762A1
; GENERAL INFORMATION:
; APPLICANT: Flint, Andrew J.
; APPLICANT: Cool, Deborah E.
; TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATES
; FILE REFERENCE: 200125.401
; CURRENT APPLICATION NUMBER: US/09/788,626
; CURRENT FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-788-626-15

Query Match
Best Local Similarity 100.0%; Score 65; DB 10; Length 310;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVHCSAGVGRGTG 12
    |||||
Db 184 VVHCSAGVGRGTG 195

RESULT 7
; US-09-788-626-7
; Sequence 7, Application US/09788626
; Patent No. US20020009762A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Flint, Andrew J.
; APPLICANT: Cool, Deborah E.
; TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE
; FILE OF INVENTION: PHOSPHATES
; FILE REFERENCE: 200125.401
; CURRENT APPLICATION NUMBER: US/09/788,626
; CURRENT FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-788-626-7

Query Match          100.0%; Score 65; DB 10; Length 313;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VVHCSAGVGRGTG 12
        |||||||||
Db      187 VVHCSAGVGRGTG 198

RESULT 8
US-09-788-626-5
; Sequence 5, Application US/09788626
; Patent No. US20020009762A1
; GENERAL INFORMATION:
; APPLICANT: Flint, Andrew J.
; APPLICANT: Cool, Deborah E.
; TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE
; FILE OF INVENTION: PHOSPHATES
; FILE REFERENCE: 200125.401
; CURRENT APPLICATION NUMBER: US/09/788,626
; CURRENT FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-626-5

Query Match          100.0%; Score 65; DB 10; Length 316;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VVHCSAGVGRGTG 12
        |||||||||
Db      190 VVHCSAGVGRGTG 201

RESULT 9
US-09-788-626-26
; Sequence 26, Application US/09788626
; Patent No. US20020009762A1
; GENERAL INFORMATION:
; APPLICANT: Flint, Andrew J.
; APPLICANT: Cool, Deborah E.
; TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE
; FILE OF INVENTION: PHOSPHATES
; FILE REFERENCE: 200125.401
; CURRENT APPLICATION NUMBER: US/09/788,626
; CURRENT FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-626-26
```

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Query Match          100.0%; Score 65; DB 10; Length 316;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VVHCSAGVGRGTG 12
        |||||||||
Db      190 VVHCSAGVGRGTG 201

RESULT 10
US-09-788-626-4
; Sequence 4, Application US/09788626
; Patent No. US20020009762A1
; GENERAL INFORMATION:
; APPLICANT: Flint, Andrew J.
; APPLICANT: Cool, Deborah E.
; TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE
; FILE OF INVENTION: PHOSPHATES
; FILE REFERENCE: 200125.401
; CURRENT APPLICATION NUMBER: US/09/788,626
; CURRENT FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-626-4

Query Match          100.0%; Score 65; DB 10; Length 317;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VVHCSAGVGRGTG 12
        |||||||||
Db      191 VVHCSAGVGRGTG 202

RESULT 11
US-09-925-300-950
; Sequence 950, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 950
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-300-950

Query Match          100.0%; Score 65; DB 10; Length 442;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VVHCSAGVGRGTG 12
        |||||||||
Db      80 VVHCSAGVGRGTG 91

RESULT 12
US-09-808-602-54
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; Sequence 54, Application US/09808602
; Patent No. US2002015115A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine A
; APPLICANT: Fernandes, Elma
; APPLICANT: Shinkets, Richard A
; APPLICANT: Herrman, John L
; APPLICANT: Majumder, Kumud
; APPLICANT: Mishra, Vishnu
; APPLICANT: Mezes, Peter S
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: No. US2002015115A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-697 CIP
; CURRENT APPLICATION NUMBER: US/09/808,602
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 09/800,198
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/186,596
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 1502
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-808-602-54
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Query Match          100.0%; Score 65; DB 9; Length 1502;
Best Local Similarity 100.0%; Pred. No. 0.005;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 VVHCSAGVGRGTG 12
        |||||
DB      1140 VVHCSAGVGRGTG 1151
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RESULT 13
US-09-808-602-55
; Sequence 55, Application US/09808602
; Patent No. US2002015115A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine A
; APPLICANT: Fernandes, Elma
; APPLICANT: Shinkets, Richard A
; APPLICANT: Herrman, John L
; APPLICANT: Majumder, Kumud
; APPLICANT: Mishra, Vishnu
; APPLICANT: Mezes, Peter S
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: No. US2002015115A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-697 CIP
; CURRENT APPLICATION NUMBER: US/09/808,602
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 09/800,198
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/186,596
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 1948
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-808-602-55
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Query Match          100.0%; Score 65; DB 9; Length 1948;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 VVHCSAGVGRGTG 12
        |||||
DB      1586 VVHCSAGVGRGTG 1597
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RESULT 14
US-10-000-954-2
; Sequence 2, Application US/10000954
; Patent No. US20020127226A1
; GENERAL INFORMATION:
; APPLICANT: Schlössinger, Joseph
; APPLICANT: Barnea, Gilad
; APPLICANT: Grumet, Martin H.
; APPLICANT: Margolis, Richard U.
```

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; TITLE OF INVENTION: A NEW CLASS OF RPPases: THEIR
; STRUCTURAL DOMAINS AND LIGANDS
```

```
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
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; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/10/000,954
; FILING DATE: 04-Dec-2001
; CLASSIFICATION: <Unknown>
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; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: 09/644,293
; FILING DATE: 23-Aug-2000
; APPLICATION NUMBER: 08/081,929
; FILING DATE: <Unknown>
```

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; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: Coruzzi, Laura A.
```

```
; REGISTRATION NUMBER: 30742
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```
; REFERENCE/DOCKET NUMBER: 7683-041-999
```

```
; TELECOMMUNICATION INFORMATION:
```

```
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
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; INFORMATION FOR SEQ ID NO: 2:
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; SEQUENCE CHARACTERISTICS:
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; LENGTH: 2308 amino acids
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; TYPE: amino acid
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; STRANDEDNESS: single
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; TOPOLOGY: unknown
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; MOLECULE TYPE: protein
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; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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Query Match          100.0%; Score 65; DB 12; Length 2308;
Best Local Similarity 100.0%; Pred. No. 0.0077;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 VVHCSAGVGRGTG 12
        |||||
DB      1923 VVHCSAGVGRGTG 1934
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RESULT 15
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US-09-788-626-20
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; Sequence 20, Application US/09788626
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; Patent No. US20020009762A1
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: Flint, Andrew J.
```

```
; APPLICANT: Cool, Deborah E.
```

```
; TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE
```

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; FILE REFERENCE: 200125.401
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; CURRENT APPLICATION NUMBER: US/09/788,626
```

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; CURRENT FILING DATE: 2001-02-13
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; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 307
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-626-20

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Query Match          98.5%; Score 64; DB 10; Length 307;
Best Local Similarity 91.7%; Pred. No. 0.0015;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY      1 VVHCSAGVGRGTG 12
        |||||:||||
Db      195 VVHCSAGIGRTG 206

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 Job time : 11 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 09:11:01 : Search time 15 Seconds
(Without alignments)
23.538 Million cell updates/sec

Title: US-09-743-492-4

Sequence: 1 VVHCSAGVGRGTG 12

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Gapop 10.0 , Gapept 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	65	100.0	235	1	US-08-015-985-5
2	65	100.0	236	1	US-08-015-985-6
3	65	100.0	242	1	US-08-015-985-7
4	65	100.0	248	1	US-08-015-985-9
5	65	100.0	250	2	US-08-685-992-7
6	65	100.0	250	2	US-09-144-925-7
7	65	100.0	253	2	US-08-685-992-10
8	65	100.0	253	2	US-08-685-992-11
9	65	100.0	253	2	US-09-144-925-10
10	65	100.0	253	2	US-09-144-925-11
11	65	100.0	254	2	US-08-685-992-9
12	65	100.0	254	2	US-08-685-992-14
13	65	100.0	254	2	US-09-144-925-14
14	65	100.0	254	2	US-09-144-925-14
15	65	100.0	257	2	US-08-685-992-6
16	65	100.0	257	2	US-09-144-925-6
17	65	100.0	260	2	US-08-685-992-4
18	65	100.0	260	2	US-08-685-992-25
19	65	100.0	260	2	US-09-144-925-4
20	65	100.0	260	2	US-09-144-925-25
21	65	100.0	261	2	US-08-685-992-3
22	65	100.0	261	2	US-09-144-925-3
23	65	100.0	278	1	US-08-201-697-16
24	65	100.0	289	1	US-08-036-210-13
25	65	100.0	289	2	US-08-449-609-13
26	65	100.0	292	1	US-08-036-210-12
27	65	100.0	292	2	US-08-449-609-12

ALIGNMENTS

28	65	100.0	699	1	US-08-348-006B-7	Sequence 7, Appl1
29	65	100.0	699	2	US-08-800-825A-7	Sequence 7, Appl1
30	65	100.0	699	4	US-09-158-657-7	Sequence 7, Appl1
31	65	100.0	793	1	US-08-015-985-3	Sequence 3, Appl1
32	65	100.0	802	1	US-08-015-985-1	Sequence 1, Appl1
33	65	100.0	1237	1	US-08-241-853-2	Sequence 2, Appl1
34	65	100.0	1237	2	US-08-850-917-2	Sequence 2, Appl1
35	65	100.0	1501	2	US-08-447-464-3	Sequence 3, Appl1
36	65	100.0	1501	2	US-08-716-679-3	Sequence 3, Appl1
37	65	100.0	1911	1	US-08-348-006B-5	Sequence 5, Appl1
38	65	100.0	1911	2	US-08-800-825A-5	Sequence 5, Appl1
39	65	100.0	1911	4	US-09-158-657-5	Sequence 5, Appl1
40	65	100.0	1911	5	PCT-US94-10166-5	Sequence 5, Appl1
41	65	100.0	2308	1	US-08-015-973-1	Sequence 1, Appl1
42	65	100.0	2308	2	US-08-448-164-1	Sequence 1, Appl1
43	65	100.0	2308	4	US-08-081-929-2	Sequence 2, Appl1
44	65	100.0	2314	4	US-09-816-703A-2	Sequence 2, Appl1
45	64	98.5	126	1	US-08-202-389-10	Sequence 10, Appl1

RESULT 1
US-08-015-985-5
Sequence 5, Application US/08015985
Patent No. 5538886
GENERAL INFORMATION:
APPLICANT: Schliesinger, Joseph
APPLICANT: Sap, Jan M.
TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
TITLE OF INVENTION: PHOSPHATASE ALPHA
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSES:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 AVENUE OF THE AMERICAS
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/015,985
FILING DATE: 10-FEB-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 869-9741/8864
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-015-985-5
Query Match 100.0%; Score 65; DB 1; Length 235;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VVHCSAGVGRGTG 12
|||||
Db 174 VVHCSAGVGRGTG 185


```
RESULT 2
US-08-015-985-6
; Sequence 6, Application US/08015985
; Patent No. 5538886
; GENERAL INFORMATION:
; APPLICANT: Schlessinger, Joseph
; APPLICANT: Sap, Jan M.
; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
; TITLE OF INVENTION: PHOSPHATASE-ALPHA
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 AVENUE OF THE AMERICAS
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/015,985
; FILING DATE: 10-FEB-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7683-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 236 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-015-985-6

Query Match          100.0%; Score 65; DB 1; Length 236;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VVHCSAGVGRGT 12
        |||||
DB      175 VVHCSAGVGRGT 186

RESULT 3
US-08-015-985-7
; Sequence 7, Application US/08015985
; Patent No. 5538886
; GENERAL INFORMATION:
; APPLICANT: Schlessinger, Joseph
; APPLICANT: Sap, Jan M.
; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
; TITLE OF INVENTION: PHOSPHATASE-ALPHA
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 AVENUE OF THE AMERICAS
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/015,985
; FILING DATE: 10-FEB-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7683-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-015-985-7

Query Match          100.0%; Score 65; DB 1; Length 242;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VVHCSAGVGRGT 12
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DB      181 VVHCSAGVGRGT 192

RESULT 4
US-08-015-985-9
; Sequence 9, Application US/08015985
; Patent No. 5538886
; GENERAL INFORMATION:
; APPLICANT: Schlessinger, Joseph
; APPLICANT: Sap, Jan M.
; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
; TITLE OF INVENTION: PHOSPHATASE-ALPHA
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 AVENUE OF THE AMERICAS
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/015,985
; FILING DATE: 10-FEB-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7683-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 248 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
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MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Modified-sites
LOCATION: 1..248
OTHER INFORMATION: /label=Xaa
OTHER INFORMATION: /note="For the Consensus Sequence, Xaa = Lack of
OTHER INFORMATION: Consensus"
US-08-015-985-9

Query Match 100.0%; Score 65; DB 1; Length 248;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVHCSAGVGRG 12
DB 187 VVHCSAGVGRG 198

RESULT 5

US-08-685-992-7
Sequence 7, Application US/08685992
Patent No. 5912138
GENERAL INFORMATION:
APPLICANT: Tonks, Nicholas
APPLICANT: Flint, Andrew J.
TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: Windows 95
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,992
FILING DATE: 25-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540
TELEX:
INFORMATION FOR SEQ. ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 250 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-685-992-7

Query Match 100.0%; Score 65; DB 2; Length 250;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVHCSAGVGRG 12
DB 180 VVHCSAGVGRG 191

RESULT 6

US-09-144-925-7
Sequence 7, Application US/09144925
Patent No. 591979
GENERAL INFORMATION:
APPLICANT: Tonks, Nicholas
APPLICANT: Flint, Andrew J.
TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02421-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: Windows 95
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,925
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/685,992
FILING DATE: July 25, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL96-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540
TELEX:
INFORMATION FOR SEQ. ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 250 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-144-925-7

Query Match 100.0%; Score 65; DB 2; Length 250;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVHCSAGVGRG 12
DB 180 VVHCSAGVGRG 191

RESULT 7

US-08-685-992-10
Sequence 10, Application US/08685992
Patent No. 5912138
GENERAL INFORMATION:
APPLICANT: Tonks, Nicholas
APPLICANT: Flint, Andrew J.
TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,992
FILING DATE: 25-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL96-03
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-685-992-10

Query Match 100.0%; Score 65; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVHCSAGVGRGTG 12
|||||
DB 183 VVHCSAGVGRGTG 194

RESULT 8
US-08-685-992-11
Sequence 11, Application US/08685992
Patent No. 5912138
GENERAL INFORMATION:
APPLICANT: Tonks, Nicholas
APPLICANT: Flint, Andrew J.
TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
INVENTION: TYROSINE PHOSPHATASES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Millitia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,992
FILING DATE: 25-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL96-03
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540

TELEX:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-685-992-11

Query Match 100.0%; Score 65; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVHCSAGVGRGTG 12
|||||
DB 183 VVHCSAGVGRGTG 194

RESULT 9
US-09-144-925-10
Sequence 10, Application US/09144925
Patent No. 5951979
GENERAL INFORMATION:
APPLICANT: Tonks, Nicholas
APPLICANT: Flint, Andrew J.
TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
INVENTION: TYROSINE PHOSPHATASES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Millitia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02421-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,925
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/685,992
FILING DATE: July 25, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL96-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-144-925-10

Query Match 100.0%; Score 65; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVHCSAGVGRGTG 12
|||||
DB 183 VVHCSAGVGRGTG 194

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RESULT 10
US-09-144-925-11
; Sequence 11, Application US/091444925
; Patent No. 5951979
; GENERAL INFORMATION:
; APPLICANT: Tonks, Nicholas
; APPLICANT: Flint, Andrew J.
; TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
; TITLE OF INVENTION: TYROSINE PHOSPHATASES
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02421-4799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,925
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/685,992
; FILING DATE: July 25, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL96-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9540
; TELEX:
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-144-925-11

Query Match      100.0%; Score 65; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VVHCSAGVGRGTG 12
Db      183 VVHCSAGVGRGTG 194
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RESULT 11
US-08-685-992-9
; Sequence 9, Application US/08685992
; Patent No. 5912138
; GENERAL INFORMATION:
; APPLICANT: Tonks, Nicholas
; APPLICANT: Flint, Andrew J.
; TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
; TITLE OF INVENTION: TYROSINE PHOSPHATASES
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/685,992
; FILING DATE: 25-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL96-03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9540
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-685-992-9

Query Match      100.0%; Score 65; DB 2; Length 254;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VVHCSAGVGRGTG 12
Db      184 VVHCSAGVGRGTG 195

RESULT 12
US-08-685-992-14
; Sequence 14, Application US/08685992
; Patent No. 5912138
; GENERAL INFORMATION:
; APPLICANT: Tonks, Nicholas
; APPLICANT: Flint, Andrew J.
; TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
; TITLE OF INVENTION: TYROSINE PHOSPHATASES
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/685,992
; FILING DATE: 25-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL96-03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
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TELEFAX: 781-861-9540
TELEX:
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 254 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-685-992-14

Query Match 100.0%; Score 65; DB 2; Length 254;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVHCSAGVGRG 12
|||||
DB 184 VVHCSAGVGRG 195

RESULT 13
US-09-144-925-9
Sequence 9, Application US/09144925
Patent No. 5951979
GENERAL INFORMATION:
APPLICANT: Tonks, Nicholas
APPLICANT: Flint, Andrew J.
TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02421-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,925
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/685,992
FILING DATE: July 25, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL96-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540
TELEX:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 254 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-144-925-9

Query Match 100.0%; Score 65; DB 2; Length 254;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVHCSAGVGRG 12
|||||
DB 184 VVHCSAGVGRG 195

RESULT 14
US-09-144-925-14
Sequence 14, Application US/09144925
Patent No. 5951979
GENERAL INFORMATION:
APPLICANT: Tonks, Nicholas
APPLICANT: Flint, Andrew J.
TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02421-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,925
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/685,992
FILING DATE: July 25, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL96-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540
TELEX:
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 254 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-144-925-14

Query Match 100.0%; Score 65; DB 2; Length 254;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVHCSAGVGRG 12
|||||
DB 184 VVHCSAGVGRG 195

RESULT 15
US-08-685-992-6
Sequence 6, Application US/08685992
Patent No. 5912138
GENERAL INFORMATION:
APPLICANT: Tonks, Nicholas
APPLICANT: Flint, Andrew J.
TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA

```

;
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FASTSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/685,992
; FILING DATE: 25-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL96-03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9540
;
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
; US-08-685-992-6
;
Query Match 100.0%; Score 65; DB 2; Length 257;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VVHCSAGVGRTG 12
Db 187 VVHCSAGVGRTG 198

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Search completed: January 17, 2003, 09:12:42
Job time : 16 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 10:58:57 ; Search time 15 Seconds
(without alignments)
76.908 Million cell updates/sec

Title: US-09-743-492-4
Perfect score: 65
Sequence: 1 VHCAGVGRG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 1580

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR-73.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	41.5	12	2 PH0931	T-cell receptor be
2	24	36.9	12	2 S47394	T-cell antigen rec
3	23	35.4	8	2 PH0803	T-cell receptor al
4	23	35.4	11	2 PT0218	T-cell receptor be
5	23	35.4	12	2 S26549	T-cell receptor be
6	23	35.4	12	2 PH1463	T-cell receptor be
7	22	33.8	11	2 PH0938	T-cell receptor be
8	22	33.8	12	2 S28215	glucan endo-1,3-be
9	22	33.8	12	2 PH1464	T-cell receptor be
10	22	33.8	12	2 PT0216	T-cell receptor be
11	21	32.3	9	2 A11497	transaldolase (EC
12	21	32.3	9	2 I50633	C-rel protein - ch
13	21	32.3	11	2 S33782	acetylactate synth
14	21	32.3	12	2 S29764	alpha-macroglobuli
15	21	32.3	12	2 S26552	T-cell receptor be
16	21	32.3	12	2 PH1470	T-cell receptor be
17	21	32.3	12	2 PH1469	T-cell receptor be
18	21	32.3	12	2 PH1468	T-cell receptor be
19	20	30.8	7	2 PT0623	T-cell receptor be
20	20	30.8	8	2 PT0691	T-cell receptor be
21	20	30.8	9	2 A12872	transaldolase (EC
22	20	30.8	12	2 S26557	T-cell receptor be
23	20	30.8	12	2 S29830	dimethylalanine mo
24	20	30.8	12	2 S47391	T-cell antigen rec
25	19	29.2	10	2 E41946	T-cell receptor ga
26	19	29.2	11	2 S66196	alcohol dehydrogen
27	19	29.2	11	2 PH1600	ig H chain V-D-J r
28	19	29.2	12	2 S26553	T-cell receptor be
29	19	29.2	12	2 PH1180	T-cell receptor al

30	19	29.2	12	2 PH1466	T-cell receptor be
31	18	27.7	6	2 PT0718	T-cell receptor be
32	18	27.7	7	2 S08606	hypothetical prote
33	18	27.7	7	2 PT0663	T-cell receptor be
34	18	27.7	8	2 PT0279	Ig heavy chain CRD
35	18	27.7	10	2 S77990	cytochrome-c oxida
36	18	27.7	11	2 C49037	TCR gamma V-J regi
37	18	27.7	12	2 S47395	T-cell antigen rec
38	17	26.2	6	2 JU0355	lipopeptide WS1279
39	17	26.2	6	2 PT0643	T-cell receptor be
40	17	26.2	6	2 PT0668	T-cell receptor be
41	17	26.2	6	2 PT0727	T-cell receptor be
42	17	26.2	7	2 PT0719	T-cell receptor be
43	17	26.2	8	2 I48934	apolipoprotein A-I
44	17	26.2	8	2 PT0627	T-cell receptor be
45	17	26.2	8	2 A25836	L-serine ammonia-1

ALIGNMENTS

RESULT 1

PH0931
T-cell receptor beta chain V-D-J region (clone 2) - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C:Accession: PH0931

R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.

J. Exp. Med. 174, 1467-1476, 1991

A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental alle

A:Reference number: PH0891; MUID:92078857; PMID:1836012

A:Accession: PH0931

A:Molecule type: mRNA

A:Residues: 1-12 <GOL>

A:Experimental source: complete Freund's adjuvant-immunized lymph node

C:Keywords: T-cell receptor

Query Match 41.5%; Score 27; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CSAGVGRG 11
I:: |||
Db 1 CASSAGRT 8

RESULT 2

S47394
T-cell antigen receptor VJ junction beta chain - human

C:Species: Homo sapiens (man)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999

C:Accession: S47394; S47369

R:Lehner, P.J.

submitted to the EMBL Data Library, August 1994

A:Description: Human HLA-A0201 restricted recognition of Influenza A is dominated by

A:Reference number: S47355

A:Accession: S47394

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-12 <LEH>

A:Cross-references: EMBL:Z35714; NID:G527523; PID:CAA84783.1; PID:G527524; EMBL:Z356

C:Keywords: T-cell receptor

Query Match 36.9%; Score 24; DB 2; Length 12;
Best Local Similarity 33.3%; Pred. No. 6.3e+02;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 4 CSAGVGRG 12
I::: | |
Db 1 CASSIGNYG 9

RESULT 3

PH0803

T-cell receptor alpha chain (J2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PH0803
R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A;Title: T cell receptor genes in a series of class I major histocompatibility complex-I allelic exclusion and antigen-specific repertoire.
A;Reference number: PH0746; MUID:92078846; PMID:1836010
A;Accession: PH0803
A;Molecule type: mRNA
A;Residues: 1-8 <CAS>
A;Cross-references: EMBL:X60912
A;Experimental source: T lymphocyte
C;Keywords: T-cell receptor

Query Match 35.4%; Score 23; DB 2; Length 8;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 CSAGV 8
I::: I I
Db 1 CAGI 5

RESULT 4

PT0218
T-cell receptor beta chain V-J region (7-10-D.3) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997
C;Accession: PT0218
R;Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.
J. Exp. Med. 173, 1091-1097, 1991
A;Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restricted.
A;Reference number: PT0209; MUID:91217621; PMID:1902501
A;Accession: PT0218
A;Molecule type: mRNA
A;Residues: 1-11 <NAK>
C;Keywords: T-cell receptor

Query Match 35.4%; Score 23; DB 2; Length 11;
Best Local Similarity 66.7%; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CSAGVG 9
I::: I I
Db 1 CGAGQG 6

RESULT 5

S26549
T-cell receptor beta chain (clone Cw3/A8, Cw3/Cas1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 17-Apr-1998 #text_change 17-Mar-1999
C;Accession: S26549; S26550
R;Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Widmann, J.
J. Exp. Med. 176, 439-447, 1992
A;Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor
A;Reference number: S26512; MUID:92364546; PMID:1380061
A;Accession: S26549
A;Molecule type: mRNA
A;Residues: 1-12 <CAS>
A;Cross-references: EMBL:X67999
A;Experimental source: cytolytic T-lymphocyte, clone Cw3/A8
A;Accession: S26550
A;Molecule type: mRNA
A;Residues: 1-12 <CA2>
A;Cross-references: EMBL:X68000
A;Experimental source: cytolytic T-lymphocyte, clone Cw3/Cas1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor

Query Match

Best Local Similarity 37.5%; Score 23; DB 2; Length 12;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 CSAGVGRT 11
I::: I I
Db 1 CASSLGET 8

RESULT 6

PH1463
T-cell receptor beta chain (clone A24/10.1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995
C;Accession: PH1463
R;Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; J. Exp. Med. 177, 811-820, 1993
A;Title: T cell receptor selection by and recognition of two class I major histocomp
A;Reference number: PH1430; MUID:93171821; PMID:8436911
A;Accession: PH1463
A;Molecule type: mRNA
A;Residues: 1-12 <CAS>
A;Experimental source: cytolytic T-lymphocyte
C;Superfamily: immunoglobulin homology
C;Keywords: receptor; T-cell

Query Match 35.4%; Score 23; DB 2; Length 12;
Best Local Similarity 37.5%; Pred. No. 9.5e+02;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 CSAGVGRT 11
I::: I I
Db 1 CASSLGMT 8

RESULT 7

PH0938
T-cell receptor beta chain V-D-J region (clone 9) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0938
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental alle
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0938
A;Molecule type: mRNA
A;Residues: 1-11 <GOL>
A;Experimental source: complete Freund's adjuvant-immunized lymph node
C;Keywords: T-cell receptor

Query Match 33.8%; Score 22; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GRTG 12
I::: I I I I
Db 7 GRTG 10

RESULT 8

S28215
glucan endo-1,3-beta-D-glucosidase (EC 3.2.1.39) GII - barley (fragment)
N;Alternate names: (1-3)-beta-D-glucanase GII
C;Species: Hordeum vulgare (barley)
C;Date: 19-Mar-1997 #sequence_revision 17-Jul-1998 #text_change 07-May-1999
C;Accession: S28215
R;Hrmova, M.; Fincher, G.B.
Biochem. J. 289, 453-461, 1993
A;Title: Purification and properties of three (1->3)-beta-D-glucanase isoenzymes from
A;Reference number: S28214; MUID:93143715; PMID:8424790
A;Accession: S28215
A;Molecule type: protein

A;Residues: 1-12 <HRM>
A;Experimental source: cultivar clipper
C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 33.8%; Score 22; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 CSAGVG 9

I : : : |

Db 4 CYGGIG 9

RESULT 9

PHI464

T-cell receptor beta chain (clone A3/63) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995

C;Accession: PHI464

R;Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, A.; K

J. Exp. Med. 177, 811-820, 1993

A;Title: T cell receptor selection by and recognition of two class I major histocompatib

A;Reference number: PHI430; MUID:93171821; PMID:8436911

A;Accession: PHI464

A;Molecule type: mRNA

A;Residues: 1-12 <CAS>

A;Experimental source: cytolytic T-lymphocyte

C;Superfamily: immunoglobulin homology

C;Keywords: receptor; T-cell

Query Match 33.8%; Score 22; DB 2; Length 12;

Best Local Similarity 37.5%; Pred. No. 1.4e+03;

Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 CSAGVGRT 11

I : : : |

Db 1 CASSTGNT 8

RESULT 10

PT0216

T-cell receptor beta chain V-J region (4-1-G.4) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997

C;Accession: PT0216

R;Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.

J. Exp. Med. 173, 1091-1097, 1991

A;Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restrict

A;Reference number: PT0209; MUID:91217621; PMID:1902501

A;Accession: PT0216

A;Molecule type: mRNA

A;Residues: 1-12 <NAK>

C;Keywords: T-cell receptor

Query Match 33.8%; Score 22; DB 2; Length 12;

Best Local Similarity 37.5%; Pred. No. 1.4e+03;

Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 CSAGVGRT 11

I : : : |

Db 1 CASSLGTT 8

RESULT 11

All1497

transaldolase (EC 2.2.1.2) III - yeast (Pichia jadinii) (fragment)

C;Species: Pichia jadinii, Candida utilis

C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 30-Sep-1993

C;Accession: All1497

R;Tsolas, O.; Sun, S.C.

Arch. Biochem. Biophys. 167, 525-533, 1975

A;Title: Isolation of a peptide containing a histidinyI-cysteinyI sequence from the acti

A;Reference number: All1497; MUID:75145197; PMID:1092268

A;Accession: All1497

A;Molecule type: protein

A;Residues: 1-9 <TSO>

C;Keywords: transferase

Query Match 32.3%; Score 21; DB 2; Length 9;

Best Local Similarity 50.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHCS 5

I : : |

Db 3 IHCN 6

RESULT 12

I50633

C-rel protein - chicken (fragment)

C;Species: Gallus gallus (chicken)

C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000

C;Accession: I50633

R;Hannink, M.; Temin, H.M.

Oncogene 5, 1843-1850, 1990

A;Title: Structure and autoregulation of the c-rel promoter.

A;Reference number: I50633; MUID:91133738; PMID:2284104

A;Accession: I50633

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-9 <HAN>

A;Cross-references: EMBL:X56440; NID:g63338; PIDN:CAA39822.1; PID:g584483

Query Match 32.3%; Score 21; DB 2; Length 9;

Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 SAGVGR 10

I : : |

Db 4 SGGAGR 9

RESULT 13

S33782

acetylactate synthase (EC 4.1.3.18) small chain, valine-sensitive - Serratia marcesce

C;Species: Serratia marcescens

C;Date: 19-Mar-1997 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999

C;Accession: S33782

R;Yang, J.H.; Kim, S.S.

Biochim. Biophys. Acta 1157, 178-184, 1993

A;Title: Purification and characterization of the valine sensitive acetylactate synth

A;Reference number: S33781; MUID:93283409; PMID:8507653

A;Accession: S33782

A;Molecule type: protein

A;Residues: 1-11 <YAN>

A;Experimental source: ATCC 25419

C;Complex: heterotetramer; two small and two large chains

C;Function:

A;Description: catalyzes the condensation of pyruvate and alpha-ketobutyrate to form

A;Pathway: valine, leucine, and isoleucine biosynthesis

A;Note: this isoenzyme exhibits homotropic allosterism with pyruvate

C;Keywords: branched-chain amino acid biosynthesis; carbon-carbon lyase; flavoprotein

Query Match 32.3%; Score 21; DB 2; Length 11;

Best Local Similarity 80.0%; Pred. No. 1.9e+03;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 VGRGTG 12

I : : |

Db 4 VGRNG 8

RESULT 14

S29764

alpha-macroglobulin proteinase inhibitor - bullfrog (fragment)

C;Species: Rana catesbeiana (bullfrog)

C:Date: 19-Mar-1997 #sequence_revision 24-Mar-1999 #text_change 07-May-1999
 C:Accession: S29764
 R:Rubenstein, D.S.; Thoenes, I.B.; Pizzo, S.V.; Enghild, J.J.
 Biochem. J. 290, 85-95, 1993
 A:Title: Identification of monomeric alpha-macroglobulin proteinase inhibitors in birds,
 teinase inhibitor from the American bullfrog Rana catesbeiana.
 A:Reference number: S29764; MUID:93176138; PMID:7679897

A:Accession: S29764
 A:Molecule type: protein
 A:Residues: 1-12 <RUB>
 A:Experimental source: plasma
 C:Function:
 A:Description: inhibits the proteinases of different catalytic class
 C:Superfamily: alpha-2-macroglobulin
 C:Keywords: monomer; proteinase inhibitor

Query Match 32.3%; Score 21; DB 2; Length 12;
 Best Local Similarity 33.3%; Pred. No. 2.1e+03;
 Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 VVHCSAGVG 9
 : : | | |
 Db 1 IHLPGCG 9

RESULT 15
 S26552
 T-cell receptor beta chain (clone Cw3/701.1) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 13-Jan-1995 #sequence_revision 17-Apr-1998 #text_change 17-Mar-1999
 C:Accession: S26552
 R:Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid
 J. Exp. Med. 176, 439-447, 1992
 A:Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor
 A:Reference number: S26512; MUID:92364546; PMID:1380061
 A:Accession: S26552
 A:Molecule type: mRNA
 A:Residues: 1-12 <CAS>
 A:Cross-references: EMBL:X68002
 A:Experimental source: cytolytic T-lymphocyte, clone Cw3/701.1
 C:Superfamily: immunoglobulin V region;--immunoglobulin homology
 C:Keywords: T-cell receptor

Query Match 32.3%; Score 21; DB 2; Length 12;
 Best Local Similarity 37.5%; Pred. No. 2.1e+03;
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 CSAGVGRT 11
 : : | |
 Db 1 CASSYGET 8

Search completed: January 17, 2003, 11:01:06
 Job time : 16 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 10:58:12 ; Search time 10 Seconds
(without alignments)

49.772 Million cell updates/sec

Title: US-09-743-492-4

Perfect score: 65

Sequence: 1 VVHCSAGVGRTG 12

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 467

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Length	ID	Description
1	21	32.3	9	TAL3_PICJA	P17441 pichia jadi
2	20	30.8	9	TAL3_PICJA	P17440 pichia jadi
3	19	29.2	10	TRU2_UREUN	P40752 urechis uni
4	19	29.2	10	URAL1_HUMAN	P32118 homo sapien
5	18	27.7	10	COXO_THUOB	P80982 thunnus obe
6	17	26.2	9	CCAP_CARMA	P38556 carcinus ma
7	17	26.2	9	DNFL_LOEMI	P16339 locusta mig
8	17	26.2	10	COXO_RAT	P80432 rattus norv
9	16	24.6	9	OXYT_EISFO	P42998 eisenia foe
10	16	24.6	9	OXYV_SQUAC	P43000 squalus aca
11	16	24.6	10	FARP_MANSE	P18523 manduca sex
12	16	24.6	10	TPIS_NICPL	P19118 nicotiana p
13	16	24.6	12	OPS3_DROVI	P17645 drosophila
14	16	24.6	12	V14K_WSSV	P82006 white spot
15	15	23.1	9	ISOT_CYPCA	P42993 cyprinus ca
16	15	23.1	9	OXYA_SCYCA	P42996 scyllorhinu
17	15	23.1	9	OXYF_SCYCA	P42997 scyllorhinu
18	15	23.1	9	OXYT_CYPCA	P23879 cyprinus ca
19	15	23.1	9	OXYT_RABIT	P32878 eryctolagus
20	15	23.1	9	OXYT_FAJCL	P42994 raja clavav
21	15	23.1	10	CU30_LOEMI	P11735 locusta mig
22	15	23.1	10	GON1_ALLMI	P37041 alligator m
23	15	23.1	10	GON1_CLUPA	P81749 clupea pall
24	15	23.1	10	HTF_NAUCI	P10939 nauphoeta c
25	15	23.1	10	UPA5_HUMAN	P30091 homo sapien
26	14	21.5	5	UF01_MOUSE	P38639 mus musculu
27	14	21.5	9	CONO_CONGE	P05486 conus geogr
28	14	21.5	9	CONO_CONST	P05487 conus stria
29	14	21.5	9	OXYA_SQUAC	P42999 squalus aca
30	14	21.5	9	OXYT_OCIVU	P80027 octopus vul
31	14	21.5	9	PGLR_DIAAB	P81179 diaprepes a
32	14	21.5	10	GON2_CHICK	P37043 gallus gall
33	14	21.5	10	GON3_ONGKE	P20367 oncorhynch

ALIGNMENTS

RESULT 1

```
TAL3_PICJA
ID TAL3_PICJA STANDARD: PRT; 9 AA.
AC P17441;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Transaldolase III (EC 2.2.1.2) (Fragment).
OS Pichia jadinii (Yeast) (Candida utilis).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Pichia.
OX NCBI_TaxID=4903;
RN [1]
RP SEQUENCE.
RX MEDLINE=75145197; PubMed=1092268;
RA Tsolas O., Sun S.C.;
RT "Isolation of a peptide containing a histidyl-cysteiny sequence
from the active center of transaldolase.";
RL Arch. Biochem. Biophys. 167:525-533(1975).
CC -!- FUNCTION: TRANSALDOLASE IS IMPORTANT FOR THE BALANCE OF
METABOLITES IN THE PENTOSE-PHOSPHATE PATHWAY.
CC -!- CATALYTIC ACTIVITY: Sedoheptulose 7-phosphate + D-glyceraldehyde
3-phosphate -> D-erythrose 4-phosphate + D-fructose 6-phosphate.
CC -!- PATHWAY: Pentose phosphate pathway; nonoxidative part.
CC -!- SIMILARITY: BELONGS TO THE TRANSALDOLASE FAMILY. SUBFAMILY 1.
DR PIR; A11497; A11497.
DR InterPro; IPR001585; Transaldolase.
DR PROSITE; PS00958; TRANSALDOLASE_2; PARTIAL.
DR PROSITE; PS01054; TRANSALDOLASE_1; PARTIAL.
KW Transferase; Pentose shunt.
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 1033 MW; 325A31A44EB1E058 CRC64;
```

Query Match 32.3%; Score 21; DB 1; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 2 VHCS 5
:|: 6
Db 3 IHCN 6

RESULT 2

```
TAL3_PICJA
ID TAL3_PICJA STANDARD: PRT; 9 AA.
AC P17440;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Transaldolase I (EC 2.2.1.2) (Fragment).
OS Pichia jadinii (Yeast) (Candida utilis).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Pichia.
OX NCBI_TaxID=4903;
RN [1]
```

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RP SEQUENCE.
RX MEDLINE=77110646; PubMed=556924;
RA Sun S.C., Joris L., Tsolas O.;
RT "Purification of crystallization of transaldolase isozyme I and
RT evidence for different genetic origin of isozymes I and III in
RT Candida utilis.";
RL Arch. Biochem. Biophys. 178:69-78(1977).
CC -1- FUNCTION: TRANSALDOLASE IS IMPORTANT FOR THE BALANCE OF
CC METABOLITES IN THE PENTOSE-PHOSPHATE PATHWAY.
CC -1- CATALYTIC ACTIVITY: Sedoheptulose 7-phosphate + D-glyceraldehyde
CC 3-phosphate = D-erythrose 4-phosphate + D-fructose 6-phosphate.
CC -1- PATHWAY: Pentose phosphate pathway; nonoxidative part.
CC -1- SIMILARITY: BELONGS TO THE TRANSALDOLASE FAMILY. SUBFAMILY 1.
DR PIR; A12872; A12872.
DR InterPro; IPR001585; Transaldolase.
DR PROSITE; PS00958; TRANSALDOLASE_2; PARTIAL.
DR PROSITE; PS01054; TRANSALDOLASE_1; PARTIAL.
KW Transferase; Pentose shunt.
FT NON_TER 1
FT NON_TER 9
FT NON_TER 9
SQ SEQUENCE 9 AA; 1008 MW; 274F31AF0EB1E058 CRC64;

Query Match 30.8%; Score 20; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.1e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHC 4
DB 3 IHC 5

RESULT 3
TKU2_UREUN STANDARD; PRT; 10 AA.
ID TKU2_UREUN
AC P40752;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Urechis tacyhkinin II.
OS Urechis uncinatus.
OC Eukaryota; Metazoa; Echiura; Xenopneusta; Urechidae; Urechis.
OX NCBI_TaxID=6432;
[1]
RN SEQUENCE, AND SYNTHESIS.
RC TISSUE=Ventral nerve cord;
RX MEDLINE=93236558; PubMed=8476410;
RA Ikeda T., Minakata H., Nomoto K., Kubota I., Muneoka Y.;
RT "Two novel tacyhkinin-related neuropeptides in the echiuroid worm,
RL Urechis uncinatus.";
RC Biochem. Biophys. Res. Commun. 192:1-6(1993).
CC -1- FUNCTION: CONTRACTILE ACTION ON THE INNER CIRCULAR BODY-WALL
CC MUSCLE OF THE ANIMAL.
CC -1- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10
FT MOD_RES 10
SQ SEQUENCE 10 AA; 984 MW; 3F58DD79C9C87698 CRC64;

Query Match 29.2%; Score 19; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 SAGVGRTG 12
DB 1 AAGMGFFG 8

RESULT 4
URAL_HUMAN STANDARD; PRT; 10 AA.
ID URAL_HUMAN
AC P32118;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 16-OCT-2003 (Rel. 40, Last annotation update)

```

```

DE Unknown protein from 2D-page of red blood cells (Spot 1) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE.
RC TISSUE=Erythrocyte;
RX MEDLINE=94147970; PubMed=8313871;
RA Golaz O., Hughes G.J., Frutiger S., Paquet N., Bairoch A.,
RA Pasquali C., Sanchez J.-C., Tissot J.-D., Appel R.D., Walzer C.,
RA Balant L., Hochstrasser D.F.;
RT "Plasma and red blood cell protein maps: update 1993.";
RL Electrophoresis 14:1223-1231(1993).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.4, ITS MW IS: 23 Kda.
DR SWISS-2DPAGE; P32118; HUMAN.
FT NON_TER 1
FT NON_TER 10
FT NON_TER 10
SQ SEQUENCE 10 AA; 977 MW; 723C65BIADD0587B CRC64;

Query Match 29.2%; Score 19; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 GVGRTG 12
DB 4 GIATTG 9

RESULT 5
COXO_THUOB STANDARD; PRT; 10 AA.
ID COXO_THUOB
AC P80982;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cytochrome c oxidase polypeptide VIIC (EC 1.9.3.1) (Fragment).
OS Thunus obesus (Bigeye tuna).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCBI_TaxID=8241;
[1]
RN SEQUENCE.
RC TISSUE=Heart, and Liver;
RX MEDLINE=97454291; PubMed=9310366;
RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
RA Kadenbach B.;
RT "The subunit structure of cytochrome-c oxidase from tuna heart and
RT liver.";
RL Eur. J. Biochem. 248:99-103(1997).
CC -1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
CC MITOCHONDRIAL ELECTRON TRANSPORT.
CC -1- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -1- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIIC FAMILY.
KW Oxidoreductase; Inner membrane; Mitochondrion.
FT NON_TER 10
FT NON_TER 10
SQ SEQUENCE 10 AA; 1059 MW; 126DE767687BIDCB CRC64;

Query Match 27.7%; Score 18; DB 1; Length 10;
Best Local Similarity 37.5%; Pred. No. 1.8e+03;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 HCSAGVCR 10
DB 2 HYAEGPGK 9

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RESULT 6 .
CCAP_CARMA          STANDARD;          PRT;          9 AA.
ID  CCAP_CARMA
AC  P38556;
DT  01-OCT-1994 (Rel. 30, Created)
DT  01-OCT-1994 (Rel. 30, Last sequence update)
DT  15-DEC-1998 (Rel. 37, Last annotation update)
DE  Cardioactive peptide (CCAP).
OS  Carcinus maenas (Common shore crab) (Green crab),
OS  Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm),
OS  Tenebrio molitor (Yellow mealworm), and
OS  Spodoptera eridania (Southern armyworm).
OC  Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
OC  Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
OC  Brachyura; Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX  NCBI_TaxID=6759, 7130, 7067, 37547;
RN  [1]
RN  SEQUENCE.
RP  SPECIES=C.maenas; TISSUE=Pericardial organs;
RC  Stangier J., Hilbich C., Beyreuther K., Keller R.;
RA  "Unusual cardioactive peptide (CCAP) from pericardial organs of the
RT  shore crab Carcinus maenas.";
RL  Proc. Natl. Acad. Sci. U.S.A. 84:575-579(1987).
RN  [2]
RN  SEQUENCE.
RP  SPECIES=M.sexata;
RC  MEDLINE=93050243; PubMed=1426284;
RA  Cheung C.C., Loi P.K., Sylwester A.W., Lee T.D., Tublitz N.J.;
RT  "Primary structure of a cardioactive neuropeptide from the tobacco
RN  hawkmoth, Manduca sexta.";
RL  FEBS Lett. 313:165-168(1992).
RN  [3]
RN  SEQUENCE.
RP  SPECIES=T.molitor, and S.eridania; TISSUE=Head;
RC  MEDLINE=94176032; PubMed=8129851;
RA  Furuya K., Liao S., Reynolds S.E., Ota R.B., Hackett M.,
RA  Schooley D.A.;
RT  "Isolation and identification of a cardioactive peptide from Tenebrio
RN  molitor and Spodoptera eridania.";
RL  Biol. Chem. Hoppe-Seyler 374:1065-1074(1993).
CC  -1- FUNCTION: THE EFFECT OF CCAP IS BOTH INO- AND CHRONOTROPIC.
CC  -1- TISSUE SPECIFICITY: STORED IN PERICARDIAL ORGANS AND RELEASED
CC  INTO THE HEMOLYMPH.
DR  PIR; A26363; A26363.
DR  PIR; S27233; S27233.
KW  Neuropeptide; Amidation.
FT  DISULFID 3 9
FT  MOD_RES 9 9
FT  SEQUENCE 9 AA; 959 MW; CSA861A9CDD44EB9 CRC64;

Query Match 26.2%; Score 17; DB 1; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.1e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CSAGVG 9
    | | |
Db 3 CNAFTG 8

RESULT 7
DNF1_LOCMI          STANDARD;          PRT;          9 AA.
ID  DNF1_LOCMI
AC  P16339;
DT  01-AUG-1990 (Rel. 15, Created)
DT  01-AUG-1990 (Rel. 15, Last sequence update)
DT  15-DEC-1998 (Rel. 37, Last annotation update)
DE  Locupressin (Diuretic neuropeptide Fl/F2).
OS  Locusta migratoria (Migratory locust).
OC  Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC  Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
OC  Acridomorpha; Acridoidea; Acrididae; Oedipodinae; Locusta.
OX  NCBI_TaxID=7004;
RN  [1]
RN  SEQUENCE.
RP  SPECIES=L.migratoria; TISSUE=Liver, and Heart;
RC  STRAIN=Wistar; TISSUE=Liver, and Heart;
RX  MEDLINE=95324529; PubMed=7601105;
RA  Schaeffer H., Noack H., Halangk W., Brandt U., von Jagow G.;
RT  "Cytochrome-c oxidase in developing rat heart. Enzymic properties and
RN  amino-terminal sequences suggest identity of the fetal heart and the
adult liver isoform.";
RL  Eur. J. Biochem. 230:235-241(1995).
CC  -1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC  CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
CC  MITOCHONDRIAL ELECTRON TRANSPORT.
CC  -1- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) -> 4 ferricytochrome
CC  c + 2 H(2)O.
CC  -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIIC FAMILY.
KW  Oxidoreductase; Mitochondrion.
FT  NON_TER 10
FT  SEQUENCE 10 AA; 1117 MW; 126DE767687B1B0B CRC64;

Query Match 26.2%; Score 17; DB 1; Length 10;
Best Local Similarity 37.5%; Pred. No. 2.6e+03;
Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 3 HCSAGVGR 10
    | | |
Db 2 HYECPGK 9

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RP  SEQUENCE.
RC  TISSUE=Subesophageal ganglion, and Thoracic ganglion;
RX  MEDLINE=88077077; PubMed=3689410;
RA  Proux J.P., Miller C.A., Li J.P., Carney R.L., Girardie A.,
RA  Delaage M., Schooley D.A.;
RT  "Identification of an arginine vasopressin-like diuretic hormone from
RN  Locusta migratoria.";
RL  Biochem. Biophys. Res. Commun. 149:180-186(1987).
CC  -1- FUNCTION: DIURETIC HORMONE.
CC  -1- SUBUNIT: F2 IS AN ANTIPARALLEL DISULFIDE LINKED DIMER OF F1.
CC  -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR  PIR: A29477; A29477.
DR  InterPro; IPR000981; Neurhyp_horm.
DR  Pfam; PF00220; hormone4; 1.
DR  PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW  Hormone; Neuropeptide; Amidation
FT  DISULFID 1 6
FT  DISULFID 1 1
FT  DISULFID 6 6
FT  MOD_RES 9 9
FT  SEQUENCE 9 AA; 976 MW; 56EB176EB451A057 CRC64;

Query Match 26.2%; Score 17; DB 1; Length 9;
Best Local Similarity 28.6%; Pred. No. 1.1e+05;
Matches 2; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VVHCSAG 7
    : | |
Db 3 ITNCPRG 9

RESULT 8
COXO_RAT            STANDARD;          PRT;          10 AA.
ID  COXO_RAT
AC  P80432;
DT  01-NOV-1995 (Rel. 32, Created)
DT  01-NOV-1995 (Rel. 32, Last sequence update)
DT  15-JUN-2002 (Rel. 41, Last annotation update)
DE  Cytochrome c oxidase polypeptide VIIC, mitochondrial (EC 1.9.3.1)
DE  (VIIIa) (Fragment).
GN  COX7C OR COX7C1.
OS  Rattus norvegicus (Rat).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX  NCBI_TaxID=10116;
RN  [1]
RN  SEQUENCE.
RC  STRAIN=Wistar; TISSUE=Liver, and Heart;
RX  MEDLINE=95324529; PubMed=7601105;
RA  Schaeffer H., Noack H., Halangk W., Brandt U., von Jagow G.;
RT  "Cytochrome-c oxidase in developing rat heart. Enzymic properties and
RN  amino-terminal sequences suggest identity of the fetal heart and the
adult liver isoform.";
RL  Eur. J. Biochem. 230:235-241(1995).
CC  -1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC  CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
CC  MITOCHONDRIAL ELECTRON TRANSPORT.
CC  -1- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) -> 4 ferricytochrome
CC  c + 2 H(2)O.
CC  -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIIC FAMILY.
KW  Oxidoreductase; Mitochondrion.
FT  NON_TER 10
FT  SEQUENCE 10 AA; 1117 MW; 126DE767687B1B0B CRC64;

Query Match 26.2%; Score 17; DB 1; Length 10;
Best Local Similarity 37.5%; Pred. No. 2.6e+03;
Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 3 HCSAGVGR 10
    | | |
Db 2 HYECPGK 9

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RESULT 9
OXYT_EISFO      STANDARD;          PRT;          9 AA.
AC P42998;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Annetocin.
OS Eisenia foetida (Common brandling worm) (Common dung-worm).
OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
OC Lumbricina; Lumbricidae; Eisenia.
OX NCBI_TaxID=6396;
RN [1]
RP SEQUENCE.
RC TISSUE=PItuitary;
RX MEDLINE=94121660; PubMed=8292046;
RA Oumi T., Ukena K., Matsushima O., Ikeda T., Fujita T., Minakata H.,
RA Nomoto K.;
RT "Annetocin: an oxytocin-related peptide isolated from the earthworm,
RT Eisenia foetida.";
RL Biochem. Biophys. Res. Commun. 198:393-399(1994).
CC -!- FUNCTION: POTENTIATES SPONTANEOUS CONTRACTIONS OF THE GUT AND ALSO
CC PULSATORY CONTRACTIONS AND BLADDER-SHAKING MOVEMENT OF THE
CC NEPHRIDIA. MAY BE INVOLVED IN OSMOREGULATION OF THE ANIMAL THROUGH
CC NEPHRIDIAL FUNCTION.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR PIR: PC2021; PC2021.
DR InterPro: IPR000981; Neurhyp_horm.
DR Pfam: PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; FALSE_NEG.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
FT SEQUENCE 9 AA; 996 MW; D4EEB76EB45412C9 CRC64;
QY 1 VVHCASG 7
DB 3 VRNCPTG 9
Query Match 24.6%; Score 16; DB 1; Length 9;
Best Local Similarity 42.9%; Pred. No. 1.1e+05;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 VVHCASG 7
DB 3 VRNCPTG 9
RESULT 10
OXYV_SQUAC      STANDARD;          PRT;          9 AA.
AC P43000;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Valitocin.
OS Squalus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalae; Squaloidei; Squalidae; Squalus.
OX NCBI_TaxID=7797;
RN [1]
RP SEQUENCE.
RX MEDLINE=73031727; PubMed=5083097;
RA Acher R., Chauvet J., Chauvet M.-T.;
RT "Phylogeny of the neurohypophysial hormones. Two new active peptides
RT isolated from a cartilaginous fish, Squalus acanthias.";
RL Eur. J. Biochem. 29:12-19(1972).
RN [2]
RP SEQUENCE.
RX MEDLINE=72128038; PubMed=4622083;
RA Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;
RT "Identification of 2 new neurohypophyseal hormones, valitocin (Val8-
RT oxytocin) and aspartocin (Asn4-oxytocin) in a selachian fish, the
RT spiny dog-fish (Squalus acanthias).";
RL C. R. Acad. Sci., D, Sci. Nat. 274:313-316(1972).
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR InterPro: IPR000981; Neurhyp_horm.
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DR InterPro: IPR001230; Prenyl_site.
DR Pfam: PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
FT SEQUENCE 9 AA; 996 MW; 17EDD76EB456D04B CRC64;
QY 1 VVHCASG 7
DB 3 IQNCPVG 9
Query Match 24.6%; Score 16; DB 1; Length 9;
Best Local Similarity 28.8%; Pred. No. 1.1e+05;
Matches 2; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 VVHCASG 7
DB 3 IQNCPVG 9
RESULT 11
FARP_MANSE      STANDARD;          PRT;          10 AA.
AC P18523;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRFamide-like neuropeptide.
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;
OC Ditrysia; Sphingioidea; Sphingidae; Sphinginae; Manduca.
OX NCBI_TaxID=7130;
RN [1]
RP SEQUENCE.
RX MEDLINE=91045350; PubMed=2235684;
RA Kington T.G., Teplow D.B., Phillips J.M., Riehm J.P., Rao K.R.,
RA Hildebrand J.G., Homborg U., Kammer A.E., Jardine I., Griffin P.R.,
RA Hunt D.F.;
RT "A new peptide in the FMRFamide family isolated from the CNS of the
RT hawkmoth, Manduca sexta.";
RL Peptides 11:849-856(1990).
CC -!- FUNCTION: INCREASES THE FORCE OF NEURALLY EVOKED CONTRACTIONS IN
CC THE MAJOR POWER-PRODUCING FLIGHT MUSCLES, THE DORSAL LONGITUDINAL
CC MUSCLES AND SO IS LIKELY TO PLAY A ROLE IN SUSTAINING OR PROMOTING
CC FLIGHT BEHAVIOR PATTERNS.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR PIR: A43977; A43977.
KW Amidation; Neuropeptide.
FT MOD_RES 1 1
FT MOD_RES 10 10
FT SEQUENCE 10 AA; 1247 MW; D3C45229D5B1F2D2 CRC64;
QY 1 VVH 3
DB 3 VVH 5
Query Match 24.6%; Score 16; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VVH 3
DB 3 VVH 5
RESULT 12
TPIS_NICPL      STANDARD;          PRT;          10 AA.
AC P19118;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Triosephosphate isomerase, cytosolic (EC 5.3.1.1) (TIM) (Fragment).
OS Nicotiana glumaginifolia (Leadwort-leaved tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4092;
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RN SEQUENCE.
RA [1]
RA Bouw G., de Loose M., Inze D., van Montagu M., Vandekerckhove J.;
RT "Alterations in the phenotype of plant cells studied by NH2-terminal
RT amino acid-sequence analysis of proteins electrophoretically from two-
RT dimensional gel-separated total extracts."
RL Proc. Natl. Acad. Sci. U.S.A. 84:4806-4810(1987).
CC -1- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate = glycerone
CC phosphate.
CC -1- PATHWAY: PLAYS AN IMPORTANT ROLE IN SEVERAL METABOLIC PATHWAYS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- MISCELLANEOUS: IN PLANTS, THERE ARE TWO TYPES OF TPIS, CYTOSOLIC
CC AND PLASTID.
CC -1- SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.
DR PIR: A27617; A27617.
DR InterPro: IPR000652; Triophos_1smrse.
DR PROSITE: PS00171; TIM: PARTIAL.
KM Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;
KM Pentose shunt.
FT NON_TER 10
SQ SEQUENCE 10 AA: 1140 MW: 8089D37862C9C9D1 CRC64;

Query Match 24.6%; Score 16; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GRT 11
   |||
Db 1 GRT 3

RESULT 13
OPS3_DROVI STANDARD; PRT; 12 AA.
ID OPS3_DROVI
AC P17645;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Opsin Rh3 (inner R7 photoreceptor cells opsin) (Fragment).
GN Rh3.
OS Drosophila virilis (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OC NCBI_TaxID=7244;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90249748; PubMed=2140105;
RA Fortini M.E., Rubin G.M.;
RT "Analysis of cis-acting requirements of the Rh3 and Rh4 genes reveals
RT a bipartite organization to rhodopsin promoters in Drosophila
RT melanogaster."
RT Genes Dev. 4:444-463(1990).
CC -1- FUNCTION: VISUAL PIGMENTS ARE THE LIGHT-ABSORBING MOLECULES THAT
CC MEDIATE VISION. THEY CONSIST OF AN APOPROTEIN, OPSIN, COVALENTLY
CC LINKED TO CIS-RETINAL.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- MISCELLANEOUS: EACH DROSOPHILA EYE IS COMPOSED OF 800 FACETS OR
CC OMATIDIA. EACH OMATIDIUM CONTAINS 8 PHOTORECEPTOR CELLS (R1-R8),
CC THE R1 TO R6 CELLS ARE OUTER CELLS, WHILE R7 AND R8 ARE INNER
CC CELLS.
CC -1- MISCELLANEOUS: OPSIN RH3 IS SENSITIVE TO UV LIGHT.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC OPSIN SUBFAMILY.
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CC EMBL: X51350; CA35742.1;
DR FLYBASE; FBgn0013091; Dvir\Rh3.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR InterPro: IPR001760; Opsin.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; PARTIAL.
DR PROSITE: PS00238; OPSIN; PARTIAL.
KM Photoreceptor; Retinal protein; Transmembrane; Phosphorylation;
KM Glycoprotein; G-protein coupled receptor; Vision.
FT CARBOHYD 10
FT NON_TER 12
SQ SEQUENCE 12 AA: 1253 MW: 04024E43495865B0 CRC64;

Query Match 24.6%; Score 16; DB 1; Length 12;
Best Local Similarity 50.0%; Pred. No. 4.7e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 AGVG 9
   :||
Db 6 SGIG 9

RESULT 14
V14K_MSSV STANDARD; PRT; 12 AA.
ID V14K_MSSV
AC P82006;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 14.5 kDa structural polypeptide (Fragment).
OS White spot syndrome virus (WSSV).
OC Viruses; dsDNA viruses, no RNA stage; Nimaviridae.
OC NCBI_TaxID=92652;
RN [1]
RP SEQUENCE.
RC STRAIN=South Carolina;
RX MEDLINE=20214217; PubMed=10752552;
RA Wang Q., Poulos B.T., Lightner D.V.;
RT "Protein analysis of geographically isolates of shrimp white spot syndrome
RT virus."
RL Arch. Virol. 145:263-274(2000).
CC -1- FUNCTION: STRUCTURAL COMPONENT OF THE VIRION.
CC NON_TER 12
FT SEQUENCE 12 AA: 1242 MW: 24B8D4FFD21A338 CRC64;

Query Match 24.6%; Score 16; DB 1; Length 12;
Best Local Similarity 75.0%; Pred. No. 4.7e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 GRTG 12
   |||
Db 9 GRRG 12

RESULT 15
ISOT_CYPCA STANDARD; PRT; 9 AA.
ID ISOT_CYPCA
AC P42993;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Isotocin.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinus.
OC NCBI_TaxID=7962;
RN [1]
RP SEQUENCE.
RC TISSUE=pituitary;
RA Acher R., Chauvet J., Chauvet M.-T., Crepy D.;
RT "Characterization of neurohypophyseal hormones from a fresh water bony
RT fish, the carp (Cyprinus carpio). Comparison with hormones from sea

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RT water bony fishs."
 RL Comp. Biochem. Physiol. 14:245-254(1965).
 CC -1- FUNCTION: ANTIDIURETIC HORMONE.
 CC -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
 DR PIR: A61364; A61364.
 DR InterPro: IPR000981; Neuhyp_horm.
 DR InterPro: IPR001230; Prenyl_site.
 DR Pfam: PF00220; hormone4; 1.
 DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.
 KW Hormone; Amidation.
 FT DISULFID 1 6
 FT MOD_RES 9 9
 SQ SEQUENCE 9 AA: 969 MW: 17PF476EB455B04B CRC64;

Query Match 23.1%; Score 15; DB 1; Length 9;
 Best local Similarity 28.6%; Pred. No. 1.1e+05;
 Matches 2; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 VVHCSAG 7
 : : 1 1
 Db 3 ISNCPIG 9

Search completed: January 17, 2003, 11:00:09
 Job time : 10 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 10:58:32 ; Search time 28 Seconds
(without alignments)
88.306 Million cell updates/sec

Title:	US-09-743-492-4
Perfect score:	65
Sequence:	1 VVHCSAGVGRGTG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

```
Searched:      671580 segs, 206047115 residues
Total number of hits satisfying chosen parameters: 20411
```

```
Minimum DB seq length: 0
Maximum DB seq length: 12
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database :
SPREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vetbrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archeap:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Query Match	Score	Request No.	Description
1	38.5	25	061331 mus musculus
2	35.4	23	Q9YV79 panulirus 1
3	32.3	21	Q92009 gallus galli
4	33.3	21	Q945C2 crypthecocidi
5	30.8	20	Q8WP04 ateles belz
6	30.8	20	Q9SP67 gallus galli
7	29.2	19	Q17140 crassostrea
8	29.2	19	Q9TFT8 bos taurus
9	27.7	18	Q99887 homo sapien
10	27.7	18	Q66874 feline cali
11	27.7	11	Q66877 feline cali
12	27.7	12	Q16452 homo sapien
13	27.7	12	Q945C4 crypthecocidi
14	27.7	12	Q91F00 human adeno
15	27.7	12	Q91E29 human adeno
16	27.7	12	Q12074 caprine art

17	18	27.7	12	15	012076	012076 caprine art
18	18	27.7	12	15	012078	012078 caprine art
19	18	27.7	12	15	012080	012080 caprine art
20	18	27.7	12	15	012082	012082 caprine art
21	18	27.7	12	15	012084	012084 caprine art
22	18	27.7	12	15	012086	012086 caprine art
23	18	27.7	12	15	012088	012088 caprine art
24	18	27.7	12	15	012090	012090 caprine art
25	18	27.7	12	15	012092	012092 caprine art
26	18	27.7	12	15	012094	012094 caprine art
27	18	27.7	12	15	012106	012106 caprine art
28	18	27.7	12	15	012108	012108 caprine art
29	18	27.7	12	15	012110	012110 caprine art
30	18	27.7	12	15	012112	012112 caprine art
31	18	27.7	12	15	012114	012114 caprine art
32	18	27.7	12	15	012116	012116 caprine art
33	18	27.7	12	15	012118	012118 caprine art
34	18	27.7	12	15	078845	078845 human immun
35	17	26.2	8	4	015900	015900 homo sapien
36	17	26.2	8	11	060615	060615 mus musculu
37	17	26.2	10	3	090VW2	090VW2 schizopyll
38	17	26.2	11	11	099JC3	099JC3 rattus sp.
39	17	26.2	12	3	099R22	099R22 cryptococcu
40	17	26.2	12	6	099R02	099R02 bos taurus
41	17	26.2	12	10	002319	002319 pinus sylve
42	17	26.2	12	10	002320	002320 pinus sylve
43	17	26.2	12	10	038715	038715 arachis hyp
44	16.5	25.4	11	5	P82698	P82698 leucophaea
45	16	24.6	7	2	Q47505	Q47505 escherichia

ALIGNMENTS

RESULT	1				
ID	061331	PRELIMINARY;	PRT;	12 AA.	
AC	Q61331;				
DT	01-NOV-1996 (TREMBLrel. 01, Created)				
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)				
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)				
DE	N-acetylglucosamine (Beta1-4) galactosyl transferase (EC 2.4.1.90) (Fragment).				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=89033997; PubMed=3141392;				
RA	Nakazawa K., Ando T., Kimura T., Narimatsu H.;				
RT	"Cloning and sequencing of a full-length cDNA of mouse N-				
RT	acetylglucosamine (beta1-4)galactosyltransferase.";				
RL	J. Biochem. 104:165-168(1988).				
DR	EMBL; D00315; BAA00217.1; -.				
KW	Glycosyltransferase; Transferase.				
FT	NON_TER	1			
FT	NON_TER	12			
SO	SEQUENCE	12 AA; 1283 MW; 304EA0668387728 CRC64;			
Query Match		38.5%;	Score 25;	DB 11; Length 12;	
Best Local Similarity		57.1%;	Pred. No. 5.3e+02;		
Matches	4; Conservative	3; Mismatches	0; Indels	0; Gaps	0;
OY	5 SAGVGT 11				
	: : :				
Dd	3 SSGGKT 9				

RESULT	2				
ID	Q9TY79	PRELIMINARY;	PRT;	12 AA.	
AC	Q9TY79;				

DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE Potassium channel (Fragment).
 GN SHAKER.
 OS Panulirus interruptus (California spiny lobster).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Palinura;
 OC Palinuroidea; Palinuridae; Panulirus.
 OX NCBI_TaxId=6735;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98330950; PubMed=9665521;
 RA Kim M., Baro D.J., Lanning C.C., Doshi M., Moskowitz H.S., Farnham J.,
 RA Harris-Warlick R.M.;
 RT "Expression of Panulirus shaker potassium channel splice variants";
 RL Recept. Channels 5:291-304(1998).
 DR EMBL: AF017131; AAC05911.1; -.
 FT NON_TER
 SO SEQUENCE 12 AA; 1227 MW; 049050CA44D4DD4 CRC64;

Query Match 35.4%; Score 23; DB 5; Length 12;
 Best Local Similarity 33.3%; Pred. No. 1.2e+03;
 Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 VHCAGVG 9
 : : 1 : 1 :
 DB 1 MISCNANAG 9

RESULT 3

ID 092009 PRELIMINARY; PRT; 9 AA.
 AC 092009;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
 DE C-REL protein (Fragment).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxId=9031;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91133738; PubMed=2284104;
 RA Hannink M., Temin H.M.;
 RT "Structure and autoregulation of the c-rel promoter";
 RL Oncogene 5:1843-1850(1990).
 RN [12]
 RP SEQUENCE FROM N.A.
 RA Hannink M., Temin H.M.;
 RL Oncogene 0:0-0(1990).
 DR EMBL: X56440; CAA38822.1; -.
 DR EMBL: X56515; CAA39866.1; -.
 FT NON_TER
 SO SEQUENCE 9 AA; 805 MW; DE317DD87865A2CD CRC64;

Query Match 32.3%; Score 21; DB 13; Length 9;
 Best Local Similarity 66.7%; Pred. No. 6.7e+05;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 SAGVGR 10
 : : 1 : 1 : 1 :
 DB 4 SGCAGR 9

RESULT 4

ID 0945C2 PRELIMINARY; PRT; 12 AA.
 AC 0945C2;
 DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE DapC protein (Fragment).
 OS Cryptocodium colonii (Dinoflagellate).
 OC Eukaryota; Alveolata; Dinophyceae; Gonyaulacales; Cryptocodiniaceae;
 OC Cryptocodium.
 OX NCBI_TaxId=2866;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21428164; PubMed=11545436;
 RA Guillebaud D., Derelle E., Bhaud Y., Moreau H.;
 RT "Role of nuclear MW domains and proline-rich proteins in
 RL dinoflagellate transcription";
 RL Probst 152:127-138(2001).
 DR EMBL: AF417569; AAL15907.1; -.
 FT NON_TER
 SO SEQUENCE 12 AA; 1436 MW; C4831B7517B1F2CD CRC64;

Query Match 32.3%; Score 21; DB 10; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHC 4
 : : 1 : 1 :
 DB 6 VHC 8

RESULT 5

ID 08WP04 PRELIMINARY; PRT; 10 AA.
 AC 08WP04;
 DT 01-MAR-2002 (TReMBLrel. 20, Created)
 DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
 DE Oculocutaneous albinism type II (Fragment).
 GN OCA2.
 OS Ateles belzebuth chamek (Chamek spider monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Ateles.
 OX NCBI_TaxId=118643;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21636947; PubMed=11778686;
 RA Senanez H.N., Lima C.R., Lemos B., Bonvicino C.R., Moreira M.A.M.,
 RA Canavez F.C.;
 RT "Gene assignment in Ateles paniscus chamek (Platyrrhini, Primates).
 RT Allocation of 18 markers of human syntenic groups 1,2,7,14,15,17 and
 RT 22";
 RL Chromosome Res. 9:631-639(2001).
 DR EMBL: AF375652; AAL31489.1; -.
 FT NON_TER
 SO SEQUENCE 10 AA; 901 MW; 22DF47DD87EA5B8 CRC64;

Query Match 30.8%; Score 20; DB 6; Length 10;
 Best Local Similarity 60.0%; Pred. No. 3.4e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 CSAGV 8
 : : 1 : 1 :
 DB 5 CGAGM 9

RESULT 6

ID 09PS67 PRELIMINARY; PRT; 12 AA.
 AC 09PS67;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Myosin (Fragment).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.

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OX NCBI_TaxID=9031;
RP [1]
RP SEQUENCE.
RX MEDLINE=92031443; PubMed=1931944;
RA Garabedian T.E., Yount R.G.;
RT "Direct photoaffinity labeling of gizzard myosin with vanadate-trapped
RL adenosine diphosphate.";
RL Biochemistry 30:10126-10132(1991).
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 12 AA; 1178 MW; C1FC2E0D9AA387D CRC64;

Query March 30.8%; Score 20; DB 13; Length 12;
Best Local Similarity 50.0%; Pred. No. 4.2e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGVGR 11
DB 3 SGAGKT 8

RESULT 7
ID 017140 PRELIMINARY; PRT; 12 AA.
AC 017140;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Putative c-myc homolog (Fragment).
OS Crassostrea virginica (Eastern oyster).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Ostreoida;
OC Ostreoidae; Ostreidae; Crassostrea.
OX NCBI_TaxID=6565;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WESTERN NORTH ATLANTIC WILD OYSTER;
RA Hare M.P., Avise J.C.;
RT "Population structure in the American Oyster as inferred by Nuclear
RT Mol. Biol. Evol. 0:0-0(1997).
DR EMBL; AF024522; AAB82269.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 12 AA; 1334 MW; FF6312ABFE1775AA CRC64;

Query Match 29.2%; Score 19; DB 5; Length 12;
Best Local Similarity 42.9%; Pred. No. 6.3e+03;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 HCSAGVG 9
DB 3 HCSAPRG 9

RESULT 8
ID 09TRT8 PRELIMINARY; PRT; 12 AA.
AC 09TRT8;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE 15 kDa histone H4 homolog (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=92132498; PubMed=1734497;
RA Veiby O.P., Sletten K., Husby G., Nordstoga K.;
RT "Amino acid sequence analyses of non-AA proteins from amyloid fibrils
RT of bovine kidney.";
```

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RL Scand. J. Immunol. 35:63-69(1992).
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 12 AA; 1406 MW; CA8BC4BC900372D CRC64;

Query Match 29.2%; Score 19; DB 6; Length 12;
Best Local Similarity 45.5%; Pred. No. 6.3e+03;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 VVHCAGVGR 11
DB 2 VVYALKRQGR 12

RESULT 9
ID 099887 PRELIMINARY; PRT; 9 AA.
AC 099887;
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE 11 <beta>-HSD2 protein (Fragment).
GN 11 <BETA>-HSD2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96133030; PubMed=8538347;
RA Stewart P.M., Krozowski Z.S., Gupta A., Milford D.V., Howie A.J.,
RA Sheppard M.C., Whorwood C.B.;
RT "Hypertension in the syndrome of apparent mineralocorticoid excess due
RT to mutation of the 11 beta-hydroxysteroid dehydrogenase type 2 gene.";
RL Lancet 347:88-91(1996).
DR EMBL; S80133; AAD14324.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 9 AA; 1020 MW; CERC2EB1F5B059C9 CRC64;

Query Match 27.7%; Score 18; DB 4; Length 9;
Best Local Similarity 50.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VVHC 4
DB 4 ISHC 7

RESULT 10
ID 066874 PRELIMINARY; PRT; 11 AA.
AC 066874;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
DE Polymerase (Fragment).
OS Feline calicivirus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
OC Vesivirus.
OX NCBI_TaxID=11978;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=255;
RX MEDLINE=95250311; PubMed=7732664;
RA Seal B.S., Neill J.D.;
RT "Capsid protein gene sequence of feline calicivirus isolates 255 and
RT LUK: further evidence for capsid protein configuration among feline
RT caliciviruses.";
RL Virus Genes 9:183-187(1995).
DR EMBL; U07130; AAA74412.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 11 AA; 1232 MW; 4EBE5F5CMAEB1E7 CRC64;
```

Query Match 27.7%; Score 18; DB 12; Length 11;
 Best Local Similarity 66.7%; Pred. No. 8.6e+03;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 VHC 4
 : :
 Db 4 LHC 6

RESULT 11
 066877 PRELIMINARY; PRT; 11 AA.
 AC 066877;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DE Polymerase (Fragment).
 OS Feline calicivirus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
 OC Vesivirus.
 OX NCBI_TaxID=11978;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LIK:
 RX MEDLINE=95250311; PubMed=7732664;
 RA Seal B.S., Neill J.D.;
 RT "Capsid protein gene sequence of feline calicivirus isolates 255 and
 RT LIK: further evidence for capsid protein configuration among feline
 RT caliciviruses";
 RL Virus Genes 9:183-187(1995).
 DR EMBL, U07131; AAA74415.1; -.
 FT NON_TER 1
 SQ SEQUENCE 11 AA; 1264 MW; 5E9F43BCCAEB1E7 CRC64;

Query Match 27.7%; Score 18; DB 12; Length 11;
 Best Local Similarity 66.7%; Pred. No. 8.6e+03;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 VHC 4
 : :
 Db 4 LHC 6

RESULT 12
 016452 PRELIMINARY; PRT; 12 AA.
 AC 016452;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DE Mutant collagen alpha 2(I) chain CB peptide alpha 2CBA
 DE (Fragment).
 GN COL1A2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92201825; PubMed=1551666;
 RA Nicholls A.C., Oliver J., Renouf D.V., Heath D.A., Pope F.M.;
 RT "The molecular defect in a family with mild atypical osteogenesis
 RT imperfecta and extreme joint hypermobility: exon skipping caused by an
 RT 11-bp deletion from an intron in one COL1A2 allele";
 RL Hum. Genet. 88:627-633(1992).
 DR EMBL, S89896; AAB21862.1; -.
 KW Collagen.
 FT NON_TER 1
 FT NON_TER 12
 SQ SEQUENCE 12 AA; 1161 MW; D5BD7D21FAE861B6 CRC64;

Query Match 27.7%; Score 18; DB 4; Length 12;
 Best Local Similarity 75.0%; Pred. No. 9.5e+03;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 9 GRTG 12
 : :
 Db 4 GRTG 7

RESULT 13
 0945C4 PRELIMINARY; PRT; 12 AA.
 ID 0945C4
 AC 0945C4;
 DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
 DE Beta-tubulin (Fragment).
 OS Cryptocodium cohnii (Dinoflagellate).
 OC Eukaryota; Alveolata; Dinophyceae; Gonyaulacales; Cryptocodiniaceae;
 OC Cryptocodium.
 OX NCBI_TaxID=2866;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Guillebaud D., Derelle E., Lozano J.C., Bingham S., Moreau H.;
 RT "A single TBP-like protein is present in the marine unicellular
 RT organism: the dinoflagellate Cryptocodium cohnii";
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AF417567; AAL15905.1; -.
 FT NON_TER 12
 SQ SEQUENCE 12 AA; 1299 MW; F2AE9D1D416D051 CRC64;

Query Match 27.7%; Score 18; DB 10; Length 12;
 Best Local Similarity 42.9%; Pred. No. 9.5e+03;
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 VHCASG 7
 : :
 Db 3 LVHIOGG 9

RESULT 14
 091F00 PRELIMINARY; PRT; 12 AA.
 ID 091F00
 AC 091F00;
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DE E1A nucleoprotein (Fragment).
 OS Human adenovirus type 5.
 OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
 OX NCBI_TaxID=28285;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hayashi S., Gillam I.C., McDonald T., Way D., Harris T.,
 RA Sedgwick E.G.;
 RT "E1A DNA of group C adenovirus integrates into human chromosomes";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AF288220; AAF91488.1; -.
 KW Nucleocapsid.
 FT NON_TER 12
 SQ SEQUENCE 12 AA; 1337 MW; 06D6D0D4171EB0 CRC64;

Query Match 27.7%; Score 18; DB 12; Length 12;
 Best Local Similarity 60.0%; Pred. No. 9.5e+03;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 CSAGV 8
 : :
 Db 6 CHGCV 10

RESULT 15
 091E29 PRELIMINARY; PRT; 12 AA.
 ID 091E29
 AC 091E29;

DT 01-OCT-2000 (TRENBLrel. 15, Created)
 DT 01-OCT-2000 (TRENBLrel. 15, last sequence update)
 DT 01-OCT-2000 (TRENBLrel. 15, last annotation update)
 DE E1A nucleoprotein (Fragment).
 OS Human adenovirus type 5.
 OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
 OX NCBI_TaxID=28285;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hayashi S., Gilliam I.C., McDonald T., Way D., Harris T.,
 RA Sedgwick E.G.;
 RT "E1A DNA of group C adenovirus integrates into human chromosomes.";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF288641; AAF91494.1; -.
 KW Nucleocapsid.
 FT NON_TER 12
 SQ SEQUENCE 12 AA; 1337 MW; 06D6DD0D4171EB0 CRC64;

Query Match 27.7%; Score 18; DB 12; Length 12;
 Best Local Similarity 60.0%; Pred. No. 9.5e+03;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 CSAGV 8
 1 11
 Db 6 CHGV 10

Search completed: January 17, 2003, 11:00:44
 Job time : 28 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 10:55:47 : Search time 34 Seconds
(without alignments)
47.030 Million cell updates/sec

Title: US-09-743-492-4

Perfect score: 65

Sequence: 1 VVHCASAGVGRTG 12

Scoring table: BLOSUM62

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 204235

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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13: /SID52/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
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22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	DB	ID	Description
1	65	100.0	12	21	AAV81786	Protein tyrosine p
2	61	93.8	11	20	AAV34167	PTP-D1 binding reg
3	51	78.5	9	21	AAV19775	Protein tyrosine p
4	50	76.9	11	19	AAV64787	Human tumour suppr
5	50	76.9	11	20	AAV07459	Protein tyrosine p
6	45	69.2	8	20	AAV94026	PTP-OB tyrosine p
7	45	69.2	8	22	AAU01458	Conserved amino ac
8	45	69.2	9	21	AAV19777	Protein tyrosine p
9	43	66.2	10	23	AAV07849	Protein tyrosine p
10	43	66.2	12	22	AAV59247	Peptide associated

11	42	64.6	10	21	AAV19603	Human dual-specific
12	42	64.6	11	18	AAV35299	Protein tyrosine p
13	41	63.1	7	20	AAV14759	Tyrosine phosphata
14	41	63.1	9	21	AAV19776	Protein tyrosine p
15	40	61.5	7	16	AAV85205	Tyrosine phosphata
16	40	61.5	7	20	AAV14760	Tyrosine phosphata
17	40	61.5	7	20	AAV25413	Human PTPB1 protei
18	39	60.0	10	21	AAV32999	Human dual-specific
19	39	60.0	10	22	AAV67168	Human dual-specific
20	39	60.0	10	22	AAV66432	Human DSP-3 active
21	38	58.5	7	20	AAV14758	Tyrosine phosphata
22	36	55.4	7	15	AAV46291	PTP-D1/D2 primer #
23	36	55.4	7	16	AAV49154	Corresp. to human
24	36	55.4	7	16	AAV71502	Conserved region o
25	36	55.4	7	19	AAV49916	Protein tyrosine p
26	36	55.4	8	23	AAV7886	Human PTPN catalyt
27	36	55.4	10	23	AAV22730	Human dual-specific
28	36	55.4	11	16	AAV72863	Rat receptor type-
29	36	55.4	11	19	AAV52305	PTP catalytic doma
30	36	55.4	11	21	AAV81784	Protein tyrosine p
31	36	55.4	11	21	AAV79019	Protein tyrosine p
32	36	55.4	11	21	AAV56099	Phosphatase domain
33	36	55.4	11	22	AAV78257	Generic conserved
34	36	55.4	11	22	AAV59585	Non-receptor PTPas
35	36	55.4	11	22	AAV59358	Protein tyrosine p
36	35	53.8	7	20	AAV14757	Tyrosine phosphata
37	35	53.8	11	18	AAV29151	Consensus catalyti
38	35	53.8	12	21	AAV70337	Subsequence-2 of A
39	34	52.3	9	20	AAV39372	Protein tyrosine p
40	32	49.2	11	23	AAV13602	Protein tyrosine p
41	31	47.7	5	20	AAV89256	Human PTP04 conser
42	31	47.7	6	19	AAV3022	Protein tyrosine p
43	31	47.7	10	22	AAV94324	Human complementar
44	31	47.7	10	22	AAV94326	Human complementar
45	31	47.7	10	22	AAV6427	Saccharomycos cere

ALIGNMENTS

RESULT 1
ID AAV81786 standard; Peptide: 12 AA.
AAV81786;
07-JUN-2000 (first entry)
Protein tyrosine phosphatase motif #1.
Human; protein tyrosine phosphatase; antibody; intracellular domain; LAR; CDP5; PTP; diagnosis; insulin resistance related disease; syndrome X; non-insulin dependent diabetes mellitus; arteriosclerosis; therapy; heart disorder; signature motif.
Unidentified.
WO200002922-A1.
20-JAN-2000.
06-JUL-1999; 99WO-JP03656.
10-JUL-1998; 98WO-JP03120.
(FUSO) FUSO PHARM IND LTD.
Yamamoto H, Tsujikawa K, Uchino Y;
WPI; 2000-182215/16.
Antibody for diagnosis and treatment of insulin resistance disorders and syndrome X recognises the intracellular domains of tyrosine

PT phosphatase -
 XX
 PS Example 3; Page 32; 83pp; Japanese.
 XX
 CC This sequence represents a motif of a protein tyrosine
 CC phosphatases. The invention relates to an antibody of the invention that
 CC has sites specifically recognising the intracellular domain
 CC of two or more protein tyrosine phosphatases (PTPs). The antibody is
 CC useful for the detection and assay of PTP including novel phosphatases
 CC generated by cloning; and diagnosis, treatment and prevention of insulin
 CC resistance related diseases and non-insulin dependent diabetes mellitus,
 CC syndrome X and arteriosclerosis and heart disorders.
 XX
 SQ Sequence 12 AA:
 Query Match 100.0%; Score 65; DB 21; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.00021;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VVHCSAGVGRG 12
 DB 1 VVHCSAGVGRG 12
 RESULT 2
 AAY34167
 ID AAY34167 standard; peptide; 11 AA.
 XX
 AC AAY34167;
 XX
 DT 09-NOV-1999 (first entry)
 XX
 DE PTP-DI binding region.
 XX
 KW PTP-DI; human; protein tyrosine phosphatase; neoplastic formation;
 KW PTPase; growth factor signal transduction; cell cycle progression;
 KM cancer; diabetes; cellular phosphotyrosine metabolism; binding site.
 XX
 OS Homo sapiens.
 XX
 PN US5955592-A.
 XX
 PD 21-SEP-1999.
 XX
 PF 27-APR-1994; 94US-0234440.
 XX
 PR 27-APR-1994; 94US-0234440.
 PR 05-AUG-1992; 92US-0923740.
 XX
 PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 XX
 PI Moller KB, Moller NPH, Ullrich A;
 XX
 DR WPI; 1999-539599/45.
 XX
 PT Nucleic acids encoding protein tyrosine phosphatase PTP-DI
 PT useful for identification of PTP-DI modulators
 XX
 PS Example 8; Column 37; 63pp; English.
 XX
 CC This sequence represents a fragment of the protein tyrosine phosphatase
 CC of the invention, designated PTP-DI. This sequence is thought to promote
 CC binding of specific molecules to PTP-DI. The new PTP proteins are a
 CC subfamily of protein tyrosine phosphatases (PTPases) involved with growth
 CC factor signal transduction, cell cycle progression, and neoplastic
 CC formation. The DNA sequence may be used in the recombinant production of
 CC PTP-DI according to standard DNA methodology. The protein expressed may
 CC then be used in assays to identify modulators of its enzymatic activity
 CC and in the production of antibodies. The nucleic acids may also be used
 CC in assays to detect and quantify expression of PTP-DI in samples. Methods
 CC identifying normal or mutant PTP-D genes, or for measuring amount or
 CC activity of the protein can serve as methods for identifying
 CC susceptibility to cancer, diabetes, or other disorders associated with

CC alterations in cellular phosphotyrosine metabolism.
 XX
 SQ Sequence 11 AA;
 XX
 CC
 Query Match 93.8%; Score 61; DB 20; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.00089;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VVHCSAGVGRG 12
 DB 1 VVHCSAGVGRG 11
 RESULT 3
 AAB19775
 ID AAB19775 standard; Peptide; 9 AA.
 XX
 AC AAB19775;
 XX
 DT 19-FEB-2001 (first entry)
 XX
 DE Protein tyrosine phosphatase HPTP-beta catalytic core.
 XX
 KW Vascular endothelial protein tyrosine phosphatase; HPTP-beta;
 KW Tie-2; receptor-type tyrosine kinase; antiangiogenic; antitumour;
 KW antimetastatic; tumour; metastasis; angiogenesis; therapy; human.
 XX
 OS Homo sapiens.
 XX
 PN EP1046715-A1.
 PD 25-OCT-2000.
 XX
 PF 23-APR-1999; 99EP-0108074.
 XX
 PR 23-APR-1999; 99EP-0108074.
 XX
 PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 XX
 PI Fachinger G, Risau B, Deutsch U;
 XX
 DR WPI; 2000-648932/63.
 XX
 PT Monitoring or modulating Tie-2 tyrosine kinase activity, useful e.g.
 PT for regulating tumor growth, using vascular-endothelial protein
 PT tyrosine phosphatase -
 XX
 PS Example 4; Fig 1a; 60pp; English.
 XX
 CC The present sequence is that of the catalytic core of HPTP-beta
 CC (see AAB19774), a human protein tyrosine phosphatase. Trapping
 CC mutants were engineered by replacing the Cys residue of this
 CC motif with Ser (see AAB19776) and the Arg residue with Ala (see
 CC AAB19777). The proteins were expressed in COS-1 cells, and used to
 CC to examine the interaction of HPTP-beta with the receptor tyrosine
 CC kinases Tie-2 and VEGFR-2. HPTP-beta polypeptides, nucleic
 CC acids and ligands are used in claimed methods for detecting and
 CC modulating Tie-2 activity. This allows the monitoring or
 CC modulation of angiogenesis, induction or inhibition of vascular
 CC growth or remodelling and blood vessel maturation, and inhibition
 CC of tumour growth or metastasis.
 XX
 SQ Sequence 9 AA:
 Query Match 78.5%; Score 51; DB 21; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 HCSAGVGRG 11
 DB 1 HCSAGVGRG 9

```

RESULT 5
AAW64787
ID AAW64787 standard; Protein; 11 AA.
XX
XX AAW64787;
AC
XX
XX 03-NOV-1998 (first entry)
DT
XX
XX Human tumour suppressor TS10q23.3 protein fragment (aa 88-98).
DE
XX
XX Tumour suppressor; TS10q23.3; human; diagnosis; tumour; prostate; breast;
KM brain; glioma; metastasis; gene therapy; anti-cancer; transgenic animal;
KW drug screening.
XX
XX Homo sapiens.
OS
XX
XX WO9833907-A1.
PN
XX
XX 06-AUG-1998.
PD
XX
XX 08-JAN-1998; 98WO-US00353.
PF
XX
XX 30-JAN-1997; 97US-0791115.
PR
XX
XX (MYRI-) MYRIAD GENETICS INC.
PA (TEXA ) UNIV TEXAS SYSTEM.
XX
XX
XX Jasser SA, Pershouse MA, Steck P, Tavtigian SV;
PI Yung WKA;
PI
XX
XX WPI; 1998-437461/37.
DR
XX
XX Tumour suppressor TS10q23.3 and related antibodies - useful for
PT diagnosis, staging and treatment of cancer, especially of breast,
PR prostate and brain
PS
XX
XX Example 5; Page 115; 161pp; English.
XX
XX This sequence represents a fragment of the human tumour suppressor
CC protein TS10q23.3 corresponding to residues 88-98. This suppressor can be
CC used to diagnose a wide range of tumours, particularly of prostate,
CC breast and brain (glioma), to stage cancers (particularly differentiation
CC between low grade brain cancer and glioma) and for prediction of
CC metastasis. This suppressor and its nucleic acid are also used to alter
CC the phenotype to specifically treat cancer cells, e.g. by in vivo or ex
CC vivo gene therapy, optionally together with other anti-cancer agents.
CC Fragments of the suppressor can be coupled to an immunogenic carrier and
CC are used to raise antibodies, to isolate antigens, as immunosassay
CC reagents, to clone related DNA or for immunotherapy. Antisense nucleic
CC acid can be used to produce transgenic animals (useful for drug
CC screening) or to eliminate dominant negative mutants.
CC
XX
XX Sequence 11 AA:
SQ
Query Match 76.9%; Score 50; DB 19; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.061;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 2 VHCAGVGRGTG 12
: || || || ||
DB 1 IHCKAGKGRGTG 11

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KM Mutation; mutant; tumour suppressor; TS10q23.3; diagnosis; breast; ovary;
KM Cowden's Syndrome; thyroid gland; endometrium; cancer; antibody; ELISA;
KM enzyme linked immunosorbant assay; gene expression; human.
XX
XX Homo sapiens.
OS
XX
XX WO9910537-A1.
PN
XX
XX 04-MAR-1999.
PD
XX
XX 26-AUG-1998; 98WO-US17636.
PF
XX
XX 30-APR-1998; 98US-0083563.
PR
XX
XX 26-AUG-1997; 97US-0057750.
PA (MYRI-) MYRIAD GENETICS INC.
PA (TEXA ) UNIV TEXAS SYSTEM.
XX
XX
XX Jasser SA, Pershouse MA, Steck P, Tavtigian SV;
PI Yung WKA;
PI
XX
XX WPI; 1999-190638/16.
DR
XX
XX Newly isolated DNA or RNA polynucleotide encoding a mutant tumour
PT suppressor (TS10q23.3) - useful for the diagnosis of Cowden's
PR syndrome and susceptibility to breast cancer
PS
XX
XX Example 5; Page 110; 244pp; English.
XX
XX The invention relates to mutant genes encoding the tumour suppressor
CC TS10q23.3. The TS10q23.3 mutant gene is useful for the diagnosis of
CC Cowden's Syndrome in cells selected from the breast, ovaries, thyroid
CC gland and endometrium (claimed). The mutant gene is also useful for
CC diagnosing a subject who has a predisposition to breast cancer. Both
CC methods involve antibodies, which specifically bind to a TS10q23.3,
CC used in an ELISA assay to evaluate the level of TS10q23.3 expression.
CC
XX
XX Sequence 11 AA:
SQ
Query Match 76.9%; Score 50; DB 20; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.061;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 2 VHCAGVGRGTG 12
: || || || ||
DB 1 IHCKAGKGRGTG 11

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PA (MERI ) MERCK & CO INC.
XX
XX Rodan GA, Rutledge SJ, Schmidt A;
XX
XX WPI; 1999-141930/12.
XX
PT Protein tyrosine phosphatase denoted PTP-OB - useful for drug
PT screening
XX
XX Example 1; Column 11; 34pp; English.
XX
CC The invention relates to a human protein tyrosine phosphatase (PTP)
CC denoted as PTP-OB, produced by bone and brain cells. A recombinant
CC host cell transfected or transformed with a nucleic acid vector
CC comprising the nucleic acid can be used for the production of the
CC PTP-OB polypeptide. The protein can be used to screen for modulators of
CC PTP-OB activity, which might be useful for treating e.g. osteoporosis
CC and cancer. Sequences AA094025-26 represent peptide fragments from the
CC conserved tyrosine phosphatase domain of PTP-OB used for designing PCR
CC primers.
XX
SQ Sequence 8 AA:
Query Match 69.2%; Score 45; DB 20; Length 8;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 VHCSAGVG 9
DB 1 VHCSAGVG 8
RESULT 7
AAU01458
ID AAU01458 standard; Peptide: 8 AA.
XX
AC AAU01458;
XX
DT 18-JUL-2001 (first entry)
XX
DE Conserved amino acids of PTP domain used to make PCR primer PH2a.
XX
XX Protein tyrosine phosphatase; PTP; human; osteoporosis; bone formation;
XX PTP-OB; cell proliferation; cell death; neoplastic transformation;
XX metastasis; tumour; cancer; lung cancer; osteosarcoma.
XX
XX Homo sapiens.
XX
XX US6214564-B1.
XX
XX 10-APR-2001.
XX
XX 22-SEP-1998; 98US-0158657.
XX
XX 01-DEC-1994; 94US-0348006.
XX 14-FEB-1997; 97US-0800825.
XX 14-SEP-1993; 93US-0122032.
XX
XX (MERI ) MERCK & CO INC.
XX
XX Rodan GA, Rutledge SJ, Schmidt A;
XX
XX WPI; 2001-280994/29.
XX
XX N-PSDB; AAS02143.
XX
PT Identifying a compound which modulates protein tyrosine phosphatase
PT activity for treating osteoporosis, comprises contacting a polypeptide
PT with a compound and measuring the ability of the compound to modulate
PT polypeptide activity -
XX
XX Example 1; Column 11; 35pp; English.
XX
XX The sequence represents the conserved amino acids of protein tyrosine

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```

CC phosphatase (PTP-OB) domain used to make degenerate PCR primer PH2a.
CC The PTP-OB nucleic acid and protein sequences (see AAS02144, AAU01459)
CC were used in a method to identify a compound able to modulate PTP-OB
CC activity, involving contacting a recombinant polypeptide comprising the
CC entire cytoplasmic domain of PTP-OB with the compound, and measuring the
CC ability of the compound to modulate the activity of the polypeptide. The
CC compounds that modulate PTP-OB activity are useful in treating disease
CC states involving PTP-OB activity such as osteoporosis, for preventing and
CC treating bone loss, and stimulation of bone formation. The compounds are
CC also useful for treating diseases in which activation or inactivation of
CC PTP-OB protein results in either cellular proliferation, cell death,
CC nonproliferation, induction of cellular neoplastic transformations or
CC metastatic tumour growth, such as cancer, preferably lung cancer or
CC osteosarcoma.
XX
SQ Sequence 8 AA:
Query Match 69.2%; Score 45; DB 22; Length 8;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 VHCSAGVG 9
DB 1 VHCSAGVG 8
RESULT 8
AAB19777
ID AAB19777 standard; Peptide: 9 AA.
XX
AC AAB19777;
XX
DT 19-FEB-2001 (first entry)
XX
DE Protein tyrosine phosphatase HTPP-beta catalytic core R to A mutant.
XX
XX Vascular-endothelial protein tyrosine phosphatase; HTPP-beta;
XX Tie-2; receptor-type tyrosine kinase; antiangiogenic; antitumour;
XX antineoplastic; tumour; metastasis; angiogenesis; therapy; human;
XX mutant; mutain.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX MISC-difference 8 /note= "Arg in native sequence"
XX
XX EP1046715-A1.
XX
XX 25-OCT-2000.
XX
XX 23-APR-1999; 99EP-0108074.
XX
XX 23-APR-1999; 99EP-0108074.
XX
XX (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
XX Fachinger G, Rissau B, Deutsch U;
XX
XX WPI; 2000-648932/63.
XX
XX Monitoring or modulating Tie-2 tyrosine kinase activity, useful e.g.
XX for regulating tumor growth, using vascular-endothelial protein
XX tyrosine phosphatase -
XX
XX Example 4; Fig 1a; 60pp; English.
XX
XX The present sequence is that of the catalytic core of HTPP-beta
XX (see AAB19774) mutated such that the native Arg residue at position
XX 9 is substituted by Ala. This trapping mutant of HTPP-beta, a
XX protein tyrosine phosphatase, was used in experiments to examine
XX the interaction of HTPP-beta with the receptor tyrosine kinases

```

CC Tie2 and VEGFR-2. HRP-beta polypeptides, nucleic acids and
CC ligands are used in claimed methods for detecting and modulating
CC Tie-2 activity. This allows the monitoring or modulation of
CC angiogenesis, induction or inhibition of vascular growth or
CC remodelling and blood vessel maturation, and inhibition of tumour
CC growth or metastasis.

XX Sequence 9 AA;

Query Match 69.2%; Score 45; DB 21; Length 9;
Best Local Similarity 88.9%; Pred. No. 7.8e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 HCSAGVGR 11
| | | | | | | |
DB 1 HCSAGVGAR 9

RESULT 9
AAB07849

ID AAB07849 standard; peptide; 10 AA.

XX AC AAB07849;

XX DT 03-JUL-2002 (first entry)

XX DE Protein tyrosine phosphatase (PTP) catalytic domain conserved sequence.

XX KW Tyrosine phosphatase-like enzyme; antidiabetic; anorectic; cytostatic;
XX KW tyrosine phosphatase-like enzyme; antiparkinsonian; anticonvulsant;
XX KW cardiatic; metabolic; immunomodulator; antiparkinsonian; anticonvulsant;
XX KW cerebroprotective; neuroprotective; nootropic; neuroleptic; anti-HIV;
XX KW antianthrax; hypotensive; vulnerary; protein tyrosine phosphatase;
XX KW PTP.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
XX FT Misc-difference 1.10
XX FT /note= "residues Xaa are unknown"

XX PN WO200220747-A2.

XX PD 14-MAR-2002.

XX PF 05-SEP-2001; 2001WO-EP10205.

XX PR 11-SEP-2000; 2000US-231568P.

XX PR 06-DEC-2000; 2000US-251403P.

XX PA (FARB) BAYER AG.

XX PI Kossida S;

XX DR WPI; 2002-339803/37.

XX PT New human tyrosine phosphatase-like enzyme polypeptide, regulators of
XX PT which are useful for preventing, treating diabetes, obesity, cancer,
XX PT cardiovascular and pulmonary diseases

XX PS Disclosure; Page 4; 117pp; English.

XX CC The invention relates to a purified human tyrosine phosphatase-like
XX CC enzyme polypeptide. The enzyme can be expressed by standard recombinant
XX CC methodology. The tyrosine phosphatase-like enzyme and encoding
XX CC polynucleotides are useful for screening for modulators which are used
XX CC for treating a tyrosine phosphatase-like enzyme dysfunction related
XX CC disease such as a central nervous system (CNS) disorder, diabetes,
XX CC obesity, chronic obstructive pulmonary disease, cardiovascular disease,
XX CC cancer, anorexia, cachexia, wasting disorders, appetite suppression, and
XX CC other eating disorder such as bulimia. CNS disorders include brain
XX CC injuries, Parkinson's disease, dementia, multiple sclerosis, stroke,
XX CC Alzheimer's disease, Huntington's disease, schizophrenia, Pick's disease,
XX CC Creutzfeldt-Jacob dementia, progressive nuclear palsy, and human

CC immunodeficiency virus (HIV) dementia, pain associated with CNS disorders
CC and cardiovascular diseases include myocardial infarction, ischemic
CC diseases of the heart, atrial and ventricular arrhythmia, hypertensive
CC vascular diseases and peripheral vascular diseases. The enzyme is useful
CC in diagnostic assays for detecting diseases and abnormalities or
CC susceptibility to diseases or abnormalities related to the presence of
CC mutations in the encoding nucleic acid sequences. The present sequence
CC represents a protein tyrosine phosphatase (PTP) catalytic domain
CC conserved fragment.

XX SQ Sequence 10 AA;

Query Match 66.2%; Score 43; DB 23; Length 10;
Best Local Similarity 70.0%; Pred. No. 0.83;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 HCSAGVGR 12
| | | | | | | |
DB 1 HCSXGGRXG 10

RESULT 10
AAB59247

ID AAB59247 standard; peptide; 12 AA.

XX AC AAB59247;

XX DT 26-MAR-2001 (first entry)

XX DE Peptide associated with SH2 domain containing proteins.

XX KW SHP-2; SHP-1; Src Homology-2; protein tyrosine phosphatase; mutant;
XX KW neoplastic disorder; obesity; angiogenesis; cancer; immune;
XX KW hematopoietic; allergy.

XX OS Unidentified.

XX PN US6156551-A.

XX PD 05-DEC-2000.

XX PF 05-JUN-1998; 98US-0092443.

XX PR 05-JUN-1998; 98US-0092443.

XX PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX PA (JOSL-) JOSLIN DIABETES CENT.

XX PI Neel BG, Shoelson S, Pluskey S, O'Reilly AM;

XX DR WPI; 2001-060166/07.

XX PT Mutant SH2 domain-containing protein tyrosine phosphatase, useful in in
XX PT vitro assays to screen for binding partners, inhibitors of tyrosine
XX PT phosphatase and for treating tyrosine phosphatase-mediated diseases

XX PS Disclosure; Column 249; 161pp; English.

XX CC The present invention relates to an activated SH2 (Src Homology-2)
XX CC -domain containing protein tyrosine phosphatase (SHP-1 or SHP-2)
XX CC mutant with a mutation in the SH2-domain. Activated mutants of
XX CC SH2-domain-containing protein tyrosine phosphatases are useful in
XX CC in vitro assays to screen for binding partners and inhibitors of
XX CC the phosphatase and in the treatment of PTP-mediated diseases or
XX CC conditions in a mammal, including neoplastic disorders, obesity and
XX CC to inhibit angiogenesis. Inhibitors identified using the activated
XX CC mutants are useful for the treatment of cancer, immunosuppression,
XX CC immunostimulation, hematopoietic stimulation and anti-allergy
XX CC treatment.

XX SQ Sequence 12 AA;

Query Match 66.2%; Score 43; DB 22; Length 12;

Best Local Similarity 58.3%; Pred. No. 1;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 VHCAGVGRG 12
: ||| | | |
DB 1 IVHCAGXRRXG 12

RESULT 11
AAB19603
ID AAB19603 standard; Peptide: 10 AA.

AC AAB19603;

DE 22-JAN-2001 (first entry)

XX Human dual-specificity phosphatase-1 (DSP-1) active site.

XX DSP-1: dual-specificity phosphatase-1; human; cell proliferation;
KW cell differentiation; cell survival; cell cycle; dephosphorylation;
KW signal transduction; MAP-kinase; cancer; graft versus host disease;
KW allergy; autoimmune disease; metabolic disease; therapy.

OS Homo sapiens.

PN WO200053636-A2.

PD 14-SEP-2000.

PF 08-MAR-2000; 2000WO-US06154.

PR 08-MAR-1999; 99US-0123255.

PA (CEPT-) CEPTYR INC.

PI Luche RM, Wei B;

DR WPI: 2000-579365/54.

XX New isolated polypeptide having the sequence of dual-specificity
PT phosphatase-1 (DSP-1) is useful for treating a patient with a disorder
PT associated with DSP-1 activity e.g. cancer and autoimmune diseases -
PS Disclosure; Page 13; 74pp; English.

XX The present sequence is that of the active site of human
CC dual-specificity phosphatase-1 (DSP-1), corresponding to amino acid
CC residues 109-118 of the full-length protein (see AAB19602). DSP-1
CC dephosphorylates phosphotyrosine and phosphothreonine/serine
CC residues in DSP-1 substrates such as activated mitogen-activated
CC protein kinase (MAP-kinase). Methods are provided for recombinant
CC production of DSP-1 polypeptides, and for using DSP-1 polypeptides,
CC antibodies and polynucleotides to detect DSP-1 expression, to screen
CC for agents that modulate DSP-1 activity, and for using such agents to
CC modulate cell proliferation, differentiation or survival. The cell
CC may display contact inhibition of cell growth, anchorage-dependent
CC growth or an altered intercellular adhesion property, or is a cell
CC present in a patient afflicted with a disorder associated with
CC DSP-1 activity, such as cancer, graft-versus host disease,
CC autoimmune disease, allergy, metabolic disease, abnormal cell
CC growth, abnormal cell proliferation and abnormal cell cycle.
CC Variants of DSP-1 are also provided. These may have amino acid
CC sequence modifications in non-critical regions so as to preserve
CC the active site.

SQ Sequence 10 AA;

Query Match 64.6%; Score 42; DB 21; Length 10;

Best Local Similarity 70.0%; Pred. No. 1.2;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 VHCAGVGRG 11
|||: ||| |

DB 1 VHCAAGVSRS 10

RESULT 12
AAW35299
ID AAW35299 standard; Peptide: 11 AA.

XX AAW35299;

DE 27-MAR-1998 (first entry)

XX Protein tyrosine phosphatase catalytic core consensus.

XX Islet cell antigen 1851; autoantigen; protein tyrosine phosphatase;

KW insulin-dependent diabetes mellitus; IDDM; diagnosis; therapy;

KW macaque; human.

OS Mammalia.

XX Key Location/Qualifiers

FT Misc-difference 3 /note= "the Cys residue appears to be essential

FT to the catalytic mechanism"

FT Misc-difference 4 /note= "any amino acid"

FT Misc-difference 7 /note= "any amino acid"

FT Misc-difference 8 /note= "any amino acid"

FT Misc-difference 10 /label= Ser, thr

PN WO9732984-A1.

PD 12-SEP-1997.

PF 05-MAR-1997; 97WO-US03532.

PR 15-OCT-1996; 96US-0027540.

PR 06-MAR-1996; 96US-0012927.

PA (UNIW) UNIV WASHINGTON.

PA (ZYMO) ZYMOGENETICS INC.

PI Hagopian W, Jelinek L, Kinsdovogel W, Lagasse J;

PI Sheppard PO;

DR WPI: 1997-457535/42.

XX Mammalian pancreatic islet cell antigen and related DNA - used to
PT detect autoantibodies indicative of insulin-dependent diabetes or
PT pre-disposition to it

PS Disclosure; Page 19; 134pp; English.

XX This peptide sequence comprises the conserved catalytic core
CC within the cytoplasmic domain of the protein tyrosine phosphatase
CC (PTP) family members. The catalytic core of macaque islet cell
CC antigen 1851 (see AAW35296) and of the human homologue (see AAW35297)
CC of 1815 differ from that of other PTP family members in that
CC alanine is replaced by aspartic acid and the second variable amino
CC acid is alanine. Islet cell antigen 1851 forms an immune complex
CC with an autoantibody in patients at risk of, or predisposed to,
CC insulin-dependent diabetes mellitus (IDDM), and can be used in
CC methods for the diagnosis and treatment of IDDM.

SQ Sequence 11 AA;

Query Match 64.6%; Score 42; DB 18; Length 11;

Best Local Similarity 63.6%; Pred. No. 1.3;

Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 VHCAGVGRG 12

DB 1 VHCXAGAAARXG 11

RESULT 13

ID AAV14759 standard; peptide: 7 AA.

AC AAV14759;

DT 11-OCT-1999 (first entry)

DE Tyrosine phosphatase conserved domain.

KM Genetic proximity; gene expression; cell characterisation; homeobox gene;
KM genetic defect; reverse transcriptase polymerase chain reaction; RT-PCR;
KM kinase gene; protein phosphatase; P450; steroid receptor; cadherin.

OS Homo sapiens.

PN WO934016-A2.

PD 08-JUL-1999.

PF 28-DEC-1998; 98MO-IL00625.

PR 16-OCT-1998; 98ITL-0126627.

PR 29-DEC-1997; 97ITL-0122793.

PA (GENE-) GENENAL LTD.

PI Vidler B;

DR WPI: 1999-419113/35.

DR N-PSDB: AA218225.

Identifying and characterizing cells by comparing the pattern of
gene expression in a selected gene family

Examples; Page 48; 102pp; English.

The invention provides a new method for identifying and characterising
cells. The method for determining the genetic proximity of a first cell
and a second cell comprises: (a) obtaining the first cell and the second
cell; (b) determining in the first cell and the second cell the pattern
of expression of genes in a selected gene family; and (c) calculating a
proximity index using a specified formula. The methods can be used for
characterising cells, e.g. for determining the origin of a cell, its
genetic status, whether it carries a genetic defect, or whether it is
transformed. They can be used for detecting a selected genetic defect in
an individual, e.g. a fetus. They can also be used for determining the
effect of a selected treatment on a test cell. They can also be used for
obtaining cells capable of expressing an homeobox related desired
property. The method uses reverse transcriptase polymerase chain
reaction (RT-PCR) for determining the pattern of gene expression in a
selected gene family. Sequences AA217803-218342 represent primers that
can be used in the RT-PCR reactions to determine the pattern of gene
expression. The gene family can be selected from a set of homeobox genes,
kinase genes, protein phosphatase genes, P450 enzyme genes, steroid
receptor superfamily genes or cadherin superfamily genes. Sequences
AAV14603-813 represent conserved peptide motifs based on which the
primers of the invention were designed.

Sequence 7 AA;

Query Match 63.1%; Score 41; DB 20; Length 7;

Best Local Similarity 100.0%; Pred. No. 7.8e+05; Mismatches 0; Indels 0; Gaps 0;

OY 3 HCSAGVG 9
1 HCSAGVG 7

DB

RESULT 14

ID AAB19776 standard; peptide: 9 AA.

AC AAB19776;

DT 19-FEB-2001 (first entry)

DE Protein tyrosine phosphatase HTPP-beta catalytic core C to S mutant.

KM Vascular-endothelial protein tyrosine phosphatase; HTPP-beta;
KM Tie-2; receptor-type tyrosine kinase; antiangiogenic; antitumour;
KM antimetastatic; tumour; metastasis; angiogenesis; therapy; human;
KM mutant; mutelin.

OS Homo sapiens.

OS Synthetic.

FT Key Location/Qualifiers

FT Misc-difference 2 /note="Cys in native sequence"

PN EP1046715-A1.

PD 25-OCT-2000.

PF 23-APR-1999; 99EP-0108074.

PR 23-APR-1999; 99EP-0108074.

PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

PI Fachinger G, Risau B, Deutsch U;

DR WPI: 2000-648932/63.

Monitoring or modulating Tie-2 tyrosine kinase activity, useful e.g.
for regulating tumor growth, using vascular-endothelial protein

tyrosine phosphatase

Example 4; Fig 1a; 60pp; English.

The present sequence is that of the catalytic core of HTPP-beta
(see AAB19774), mutated such that the native Cys residue at position
2 is substituted by Ser. This trapping mutant of HTPP-beta, a
protein tyrosine phosphatase, was used in experiments to examine
the interaction of HTPP-beta with the receptor tyrosine kinases
Tie-2 and VEGFR-2. HTPP-beta polypeptides, nucleic acids and
ligands are used in claimed methods for detecting and modulating
Tie-2 activity. This allows the monitoring or modulation of
angiogenesis, induction or inhibition of vascular growth or
remodelling and blood vessel maturation, and inhibition of tumour
growth or metastasis.

Sequence 9 AA;

Query Match 63.1%; Score 41; DB 21; Length 9;

Best Local Similarity 88.9%; Pred. No. 7.8e+05; Mismatches 1; Indels 0; Gaps 0;

OY 3 HCSAGVGRT 11
1 HSSAGVGRT 9

DB

RESULT 15

ID AAR85205 standard; peptide: 7 AA.

AC AAR85205;

DT 12-FEB-1996 (first entry)

XX Protein tyrosine phosphatase conserved sequence.
DE
XX
XX Density enhanced Type III receptor-like protein tyrosine phosphatase;
KW huDEP-1.
KM
XX
XX Synthetic.
OS
XX
XX WO9530008-A1.
PN
XX
XX 09-NOV-1995.
PD
XX
XX 03-MAY-1995; 95WO-US05512.
PF
XX
XX 03-MAY-1994; 94US-0237940.
PR
XX
XX (COLD-) COLD SPRING HARBOR LAB.
PA
XX
XX Oestman A, Tonks NK;
PI
XX
XX WPI; 1995-393079/50.
DR
XX
XX New density enhanced protein tyrosine phosphatase - used to develop
PT prods. to modify transcription, translation and/or activity of
PT tyrosine phosphatase(s).
PS
XX
XX Example 1; Page 15; 51pp; English.
PS
XX
XX 2 Conserved amino acid sequences (AAR85204-05) common to many protein
CC tyrosine phosphatases (PTs) were used to design degenerate primers
CC (see PAT6028-29) used for the PCR amplification of cDNA from a HeLa
CC library, allowing isolation of a clone encoding a novel density-
CC enhanced Type III receptor-like PTP, huDEP-1 (see PAT6027).
XX
XX
SQ Sequence 7 AA:

Query Match 61.5%; Score 40; DB 16; Length 7;
Best Local Similarity 85.7%; Pred. No. 7.8e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HCSAGVG 9
Db 1 HCSAGIG 7

Search completed: January 17, 2003, 10:59:52
Job time : 35 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 11:00:48 ; Search time 11 Seconds
(Without alignments)
21.686 Million cell updates/sec

Title: US-09-743-492-4

Perfect score: 65

Sequence: 1 VVHCSAGVGRKG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 120991 seqs, 19878514 residues

Total number of hits satisfying chosen parameters: 25634

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Published Applications-AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCRT_NEW_PUB pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	61.5	7	10	US-09-848-294-13
2	40	61.5	11	10	US-09-876-527-13
3	38	58.5	10	10	US-09-964-277-16
4	36	55.4	7	9	US-10-087-993-2
5	36	55.4	7	9	US-10-087-993-5
6	36	55.4	10	9	US-09-955-732-16
7	36	55.4	11	10	US-09-788-626-1
8	36	55.4	11	10	US-09-918-3968-1
9	36	55.4	11	12	US-10-000-954-1
10	35	53.8	10	10	US-09-770-595A-4
11	35	53.8	12	10	US-09-770-595A-7
12	34	52.3	10	10	US-09-770-595A-5
13	32	49.2	7	9	US-10-020-215-7
14	32	49.2	7	10	US-09-822-295-6
15	31	47.7	5	9	US-10-020-215-9
16	31	47.7	5	10	US-09-822-295-14
17	28	43.1	5	9	US-10-020-215-10
18	27	41.5	7	10	US-09-870-379-9
19	26	40.0	12	9	US-09-981-876-265

20	25	38.5	6	10	US-09-905-831-2	Sequence 2, Appl
21	25	38.5	11	10	US-09-756-594-31	Sequence 31, Appl
22	24	36.9	8	10	US-09-817-198A-12	Sequence 12, Appl
23	24	36.9	10	9	US-09-996-288-115	Sequence 115, Appl
24	24	36.9	10	9	US-09-996-288-144	Sequence 144, Appl
25	24	36.9	10	9	US-09-996-288-197	Sequence 197, Appl
26	24	36.9	10	9	US-09-910-557-59	Sequence 59, Appl
27	23	35.4	6	10	US-09-817-159A-11	Sequence 11, Appl
28	23	35.4	6	10	US-09-817-198A-10	Sequence 10, Appl
29	23	35.4	8	9	US-10-118-984-12	Sequence 12, Appl
30	23	35.4	8	9	US-10-118-984-29	Sequence 29, Appl
31	23	35.4	8	10	US-09-728-721-12	Sequence 12, Appl
32	23	35.4	8	10	US-09-728-721-29	Sequence 29, Appl
33	23	35.4	8	10	US-09-817-199A-14	Sequence 14, Appl
34	23	35.4	8	12	US-10-105-931-12	Sequence 12, Appl
35	23	35.4	8	12	US-10-105-931-29	Sequence 29, Appl
36	23	35.4	10	10	US-09-765-086-42	Sequence 42, Appl
37	23	35.4	11	8	US-08-424-550B-521	Sequence 521, Appl
38	23	35.4	11	10	US-09-867-852-111	Sequence 111, Appl
39	23	35.4	11	10	US-09-867-852-113	Sequence 113, Appl
40	22	33.8	8	9	US-10-012-756-18	Sequence 18, Appl
41	22	33.8	10	9	US-09-996-288-112	Sequence 112, Appl
42	22	33.8	10	9	US-09-996-288-142	Sequence 142, Appl
43	22	33.8	10	9	US-09-996-288-146	Sequence 146, Appl
44	22	33.8	10	9	US-09-996-288-195	Sequence 195, Appl
45	22	33.8	10	9	US-09-996-288-195	Sequence 195, Appl

ALIGNMENTS

RESULT 1
US-09-848-294-13
Sequence 13, Application US/09848294
Patent No. US20020049179A1
GENERAL INFORMATION:
APPLICANT: Tonks, Nicholas K.
TITLE OF INVENTION: Isolation of A cDNA Encoding A NO. US20020049179A1el
TITLE OF INVENTION: Protein Tyrosine Phosphatase which localizes to Focal
FILE REFERENCE: CSH90-04FZA
CURRENT APPLICATION NUMBER: US/09/848,294
CURRENT FILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: 09/235,251
PRIOR FILING DATE: 1999-01-22
PRIOR APPLICATION NUMBER: 08/759,536
PRIOR FILING DATE: 1996-12-04
PRIOR APPLICATION NUMBER: 08/107,420
PRIOR FILING DATE: 1993-08-16
PRIOR APPLICATION NUMBER: 07/663,579
PRIOR FILING DATE: 1991-03-01
PRIOR APPLICATION NUMBER: 07/494,036
PRIOR FILING DATE: 1990-03-14
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 13
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Conserved Protein Sequence
US-09-848-294-13

Query Match

Best Local Similarity 61.5%; Score 40; DB 10; Length 7;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 HCSAGVG 9

DB 1 HCSAGIG 7

RESULT 2

US-09-876-527-13
; Sequence 13, Application US/09876527
; Patent No. US20020102616A1
; GENERAL INFORMATION:
; APPLICANT: Kindsvogel, Wayne
; Jelinek, Laura J.
; Sheppard, Paul O.
; Hagopian, William A.
; Lagasse, James M.
; TITLE OF INVENTION: ISLET CELL ANTIGEN 1851
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/876,527
; FILING DATE: 07-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/811,481
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Lingenfelter, Susan
; REGISTRATION NUMBER: P-41,156
; REFERENCE/DOCKET NUMBER: 95-36
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6675
; TELEFAX: 206-442-6678
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-876-527-13
Query Match 61.5% Score 40; DB 10; Length 11;
Best Local Similarity 63.6% Pred. No. 0.5;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2 VHCXAGVGRG 12
||| ||| |
Db 1 VHCXAGXXRG 11

RESULT 3
US-09-964-277-16
; Sequence 16, Application US/09964277
; Patent No. US20020137170A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.434
; CURRENT APPLICATION NUMBER: US/09/964,277
; CURRENT FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16 *
; LENGTH: 10

TYPE: PRT
; ORGANISM: Homo sapiens
US-09-964-277-16
Query Match 58.5% Score 38; DB 10; Length 10;
Best Local Similarity 60.0% Pred. No. 0.96;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 VHCXAGVGR 11
||| ||| |
Db 1 VHCXAGISRS 10

RESULT 4
US-10-087-993-2
; Sequence 2, Application US/10087993
; Patent No. US20020169303A1
; GENERAL INFORMATION:
; APPLICANT: Ullrich, Axel
; Aoki, Naohito
; Kim, Yeong Woong
; Wang, Hong Yang
; Chen, Zhengjun
; Naylor, Oliver
; Kharitonkov, Alexei Igorevich
; TITLE OF INVENTION: NOVEL PRP20, PCP-2, Bp1, CLK,
; AND SIRP POLYPEPTIDES AND RELATED
; PRODUCTS AND METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" diskette, 1.44 Mb
; storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/087,993
; FILING DATE: 05-Mar-2002
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/877,150
; FILING DATE: June 17, 1997
; APPLICATION NUMBER: U.S. 60/019,629
; FILING DATE: June 17, 1996
; APPLICATION NUMBER: U.S. 60/023,485
; FILING DATE: August 9, 1996
; APPLICATION NUMBER: U.S. 60/030,860
; FILING DATE: No. US20020169303A1ember 13, 1996
; APPLICATION NUMBER: U.S. 60/034,286
; FILING DATE: December 19, 1996
; APPLICATION NUMBER: U.S. 60/030,964
; FILING DATE: No. US20020169303A1ember 15, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 225/298
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: "Xaa" in position 6 stands for
either Ser, Ile or Val.
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-087-993-2

Query Match 55.4%; Score 36; DB 9; Length 7;
Best Local Similarity 85.7%; Pred. No. 1e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 HCSAGVG 9
|||||
DB 1 HCSAGXG 7

RESULT 5
US-10-087-993-5
Sequence 5, Application US/10087993
Patent No. US20020169303A1
GENERAL INFORMATION:
APPLICANT: Ulrich, Axel
Aoki, Naohito
Kim, Yeong Woong
Wang, Hong Yang
Chen, Zhengjun
Naylor, Oliver
Kharitonkov, Alexei Igorevich
TITLE OF INVENTION: NOVEL PTP20, PCP-2, BDP1, CLK,
AND SHP POLYPEPTIDES AND RELATED
PRODUCTS AND METHODS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/087,993
FILING DATE: 05-Mar-2002
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/877,150
FILING DATE: June 17, 1997
APPLICATION NUMBER: U.S. 60/019,629
FILING DATE: June 17, 1996
APPLICATION NUMBER: U.S. 60/023,485
FILING DATE: August 9, 1996
APPLICATION NUMBER: U.S. 60/030,860
FILING DATE: NO. US20020169303A1member 13, 1996
APPLICATION NUMBER: U.S. 60/034,286
FILING DATE: December 19, 1996
APPLICATION NUMBER: U.S. 60/030,964
FILING DATE: NO. US20020169303A1member 15, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 225/298
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
TELEFAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: "Xaa" in position 6 stands for
either Ser, Ile or Val.
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-087-993-5

Query Match 55.4%; Score 36; DB 9; Length 7;
Best Local Similarity 85.7%; Pred. No. 1e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 HCSAGVG 9
|||||
DB 1 HCSAGXG 7

RESULT 6
US-09-955-732-16
Sequence 16, Application US/09955732
Publication No. US20020182203A1
GENERAL INFORMATION:
APPLICANT: Lucbe, Ralf M.
APPLICANT: Wei, Bo
TITLE OF INVENTION: DSP-15 DUAL-SPECIFICITY PHOSPHATASE
FILE REFERENCE: 200125,433
CURRENT APPLICATION NUMBER: US/09/955,732
CURRENT FILING DATE: 2001-09-18
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 16
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
US-09-955-732-16

Query Match 55.4%; Score 36; DB 9; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.1;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 VHCSAGVGR 11
|||||
DB 1 VHCKMVSRS 10

RESULT 7
US-09-788-626-1
Sequence 1, Application US/09788626
Patent No. US20020009762A1
GENERAL INFORMATION:
APPLICANT: Flint, Andrew J.
APPLICANT: Cool, Deborah E.
TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE
PHOSPHATASE
FILE REFERENCE: 200125,401
CURRENT APPLICATION NUMBER: US/09/788,626
CURRENT FILING DATE: 2001-02-13
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(1)
OTHER INFORMATION: Xaa = Ile or Val
NAME/KEY: VARIANT
LOCATION: (4)...(4)

NAME/KEY: Modified-site
LOCATION: 10
OTHER INFORMATION: /label= Xaa
/note= "Xaa = Ser or Thr"
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-000-954-1

Query Match 55.4%; Score 36; DB 12; Length 11;
Best Local Similarity 60.0%; Pred. No. 2.3;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 3 HCSAGVGRGT 12
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Db 2 HCXAGXXRXG 11

RESULT 10
US-09-770-595A-4
Sequence 4, Application US/09770595A
Patent No. US20020048803A1
GENERAL INFORMATION:
APPLICANT: Revenkova, Ekaterina
APPLICANT: Paszkowski, Jurek
TITLE OF INVENTION: Map Kinase Phosphatase Mutant
FILE REFERENCE: S-30589A
CURRENT APPLICATION NUMBER: US/09/770.595A
CURRENT FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 10
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-09-770-595A-4

Query Match 53.8%; Score 35; DB 10; Length 10;
Best Local Similarity 60.0%; Pred. No. 3;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 VHCSAGVGRGT 11
||| |||
Db 1 VHCCGVGSRS 10

RESULT 11
US-09-770-595A-7
Sequence 7, Application US/09770595A
Patent No. US20020048803A1
GENERAL INFORMATION:
APPLICANT: Revenkova, Ekaterina
APPLICANT: Paszkowski, Jurek
TITLE OF INVENTION: Map Kinase Phosphatase Mutant
FILE REFERENCE: S-30589A
CURRENT APPLICATION NUMBER: US/09/770.595A
CURRENT FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 12
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-09-770-595A-7

Query Match 53.8%; Score 35; DB 10; Length 12;
Best Local Similarity 60.0%; Pred. No. 3.6;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 VHCSAGVGRGT 11
||| |||
Db 2 VHCCGVGSRS 11

RESULT 12

US-09-770-595A-5
Sequence 5, Application US/09770595A
Patent No. US20020048803A1
GENERAL INFORMATION:
APPLICANT: Revenkova, Ekaterina
APPLICANT: Paszkowski, Jurek
TITLE OF INVENTION: Map Kinase Phosphatase Mutant
FILE REFERENCE: S-30589A
CURRENT APPLICATION NUMBER: US/09/770.595A
CURRENT FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE: <221> MISC_FEATURE<222> (1)..(10)<223> Xaa = any amino acid
OTHER INFORMATION: Description of Artificial Sequence: mammalian
OTHER INFORMATION: sequence motif defining the family of PTPs
US-09-770-595A-5

Query Match 52.3%; Score 34; DB 10; Length 10;
Best Local Similarity 50.0%; Pred. No. 4.5;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 VHCSAGVGRGT 11
||| |||
Db 1 HCHXAGXXRS 10

RESULT 13
US-10-020-215-7
Sequence 7, Application US/10020215
Publication No. US20030008347A1
GENERAL INFORMATION:
APPLICANT: PLOWMAN, GREGORY
APPLICANT: PILES, EIOR
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF ALP RELATED DISORDERS
FILE REFERENCE: 038602/1290
CURRENT APPLICATION NUMBER: US/10/020.215
CURRENT FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: 09/095,443
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/049,477
PRIOR FILING DATE: 1997-06-11
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (3)
OTHER INFORMATION: Unspecified amino acid
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (6)
OTHER INFORMATION: Unspecified amino acid
US-10-020-215-7

Query Match 49.2%; Score 32; DB 9; Length 7;
Best Local Similarity 71.4%; Pred. No. 1e+05; 2; Indels 0; Gaps 0;

OY 3 HCSAGVG 9
||| |||
Db 1 HCHXAGXG 7

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RESULT 14
US-09-822-295-6
; Sequence 6, Application US/09822295
; Patent No. US20020119501A1
; GENERAL INFORMATION:
; APPLICANT: Bahija Jallal
; Gregory D. Plowman
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
; PTP04 RELATED DISORDERS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FASTSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/822,295
; FILING DATE: 02-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/081,345
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 234/253
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: "Xaa" in positions 3 and 6 stand
; for an unspecified amino acid.
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-822-295-6

Query Match          49.2%; Score 32; DB 10; Length 7;
Best Local Similarity 71.4%; Pred. No. 1e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 HCSAGVG 9
      |||||
Db      1 HCSAGVG 7

RESULT 15
US-10-020-215-9
; Sequence 9, Application US/10020215
; Publication No. US20030008347A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: PELES, EIOR
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF ALP RELATED DISORDERS
; FILE REFERENCE: 038602/1290
; CURRENT APPLICATION NUMBER: US/10/020,215
; FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 09/095,443
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; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/049,477
; PRIOR FILING DATE: 1997-06-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Illustrative
US-10-020-215-9

Query Match          47.7%; Score 31; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 HCSAG 7
      |||||
Db      1 HCSAG 5
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Search completed: January 17, 2003, 11:04:24
Job time : 11 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 10:59:18 : Search time 14 seconds
(without alignments)
25.220 Million cell updates/sec

Title: US-09-743-492-4
Perfect score: 65
Sequence: 1 VVHCSAGVGRIG 12

Scoring table:
BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

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Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	61	93.8	11	2	US-08-342-930-4
2	50	76.9	11	4	US-08-791-115B-17
3	46	70.8	8	2	US-08-342-930-12
4	45	69.2	8	1	US-08-348-006B-4
5	45	69.2	8	1	US-08-800-825A-4
6	45	69.2	8	4	US-09-158-657-4
7	43	66.2	10	1	US-08-036-210-2
8	43	66.2	10	1	US-08-036-210-32
9	43	66.2	10	2	US-08-449-609-2
10	43	66.2	10	2	US-08-449-609-32
11	40	61.5	7	3	US-08-854-585-4
12	40	61.5	7	5	PCT-US95-05512-4
13	40	61.5	11	4	US-08-791-115B-18
14	40	61.5	11	4	US-08-811-481-13
15	39	60.0	9	2	US-08-990-379-18
16	37	56.9	8	1	US-08-036-210-45
17	37	56.9	8	1	US-08-449-609-45
18	36	55.4	7	1	US-08-036-210-41
19	36	55.4	7	2	US-08-446-345-13
20	36	55.4	7	2	US-08-449-609-41
21	36	55.4	7	3	US-08-951-260A-3
22	36	55.4	7	3	US-09-100-804-9
23	36	55.4	11	1	US-08-201-697-9
24	36	55.4	11	2	US-08-342-930-3
25	36	55.4	11	2	US-08-447-464-1
26	36	55.4	11	2	US-08-716-679-1
27	36	55.4	11	2	US-08-685-992-36

28	36	55.4	11	2	US-09-144-925-36	Sequence 36, Appl
29	36	55.4	11	3	US-08-246-441-9	Sequence 9, Appl
30	36	55.4	11	4	US-08-081-929-1	Sequence 11, Appl
31	35	53.8	6	2	US-08-447-464-11	Sequence 1, Appl
32	35	53.8	6	2	US-08-716-679-11	Sequence 11, Appl
33	35	53.8	6	2	US-08-884-569A-15	Sequence 15, Appl
34	34	52.3	7	2	US-08-530-290-4	Sequence 4, Appl
35	32	49.2	7	4	US-09-081-345-6	Sequence 6, Appl
36	32	49.2	7	4	US-09-095-443-7	Sequence 7, Appl
37	31	47.7	5	4	US-09-081-345-14	Sequence 14, Appl
38	31	47.7	5	4	US-08-884-569A-13	Sequence 13, Appl
39	30	46.2	8	2	US-08-990-379-17	Sequence 17, Appl
40	30	46.2	10	4	US-09-164-193-11	Sequence 11, Appl
41	30	46.2	10	4	US-09-221-448A-11	Sequence 11, Appl
42	29	44.6	7	5	PCT-US94-10166-4	Sequence 4, Appl
43	28	43.1	11	1	US-07-732-114A-6	Sequence 6, Appl
44	28	43.1	11	1	US-08-170-114A-6	Sequence 6, Appl
45	26	40.0	6	4	US-09-020-880-50	Sequence 50, Appl

ALIGNMENTS

RESULT 1
US-08-342-930-4
Sequence 4, Application US/08342930
Patent No. 5821084
GENERAL INFORMATION:
APPLICANT: OLMSTED, ELIZABETH A.
APPLICANT: MAURO, LAURA J.
APPLICANT: DAVIS, ALAN R.
APPLICANT: DIXON, JACK E.
TITLE OF INVENTION: OSTEOBLAST-TESTICULAR PROTEIN TYROSINE
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & ROEBSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/342,930
FILING DATE: 21-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KONSKI, ANTOINETTE F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 20344-20975.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-342-930-4
Query Match 93.8%, Score 61; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00036;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VVHCSAGVGRIG 12
|||||

Db 1 VHC5AGVGRG 11

RESULT 2

US-08-791-115B-17
 ; Sequence 17, Application US/08791115B
 ; Patent No. 6262242
 ; GENERAL INFORMATION:
 ; APPLICANT: Steck, Peter
 ; APPLICANT: Pershouse, Mark A.
 ; APPLICANT: Jasser, Samar
 ; APPLICANT: Yung, W.K. Alfred
 ; APPLICANT: Tavligian, Sean V.
 ; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Rothwell, Piggy, Ernst & Kurz, P.C.
 ; STREET: 555 Thirteenth Street, N.W., Suite 701-E
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 22204
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/791,115B
 ; FILING DATE: 30-JAN-1997
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ihnen, Jeffrey L.
 ; REGISTRATION NUMBER: 38,957
 ; REFERENCE/DOCKET NUMBER: 2318-134.A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-683-6040
 ; TELEFAX: 202-683-7031
 ; INFORMATION FOR SEQ ID NO: 17:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 11 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; US-08-791-115B-17

Query Match

Best Local Similarity 76.9%; Score 50; DB 4; Length 11;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 VHC5AGVGRG 12

Db 1 IHCKAGKGRG 11

RESULT 3

US-08-342-930-12
 ; Sequence 12, Application US/08342930
 ; Patent No. 5821084
 ; GENERAL INFORMATION:
 ; APPLICANT: OLMSTED, ELIZABETH A.
 ; APPLICANT: MAURO, LAURA J.
 ; APPLICANT: DAVIS, ALAN R.
 ; APPLICANT: DIXON, JACK E.
 ; TITLE OF INVENTION: OSTEOBLAST-TESTICULAR PROTEIN TYROSINE
 ; PHOSPHATASE
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORRISON & FOERSTER
 ; STREET: 755 Page Mill Road
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/342,930
 ; FILING DATE: 21-NOV-1994
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: KOSKI, ANTOINETTE F.
 ; REGISTRATION NUMBER: 34,202
 ; REFERENCE/DOCKET NUMBER: 20344-20975.00
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 813-5600
 ; TELEFAX: (415) 494-0792
 ; TELEX: 706141
 ; INFORMATION FOR SEQ ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 8 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-342-930-12

Query Match

Best Local Similarity 70.8%; Score 46; DB 2; Length 8;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 HCSAGVGR 10

Db 1 HCSAGVGR 8

RESULT 4

US-08-348-006B-4
 ; Sequence 4, Application US/08348006B
 ; Patent No. 5658756
 ; GENERAL INFORMATION:
 ; APPLICANT: RODAN, GIDEON A.
 ; APPLICANT: SCHMIDT, AZRIEL
 ; APPLICANT: RUTLEDGE, SU JANE
 ; TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
 ; TYROSINE PHOSPHATASE
 ; NUMBER OF SEQUENCES: 7
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: J. MARK HAND
 ; STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
 ; CITY: RAHWAY
 ; STATE: NEW JERSEY
 ; COUNTRY: USA
 ; ZIP: 07065-0900
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/348,006B
 ; FILING DATE:
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION NUMBER:
 ; APPLICATION NUMBER: US 08/122,032
 ; FILING DATE: 14-SEP-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: HAND, J., MARK
 ; REGISTRATION NUMBER: 36,545
 ; REFERENCE/DOCKET NUMBER: 189921A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 908-594-3905
 ; TELEFAX: 908-594-4720
 ; INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-348-006B-4

Query Match 69.2%; Score 45; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 VHCSAGVG 9
|||||
Db 1 VHCSAGVG 8

RESULT 5
US-08-800-825A-4
Sequence 4, Application US/08800825A
Patent No. 5866397
GENERAL INFORMATION:
APPLICANT: RODAN, GIDEON A.
APPLICANT: SCHMIDT, AZRIEL
APPLICANT: RUTLEDGE, SU JANE
TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASE
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: J. MARK HAND - MERCK & CO., INC.
STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,825A
FILING DATE: 14-FEB-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HAND, J. MARK
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 18992DA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-3905
TELEFAX: 732-594-4720
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-800-825A-4

Query Match 69.2%; Score 45; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 VHCSAGVG 9
|||||
Db 1 VHCSAGVG 8

RESULT 6
US-09-158-657-4
Sequence 4, Application US/09158657
Patent No. 6214564

GENERAL INFORMATION:
APPLICANT: RODAN, GIDEON A.
APPLICANT: SCHMIDT, AZRIEL
APPLICANT: RUTLEDGE, SU JANE
TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASE
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: J. MARK HAND - MERCK & CO., INC.
STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/158,657
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/800,825
FILING DATE: 14-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: HAND, J. MARK
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 18992DA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-3905
TELEFAX: 732-594-4720
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-158-657-4

Query Match 69.2%; Score 45; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 VHCSAGVG 9
|||||
Db 1 VHCSAGVG 8

RESULT 7
US-08-036-210-2
Sequence 2, Application US/08036210
Patent No. 5585233
GENERAL INFORMATION:
APPLICANT: Moller, Niels P.H.
APPLICANT: Moller, Karin B.
APPLICANT: Ullrich, Axel
TITLE OF INVENTION: PTP-631: A NOVEL PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/036,210
FILING DATE: 23-MAR-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7683-025
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-036-210-2

Query Match          66.2%; Score 43; DB 1; Length 10;
Best Local Similarity 70.0%; Pred. No. 0.29;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      3 HCSAGVGRGTG 12
      ||| | | | |
Db      1 HCSXGXGRXG 10

RESULT 8
US-08-036-210-32
Sequence 32, Application US/08036210
Patent No. 5585233
GENERAL INFORMATION:
APPLICANT: Moller, Niels P.H.
APPLICANT: Ullrich, Karin B.
TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/036,210
FILING DATE: 23-MAR-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7683-025
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
```

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US-08-036-210-32

Query Match          66.2%; Score 43; DB 1; Length 10;
Best Local Similarity 70.0%; Pred. No. 0.29;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      3 HCSAGVGRGTG 12
      ||| | | | |
Db      1 HCSXGXGRXG 10

RESULT 9
US-08-449-609-2
Sequence 2, Application US/08449609
Patent No. 5952212
GENERAL INFORMATION:
APPLICANT: Moller, Niels P.H.
APPLICANT: Ullrich, Axel
TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,609
FILING DATE: 24-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/036,210
FILING DATE: 23-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7683-025
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-449-609-2

Query Match          66.2%; Score 43; DB 2; Length 10;
Best Local Similarity 70.0%; Pred. No. 0.29;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      3 HCSAGVGRGTG 12
      ||| | | | |
Db      1 HCSXGXGRXG 10

RESULT 10
US-08-449-609-32
Sequence 32, Application US/08449609
Patent No. 5952212
GENERAL INFORMATION:
APPLICANT: Moller, Niels P.H.
```

APPLICANT: Moller, Karin B.
APPLICANT: Ullrich, Axel
TITLE OF INVENTION: PPT-531: A NOVEL PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,609
FILING DATE: 24-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/036,210
FILING DATE: 23-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7683-025
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-449-609-32

Query Match 66.2%; Score 43; DB 2; Length 10;
Best Local Similarity 70.0%; Pred. No. 0.29;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 HCSAGVGTG 12
||| ||| |
Db 1 HCSXGGRXG 10

RESULT 11
US-08-854-585-4
Sequence 4, Application US/08854585
Patent No. 6114140
GENERAL INFORMATION:
APPLICANT: Tonks, Nicholas K. and stman, Arne
TITLE OF INVENTION: Densily Enhanced Protein Tyrosine Phosphatase
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, Suite 6300
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,585
FILING DATE:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/237,940
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 27866/31954
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-854-585-4

Query Match 61.5%; Score 40; DB 3; Length 7;
Best Local Similarity 85.7%; Pred. No. 2e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HCSAGVG 9
||||| |
Db 1 HCSAGIG 7

RESULT 12
PCT-US95-05512-4
Sequence 4, Application PC/TUS9505512
GENERAL INFORMATION:
APPLICANT: Tonks, Nicholas K. and stman, Arne
TITLE OF INVENTION: Densily Enhanced Protein Tyrosine
TITLE OF INVENTION: Phosphatase
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESS: Borun
STREET: 233 South Wacker Drive, Suite 6300
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05512
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 27866/31954
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US95-05512-4

Query Match 61.5%; Score 40; DB 5; Length 7;
Best Local Similarity 85.7%; Pred. No. 2e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HCSAGVG 9

Db 1 HCSAGIG 7

|||||:1

RESULT 13

US-08-791-115B-18

; Sequence 18, Application US/08791115B

; Patent No. 6262242

; GENERAL INFORMATION:

; APPLICANT: Steck, Peter

; APPLICANT: Pershouse, Mark A.

; APPLICANT: Jasser, Samar

; APPLICANT: Yung, W.K. Alfred

; APPLICANT: Tavligian, Sean V.

; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10023.3

; NUMBER OF SEQUENCES: 27

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.

; STREET: 555 Thirteenth Street, N.W., Suite 701-E

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 22204

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/791,115B

; FILING DATE: 30-JAN-1997

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Ihnen, Jeffrey L.

; REGISTRATION NUMBER: 38,957

; REFERENCE/DOCKET NUMBER: 2318-134.A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-683-6040

; TELEFAX: 202-683-7031

; INFORMATION FOR SEQ ID NO: 18:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; FEATURE:

; NAME/KEY: Modified-site

; LOCATION: 1

; OTHER INFORMATION: /note="may be either I =

; OTHER INFORMATION: Isoleucine or V = Valine"

; FEATURE:

; NAME/KEY: Modified-site

; LOCATION: 4..8

; OTHER INFORMATION: /note="X = Any amino acid"

; FEATURE:

; NAME/KEY: Modified-site

; LOCATION: 10

; OTHER INFORMATION: /note="may be either S = Serine or

; OTHER INFORMATION: T = Threonine"

US-08-791-115B-18

Query Match 61.5%; Score 40; DB 4; Length 11;

Best Local Similarity 54.5%; Pred. No. 0.98;

Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 VHCSAGVGRFG 12

Db 1 IPCXAGXXRSG 11

RESULT 14

US-08-811-481-13

; Sequence 13, Application US/08811481

; Patent No. 6300093

; GENERAL INFORMATION:

; APPLICANT: Kindsvogel, Wayne

; APPLICANT: Jelinek, Laura J.

; APPLICANT: Sheppard, Paul O.

; APPLICANT: Hagopian, William A.

; APPLICANT: Lagasse, James M.

; TITLE OF INVENTION: ISLET CELL ANTIGEN 1851

; NUMBER OF SEQUENCES: 34

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ZymoGenetics, Inc.

; STREET: 1201 Eastlake Avenue East

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98102

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/811,481

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Lingenfelter, Susan

; REGISTRATION NUMBER: P-41,156

; REFERENCE/DOCKET NUMBER: 95-36

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 206-442-6675

; TELEFAX: 206-442-6678

; TEXES:

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FEATURE:

US-08-811-481-13

Query Match 61.5%; Score 40; DB 4; Length 11;

Best Local Similarity 63.6%; Pred. No. 0.98;

Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 VHCSAGVGRFG 12

Db 1 VHCSAGXXRSG 11

RESULT 15

US-08-990-379-18

; Sequence 18, Application US/08990379

; Patent No. 5998188

; GENERAL INFORMATION:

; APPLICANT: Stork, Philip J

; APPLICANT: Misra-Press, Anita

; TITLE OF INVENTION: Mitogen Activated Protein Kinase Phosphatase cDNAs and

; TITLE OF INVENTION: Their Biologically Active Expression Products

; FILE REFERENCE: 4104-00032205A

; CURRENT APPLICATION NUMBER: US/08/990,379

; EARLIER FILING DATE: 1997-12-15

; EARLIER APPLICATION NUMBER: PCT/US96/10402

; EARLIER FILING DATE: 1996-06-14

; EARLIER APPLICATION NUMBER: 60/000,263

; EARLIER FILING DATE: 1995-06-16

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO: 18
 ; LENGTH: 9
 ; TYPE: prt
 ; ORGANISM: Rattus norvegicus
 US-08-990-379-18

Query Match 60.0%; Score 39; DB 2; Length 9;
 Best Local Similarity 66.7%; Pred. No. 2e+05;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 VHCSAGVGR 10
 ||| ||: |
 Db 1 VHCQAGISR 9

Search completed: January 17, 2003, 11:01:27
 Job time : 15 secs

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